

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 8, 2005, 19:02:58 ; Search time 5525.28 Seconds  
(without alignments)  
2823.852 Million cell updates/sec

Title: US-10-063-670-6

Perfect score: 1657

Sequence: 1 MARCSLVLLTTSITWTRLL.....NPESKSPSKTVRCLEAEV 322

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh  
-O=/cpn2.1/USPTO.spool.h/US10063670/runat\_06102005\_112746\_227/app.query.fasta\_1.910  
-DB=GenEmbl -QFMT=fastp -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10063670 @CNC 1.1 4930 @runat\_06102005\_112746\_227 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1657	100.0	1285	9 AF127670 Homo sapi
2	1657	100.0	1755	6 AX136227 Sequence
3	1657	100.0	1755	6 BD123566 Secretary
4	1657	100.0	1755	9 AK075443 Homo sapi

5	1657	100.0	2029	6	BD2222718	Human sig
6	1657	100.0	2029	6	AR204700	Sequence
7	1657	100.0	2312	6	CQ720788	Sequence
8	1657	100.0	2372	6	BD172392	Secreted
9	1657	100.0	2372	6	BD172711	Secreted
10	1657	100.0	2372	6	BD173030	Secreted
11	1657	100.0	2372	6	BD173349	Secreted
12	1657	100.0	2372	6	BD175383	Secretory
13	1657	100.0	2372	6	AR410761	Sequence
14	1657	100.0	2372	6	AR439125	Sequence
15	1657	100.0	2372	6	AR473145	Sequence
16	1657	100.0	2372	6	AR527131	Sequence
17	1657	100.0	2372	6	AR566164	Sequence
18	1657	100.0	2372	6	AX092274	Sequence
19	1657	100.0	2372	6	AX454446	Sequence
20	1657	100.0	2372	6	AX490924	Sequence
21	1657	100.0	2372	6	AX697609	Sequence
22	1657	100.0	2372	6	BD075532	Secretory
23	1657	100.0	2372	9	AY358925	Homo sapi
24	1643	99.2	2282	9	BC026231	Homo sapi
25	1638	98.9	2313	9	AF118108	Homo sapi
26	1174	70.9	1613	4	AY372937	Bos tauru
27	1103	66.6	2027	10	BC038653	Mus muscu
28	1103	66.6	2027	10	BC038892	Mus muscu
29	1095	66.1	1516	10	MMU311501	Mus muscu
30	803	48.5	716	6	AX136529	Sequence
31	803	48.5	716	6	BD123769	Secretory
32	755	45.6	165698	9	AC009532	Homo sapi
33	726.5	43.8	603	4	AY304537	Sus scrofa
34	592	35.7	451	6	BD076146	5' EST of
35	572	34.5	1419	5	BX932088	Gallus ga
36	389	23.5	235382	2	AC130104	Rattus no
37	389	23.5	239307	2	AC129402	Rattus no
38	306	18.5	469	6	CQ093590	Sequence
39	306	18.5	469	6	CQ132364	Sequence
40	306	18.5	469	6	CQ170929	Sequence
41	306	18.5	469	6	CQ215560	Sequence
42	306	18.5	469	6	CQ254154	Sequence
43	306	18.5	469	6	CQ291166	Sequence
44	285	17.2	363	6	AX939196	Sequence
45	285	17.2	363	6	BD077623	5' EST of
46	284.5	17.2	59529	2	AC110451_3	Continuation (4 of
47	281.5	17.0	457	6	CQ093209	Sequence
48	281.5	17.0	457	6	CQ290845	Sequence
49	277	16.7	373	6	AX968782	Sequence
50	277	16.7	373	6	BD073800	Sequence
51	241	14.2	3322	5	BC074228	Xenopus l
52	234.5	14.2	1537	6	AR365492	Sequence
53	234.5	14.2	1537	9	BABECMR	Baboon lym
54	233.5	14.1	1089	10	CRUCD44	M33827 Hamster hya
55	231	13.9	2747	6	AX401912	Sequence
56	231	13.9	2747	10	RATCD44A	M61875 Rattus norv
57	229.5	13.9	1177	10	MUSCDA44A	M27129 Mouse CD44
58	229.5	13.9	1337	5	MUSPGP1	M30655 Mouse phago
59	229.5	13.9	3328	5	BC061327	BC061327 xenopus t
60	229	13.8	1932	10	BC061531	BC061531 Rattus no
61	227	13.7	1383	10	RNU52179	U52179 Rattus norv
62	227	13.7	1384	10	RNU46957	U46957 Rattus norv
63	227	13.7	1384	10	AF065147	AF065147 Rattus no
64	226	13.6	1183	10	MUSCDA44B	M27130 Mouse CD44
65	226	13.6	2799	10	BC005676	BC005676 Mus muscu
66	224.5	13.5	1418	10	MMPGPIIM	X65081 M.musculus
67	224	13.5	3164	10	RATMETAA	M61874 Rattus norv
68	224	13.5	3207	6	I19505	I19505 Sequence 1
69	223	13.5	3207	6	AK0543	AK0543 R.norvegicu
70	222	13.4	141	6	CQ106718	CQ106718 Sequence
71	222	13.4	141	6	CQ145372	CQ145372 Sequence
72	222	13.4	141	6	CQ180810	CQ180810 Sequence
73	222	13.4	141	6	CQ228565	CQ228565 Sequence
74	222	13.4	141	6	CQ266722	CQ266722 Sequence
75	222	13.4	141	6	CQ303674	CQ303674 Sequence
76	221.5	13.4	4038	10	RNU96138	U96138 Rattus norv
77	220.5	13.3	1520	10	MMPGPIIM2M	X65082 M.musculus

78	220.5	13.3	1618	5	AY029553	AY029553 Anas plat	151	144	8.7	1616	10	BC021155	BC021155 Mus muscu
79	219	13.2	1202	5	AF332869	AF332869 Anas plat	152	143	8.6	1683	10	RNU46958	U46958 Rattus norv
80	218	13.0	1278	10	MUSPGP1A	J05162 Mouse phosph	153	142.5	8.6	8444	6	AX686192	AX686192 Sequence
81	216	13.0	1927	10	MAU10881	U10881 Mesocricetu	154	141.5	8.5	3625	6	AX149461	AX149461 Sequence
82	215	13.0	1342	9	HUMCD44A	M24915 Human CD44	155	141.5	8.5	8495	6	AX686194	AX686194 Sequence
83	215	13.0	1354	6	BD015203	BD015203 TLiSa cel	156	141	8.5	208621	2	AC150078	AC150078 Gallus ga
84	213.5	12.9	1355	4	BTCD44MR	G62881 B.taurus mR	c 157	140.5	8.5	3911	10	BC031166	BC031166 Mus muscu
85	213.5	12.9	1355	4	S63418	S63418 CD44=cell1-s	158	140.5	8.5	7931	10	AF290914	AF290914 Mus muscu
86	213.5	12.9	1766	10	MMPGP1M3M	X66083 M.musculus	159	140	8.4	8069	9	AK160380	AK160380 Homo sapi
87	213	12.9	1794	6	AX587906	AX587906 Sequence	160	139.5	8.4	7104	4	CFU65989	US5989 Canis famli
88	213	12.9	1794	6	AX658338	AX658338 Sequence	161	138.5	8.4	1411	6	AX202114	AX202114 Sequence
89	213	12.9	1794	9	HUMCD44B	M59040 Human cell	162	138	8.3	7382	10	MUSAGGRECA	L07049 Mus musculus
90	212.5	12.8	2962	10	NAU10880	U10880 Mesocricetu	163	137	8.3	1406	4	RABPS4EA	M86381 Oryctolagus
91	212	12.8	1083	6	AX824985	AX824985 Sequence	164	137	8.3	3260	6	AX686401	AX686401 Sequence
92	212	12.8	4606	9	HSN803952	AL832642 Homo sapi	165	137	8.3	3260	6	AF160476	AF160476 Homo sapi
93	212	12.8	5165	6	CQ413028	CQ413028 Sequence	166	137	8.3	3591	6	CQ719622	CQ719622 Sequence
94	210	12.7	1297	6	AR3800331	AR3800331 Sequence	167	137	8.3	4492	9	AY227444	AY227444 Homo sapi
95	210	12.7	1297	9	HSU40373	UQ0373 Human cell	168	137	8.3	4575	9	AK024503	AK024503 Homo sapi
96	210	12.7	1339	9	AV101193	AV101193 Homo sapi	169	137	8.3	5604	9	AK074051	AK074051 Homo sapi
97	210	12.7	1356	9	BC067348	BC067348 Homo sapi	170	137	8.3	6939	10	RATPGCA	J03485 Rat alterna
98	210	12.7	1997	10	MMPGP1M4M	X66084 M.musculus	171	137	8.3	8214	9	AB052958	AB052958 Homo sapi
99	207.5	12.5	1107	4	AF045939	AF045939 Ceratophe	172	137	8.3	8251	9	AY311388	AY311388 Homo sapi
100	206.5	12.5	1094	5	AY032667	AY032667 Anas plat	173	137	8.3	8266	9	HSN295695	U295695 Homo sapi
101	206	12.4	3518	10	BC051388	BC051388 Mus muscu	174	136	8.2	4706	10	AY007370	AY007370 Rattus no
102	205.5	12.4	1368	5	CR386646	CR386646 Gallus ga	175	136	8.2	8157	10	AF364951	AF364951 Mus muscu
103	205.5	12.4	3091	6	CQ875295	CQ875295 Sequence	176	135.5	8.2	3076	10	BC052032	BC052032 Mus muscu
104	205.5	12.4	3091	6	HSN251595	AJ251595 Homo sapi	177	135.5	8.2	3153	10	MMBREVGEN	X87096 M.musculus
105	204.5	12.3	2613	10	MMU251594	AJ251594 Mus muscu	178	133.5	8.1	1734	6	AR220822	AR220822 Sequence
106	204.5	12.3	5303	6	CQ766842	CQ766842 Sequence	179	132.5	8.0	2160	6	AX748299	AX748299 Sequence
107	203.5	12.3	3035	5	AF153205	AF153205 Gallus ga	180	132.5	8.0	2160	6	AK093774	AK093774 Homo sapi
108	203	12.3	1483	6	AX060538	AX060538 Sequence	181	132.5	8.0	4178	9	BC036445	BC036445 Homo sapi
109	202.5	12.2	1055	4	CFCD44AG	Z27115 C.familiari	182	131.5	7.9	5144	6	CQ723852	CQ723852 Sequence
110	202.5	12.2	1468	6	AX060536	AX060536 Sequence	183	131	7.9	3245	9	BC010571	BC010571 Homo sapi
111	199.5	12.0	1482	6	CQ766874	CQ766874 Sequence	184	131	7.9	3275	9	BC009117	BC009117 Homo sapi
112	199.5	12.0	1737	9	HSCD441	X56794 H.sapiens C	185	131	7.9	3292	9	BC027971	BC027971 Homo sapi
113	199.5	12.0	1824	6	AX769855	AX769855 Sequence	186	131	7.9	3438	6	AX056675	AX056675 Sequence
114	199.5	12.0	2100	6	AX056982	AX056982 Sequence	187	131	7.9	3476	6	AX0704756	AX0704756 Sequence
115	199.5	12.0	2100	6	AX824987	AX824987 Sequence	188	131	7.9	3476	6	AX574524	AX574524 Sequence
116	199.5	12.0	2292	9	AV101192	AV101192 Homo sapi	189	131	7.9	3476	9	AX358372	AX358372 Homo sapi
117	199.5	12.0	2308	6	BD015204	BD015204 TLiSa cel	190	130.5	7.9	2534	10	RNRNABGPI	X86406 R.norvegicu
118	199.5	12.0	2316	9	HSCD44E	X55150 Human mRNA	191	130.5	7.9	2868	10	RNALPBRE	X79881 R.norvegicu
119	199.5	12.0	4675	6	AR454624	AR454624 Sequence	192	130.5	7.9	3077	10	RNU37142	X71142 Rattus norv
120	198.5	12.0	1586	9	S66400	S66400 CD44=CD44SP	193	130.5	7.9	4040	5	AF325324	AF325324 Xenopus l
121	197	11.9	2097	6	AX824989	AX824989 Sequence	194	130.5	7.9	7137	9	HUMAGPRO	M55172 Human latge
122	197	11.9	2265	9	HSEPIC	X66733 H.sapiens m	195	130.5	7.9	7909	9	D87433	D87433 Homo sapien
123	197	11.9	2387	9	BC004372	BC004372 Homo sapi	196	130.5	7.9	7916	9	AB052956	AB052956 Homo sapi
124	196	11.8	1823	9	HUMKCAA	M25078 Human Herm	197	130	7.8	7870	9	HSN275213	AU275213 Homo sapi
125	186	11.2	1338	4	ECCD44	X66862 Equus cabal	198	128.5	7.8	1540	6	CQ716123	CQ716123 Sequence
126	178.5	10.8	1697	6	CQ723838	CQ723838 Sequence	199	128.5	7.8	3259	4	BTBREV	X75887 B.taurus Br
127	170	10.3	106	6	CQ106350	CQ106350 Sequence	200	128.5	7.8	7136	6	CQ716466	CQ716466 Sequence
128	170	10.3	106	6	CQ303364	CQ303364 Sequence	201	127.5	7.7	1893	9	AY262759	AY262759 Homo sapi
129	158	9.5	157583	5	BX571951	BX571951 Zebrafish	202	127.5	7.7	1985	6	BD172402	BD172402 Secreted
130	157	9.5	133410	5	BA470202	BA470202 Zebrafish	203	127.5	7.7	1985	6	BD172721	BD172721 Secreted
131	155	9.4	1608	9	AX129808	AX129808 Homo sapi	204	127.5	7.7	1985	6	BD173040	BD173040 Secreted
132	153.5	9.3	270	6	AX033418	AX033418 Sequence	205	127.5	7.7	1985	6	BD173359	BD173359 Secreted
133	152.5	9.2	7447	4	BTU76615	U76615 Bos taurus	206	127.5	7.7	1985	6	BD175393	BD175393 Secretory
134	151	9.1	2863	6	AX747085	AX747085 Sequence	207	127.5	7.7	1985	6	CQ881212	CQ881212 Sequence
135	151	9.1	2863	9	AK091600	AK091600 Homo sapi	208	127.5	7.7	1985	6	AR410771	AR410771 Sequence
136	149.5	9.0	6597	5	GGU78555	U78555 Gallus gall	209	127.5	7.7	1985	6	AR439135	AR439135 Sequence
137	148.5	9.0	6452	5	CHKSPCP	L21913 Chicken cho	210	127.5	7.7	1985	6	AR473155	AR473155 Sequence
138	147	8.9	6477	5	CHKAGRECA	M88101 White legho	211	127.5	7.7	1985	6	AR527141	AR527141 Sequence
139	145.5	8.8	769	9	HUMZD93D04	AF066484 Homo sapi	212	127.5	7.7	1985	6	AR566174	AR566174 Sequence
140	145.5	8.8	781	6	CQ730585	CQ730585 Sequence	213	127.5	7.7	1985	6	AX375960	AX375960 Sequence
141	145.5	8.8	834	9	HSN41936	AJ41936 Homo sapi	214	127.5	7.7	1985	6	AX697621	AX697621 Sequence
142	145.5	8.8	1430	9	BC030205	BC030205 Homo sapi	215	127.5	7.7	1985	6	BD075542	BD075542 Secretory
143	145.5	8.8	1481	4	AF314813	AF314813 Sus scrof	216	127.5	7.7	1985	9	AY358500	AY358500 Homo sapi
144	145.5	8.8	12307	5	CHKPRGL	DI3542 Chicken mRN	217	127.5	7.7	2004	9	BC062320	BC062320 Homo sapi
145	145	8.8	466	6	CQ713460	CQ713460 Sequence	218	127.5	7.7	2558	9	AF229053	AF229053 Homo sapi
146	145	8.8	834	9	HSN421518	AJ421518 Homo sapi	219	127.5	7.7	2878	9	AF228710	AF228710 Homo sapi
147	145	8.8	1414	6	AR0633905	AR0633905 Sequence	220	127.5	7.7	3306	9	BC022938	BC022938 Homo sapi
148	145	8.8	1414	6	AR144434	AR144434 Sequence	221	127.5	7.7	79444	2	AC150153	AC150153 Gallus ga
149	145	8.8	1414	6	AR281307	AR281307 Sequence	222	127.5	7.7	143178	2	AC150117	AC150117 Gallus ga
150	144	8.7	1605	10	MMU83903	U83903 Mus musculu	c 223	127.5	7.7	166863	2	AC150140	AC150140 Gallus ga



224	127.5	7.7	168751	2	AC068969	AC068969 Homo sapi	297	113.5	6.8	4634	5	AF116856	AF116856 Gallus ga
225	127.5	7.7	170883	9	AC067805	AC067805 Homo sapi	c 298	113.5	6.8	64675	2	BX322628_3	Continuation (4 of
c 226	127.5	7.7	197370	9	AC103982	AC103982 Homo sapi	c 299	113.5	6.8	110000	2	BX322628_2	Continuation (3 of
227	127	7.7	2465	6	AX400824	AX400824 Sequence	300	113.5	6.8	170883	5	AC067805	Continuation (3 of
228	127	7.7	2465	10	AF072892	AF072892 Rattus no	301	113.5	6.8	218103	9	AX465199	AX465199 Zebrafish
229	126.5	7.6	199942	2	AC150038	AC150038 Gallus ga	302	113.5	6.8	271812	2	BX530095	BX530095 Danio rer
230	136	7.6	10427	10	MUSPGM	D28599 Mouse mRNA	303	113	6.8	1925	9	BC050524	BC050524 Homo sapi
231	125.5	7.6	2780	10	AF098460	AF098460 Mus muscu	304	113	6.8	2087	6	AX338947	AX338947 Sequence
232	125.5	7.6	4738	10	BC066853	BC066853 Mus muscu	305	113	6.8	2087	9	XELPHR3A	D32039 Human pgh3
233	125	7.5	201	11	BV206501	BV206501 sqmm22108	306	113	6.8	2809	5	HMLDLR2A	M62978 X.laevig lo
234	125	7.5	1414	6	AX336169	AX336169 Sequence	307	113	6.8	8224	6	CO728127	CO728127 Sequence
235	125	7.5	1414	9	HUMTSG6A	M31165 Human tumor	308	113	6.8	8224	6	AR362654	AR362654 Sequence
236	124.5	7.5	2430	10	AF139572	AF139572 Mus muscu	309	113	6.8	8224	6	AX58277	AX58277 Sequence
237	124	7.5	1682	5	CR762351	CR762351 Xenopus t	310	113	6.8	8224	9	HSVERS	X15998 H.sapiens m
238	124	7.5	249541	2	AC095672	AC095672 Rattus t	311	113	6.8	138091	2	AC113583	AC113583 Tetraodon
239	124	7.5	249774	2	AC126196	AC126196 Rattus no	c 312	113	6.8	199942	6	CO704239	CO704239 Gallus ga
240	123	7.4	2116	4	AF060459	AF060459 Bos tauru	313	112	6.8	340	6	CO704239	Continuation (3 of
241	123	7.4	5077	4	AF060458	AF060458 Bos tauru	314	112	6.8	1173	14	AX628532	AX628532 Human her
242	123	7.4	7330	4	AF060457	AF060457 Bos tauru	315	112	6.8	1173	14	AJ626542	AJ626542 Human her
243	123	7.4	10291	4	AF060456	AF060456 Bos tauru	316	112	6.8	1173	14	AJ626547	AJ626547 Human her
244	122	7.4	1183	4	RABAGGRECA	L38480 Oryctolagus	317	112	6.8	1190	6	I67656	I67656 Sequence 1
c 245	122	7.4	150209	2	CR759744	CR759744 Danio rer	318	112	6.8	2026	5	BC068325	BC068325 Danio rer
246	121.5	7.3	959	6	CR723845	CR723845 Sequence	319	112	6.8	3070	8	AK110196	AK110196 Oryza sat
247	121	7.3	1587	6	AR432563	AR432563 Sequence	320	112	6.8	12979	14	HEHVS1SU	X02138 Hesper simp
248	121	7.3	1587	6	BD078622	BD078622 Human pro	c 321	112	6.8	26245	14	HSIUS	L00036 Human herpe
249	121	7.3	1704	9	AY007241	AY007241 Homo sapi	c 322	112	6.8	79444	2	AC150153	AC150153 Gallus ga
c 250	121	7.3	155548	2	CR848047	CR848047 Danio rer	c 323	112	6.8	143178	2	AC150117	AC150117 Gallus ga
251	120.5	7.2	5614	5	AB119257	AB119257 Homo sapi	324	112	6.8	152261	14	HE1CG	X14112 Human herpe
252	120	7.2	1626	9	BC029864	BC029864 Homo sapi	325	112	6.8	166863	2	AC150140	AC150140 Gallus ga
253	120	7.2	1630	9	BC029864	BC029864 Homo sapi	326	112	6.8	176022	2	BX294110	BX294110 Danio rer
254	120	7.2	2354	5	BC046259	BC046259 Xenopus l	327	112	6.8	208621	2	AC150078	AC150078 Gallus ga
255	120	7.2	4069	5	BC078043	BC078043 Xenopus l	c 328	112	6.8	232749	2	CR354535	CR354535 Danio rer
c 256	120	7.2	300750	1	AP005217	AP005217 Corynebact	c 329	111.5	6.7	15515	1	AE000044	AE000044 Mycoplasma
257	119.5	7.2	1236	14	AJ626545	AJ626545 Human her	330	111	6.7	1478	4	ECRTLTIG	X78077 Equus cabal
c 258	119.5	7.2	221762	2	BX908731	BX908731 Danio rer	331	111	6.7	1720	6	BD195591	BD195591 70 human
259	119	7.2	480	10	MMLINK4	AF137277 Mus muscu	332	111	6.7	1720	6	CO775636	CO775636 Sequence
260	119	7.2	1736	10	AB049055	AB049055 Mus muscu	333	111	6.7	1720	6	AR352846	AR352846 Sequence
261	119	7.2	197370	9	AC103982	AC103982 Homo sapi	c 334	111	6.7	184365	2	AC079639	AC079639 Mus muscu
262	118.5	7.2	1794	9	AB049054	AB049054 Homo sapi	c 335	110.5	6.7	193188	10	AL844155	AL844155 Mouse DNA
263	118.5	7.2	5923	9	HSU26655	U26655 Human versi	c 336	110.5	6.7	229628	8	AP005091	AP005091 Oryza sat
264	118.5	7.2	11185	6	CO776629	CO776629 Sequence	c 337	110.5	6.7	300299	1	AE017288	AE017288 Leptospir
265	118.5	7.2	11185	6	AX330530	AX330530 Sequence	338	110	6.6	1308	6	BD231671	BD231671 31 human
266	118.5	7.2	11185	6	AX410665	AX410665 Sequence	339	110	6.6	110000	2	BX322628_0	BX322628 Danio rer
267	118.5	7.2	11185	9	HSU16306	U16306 Human chond	c 340	110	6.6	110000	2	BX322628_1	Continuation (2 of
268	118.5	7.2	12319	6	AX281831	AX281831 Sequence	341	110	6.6	140093	8	AP005091	AP005091 Oryza sat
269	118.5	7.2	164846	2	AC107727	AC107727 Mus muscu	342	110	6.6	147748	8	AP005091	AP005091 Oryza sat
270	118	7.1	2318	10	MUSPGM3B	D32040 Mouse pgm3	c 343	110	6.6	183682	9	AL133330	AL133330 Human DNA
271	118	7.1	7375	6	CO777492	CO777492 Sequence	c 344	110	6.6	271812	2	BX530095	BX530095 Danio rer
272	118	7.1	7375	10	MUSPGMV	D16263 Mus musculu	c 345	110	6.6	292007	2	AC128762	AC128762 Rattus no
273	117.5	7.1	1194	14	AJ626546	AJ626546 Human her	346	109.5	6.6	1335	4	SSLINK	Y00165 Sus scrofa
274	117.5	7.1	61052	2	AC123513	AC123513 Dictyoste	347	109.5	6.6	103201	2	AC149525	AC149525 Xenopus t
c 275	117.5	7.1	136240	3	AC117070	AC117070 Dictyoste	348	109	6.6	2447	10	AF060879	AF060879 Rattus no
c 276	117.5	7.1	207418	2	AC109112	AC109112 Rattus no	349	109	6.6	6310	9	AF026547	AF026547 Homo sapi
277	117.5	7.1	246369	2	AC125707	AC125707 Rattus no	350	109	6.6	6312	6	CO727544	CO727544 Sequence
278	117	7.1	209852	2	AC151363	AC151363 Gasterost	351	109	6.6	110000	2	AC096220_0	AC096220 Rattus no
c 279	117	7.1	214941	2	AC150409	AC150409 Branchios	c 352	109	6.6	232127	2	AC113724	AC113724 Rattus no
c 280	116.5	7.0	226416	2	AC103519	AC103519 Rattus no	353	109	6.6	235684	2	AC129422	AC129422 Rattus no
c 281	116.5	7.0	230817	2	AC106909	AC106909 Rattus no	354	109	6.6	272258	2	AC123370	AC123370 Rattus no
282	116	7.0	1785	9	BC052287	BC052287 Homo sapi	355	108.5	6.5	1194	14	AJ626543	AJ626543 Human her
283	116	7.0	1910	5	CHLNKFA	M13212 Chicken car	c 356	108.5	6.5	1378	1	AY127887	AY127887 Anaplasma
284	116	7.0	136886	2	AC149262	AC149262 Spheroelid	c 357	108.5	6.5	1399	1	AY127894	AY127894 Anaplasma
285	115	6.9	1249	10	BC022136	BC022136 Mus muscu	c 358	108.5	6.5	4128	1	AF527423	AF527423 Anaplasma
286	114.5	6.9	5191	6	I56080	I56080 Sequence 1	c 359	108.5	6.5	4185	1	AMU60779	AMU60779 Anaplasma m
287	114.5	6.9	5191	10	RATNCAN	M97161 Rattus norv	360	108.5	6.5	37711	3	CEZK896	Z82288 Caenorhabdi
288	114	6.9	1406	10	AB049056	AB049056 Rattus no	c 361	108.5	6.5	110000	8	CR382129_31	Continuation (32 o
289	114	6.9	8924	6	CO580640	CO580640 Sequence	362	108.5	6.5	189608	5	AL929208	AL929208 Zebrafish
c 290	114	6.9	55864	2	AC018100	AC018100 Drosophil	363	108	6.5	317	10	RATLNKPA	AY22339 Rat link pr
c 291	114	6.9	110000	3	AC116305_1	Continuation (2 of	364	108	6.5	685	4	AY226857806	AY226857 Bos tauru
292	114	6.9	157225	3	AC010042	AC010042 Drosophil	365	108	6.5	1319	10	AY269788	AY269788 Mus muscu
c 293	114	6.9	178338	3	AC023675	AC023675 Drosophil	c 366	108	6.5	1320	4	AF529268	AF529268 Ovis arie
c 294	114	6.9	192662	10	AC134397	AC134397 Mus muscu	367	108	6.5	1433	10	AY262757	AY262757 Mus muscu
c 295	114	6.9	272888	2	AC139198	AC139198 Mus muscu	368	108	6.5	1492	9	HSCRTL115	X78076 H.sapiens C
c 296	114	6.9	284442	3	AE003558	AE003558 Drosophil	369	108	6.5	1492	9	HSLINKC	X17405 Human mRNA

370	108	6.5	1493	6	C0728128	C0728128 Sequence	443	104	6.3	6926	3	AF239611	AF239611 Drosophil
371	108	6.5	1721	9	BS057808	BC057808 Homo sapi	c 445	104	6.3	53580	5	AC096866	AC096866 Takifugu
372	108	6.5	1759	9	HU43328	U43328 Human link	c 446	104	6.3	161126	8	NC80A10	BX294012 Neurospor
c 373	108	6.5	1790	6	AX344529	AX344529 Sequence	c 446	104	6.3	198756	2	AC135657	AC135657 Rattus no
c 374	108	6.5	1790	6	AX347277	AX347277 Sequence	c 447	104	6.3	346301	1	BX640432	BX640432 Bordetell
375	108	6.5	68574	2	AC113212	AC113212 Homo sapi	448	103.5	6.2	1042	10	MMU37531	U37531 Mus muscullu
c 376	108	6.5	164286	9	AC020899	AC020899 Homo sapi	c 450	103.5	6.2	1099	3	AF436624	AF436624 Macromonta
377	108	6.5	167872	2	AC007554	AC007554 Homo sapi	c 450	103.5	6.2	1310	3	AK173560	AK173560 Ciona inta
378	108	6.5	226416	2	AC103519	AC103519 Rattus no	c 451	103.5	6.2	8433	6	C0610163	C0610163 Sequence
379	108	6.5	247266	2	AC110520	AC110520 Mus muscu	c 452	103.5	6.2	30630	3	AC116032	AC116032 Dictyoste
380	107.5	6.5	6279	6	CQ580641	CQ580641 Sequence	453	103.5	6.2	54309	2	AC017353	AC017353 Drosophil
c 381	107.5	6.5	12371	1	AE011324	AE011324 Leptospir	454	103.5	6.2	157482	3	AC092227	AC092227 Drosophil
382	107.5	6.5	77928	2	AC149263	AC149263 Spherooid	455	103.5	6.2	175058	2	CR753843	CR753843 Danio rer
383	107	6.5	427	5	CHKLKPA3	M35037 Chicken car	c 456	103.5	6.2	177426	2	CR339044	CR339044 Danio rer
384	107	6.5	1400	6	AR0316272	AR0316272 Sequence	c 457	103.5	6.2	186803	3	AC092225	AC092225 Drosophil
385	107	6.5	1400	6	AR087156	AR087156 Sequence	c 458	103.5	6.2	225861	2	CH628381	CH628381 Danio rer
386	107	6.5	1520	6	I44674	I44674 Sequence 1	c 459	103.5	6.2	276521	3	AE003642	AE003642 Drosophil
387	107	6.5	1520	10	RNBEHAB	Z28366 R.norvegicu	c 460	103.5	6.2	305502	3	DROSADH03	AE003409 Drosophil
388	107	6.5	1851	6	AX302626	AX302626 Sequence	c 461	103.5	6.2	348551	8	BX649606	BX649606 Aspergill
389	107	6.5	2011	6	AX149447	AX149447 Sequence	462	103	6.2	402	6	AX778505	AX778505 Sequence
390	107	6.5	2589	6	I32212	I32212 Sequence 3	463	103	6.2	1296	6	AR549679	AR549679 Sequence
391	107	6.5	2585	6	A39780	A39780 Sequence 14	464	103	6.2	1519	4	FDBEHAB	Z28367 F.domesticu
392	107	6.5	2885	6	A74265	A74265 Sequence 21	465	103	6.2	1519	6	I44675	I44675 Sequence 2
393	107	6.5	4544	8	AK119845	AK119845 Oryza sat	c 466	103	6.2	1962	6	BD195649	BD195649 70 human
394	107	6.5	4614	6	BD271910	BD271910 Process f	c 467	103	6.2	1962	6	CQ775694	CQ775694 Sequence
395	107	6.5	4614	6	I32211	I32211 Sequence 1	c 468	103	6.2	1962	6	AR352704	AR352704 Sequence
396	107	6.5	5259	10	MNNEUROCM	X84727 M.musculus	c 469	103	6.2	2019	10	BC063758	BC063758 Mus muscu
397	107	6.5	5388	6	CQ608451	CQ608451 Sequence	470	103	6.2	2168	3	BT001711	BT001711 Drosophil
398	107	6.5	5743	8	SCFL01	X78160 S.cerevisia	c 471	103	6.2	10126	1	AE012547	AE012547 Xanthomon
399	107	6.5	7147	10	BC065118	BC065118 Mus muscu	472	103	6.2	224000	1	AE012859	AE012859 Rattus no
c 400	107	6.5	7782	6	CQ608450	CQ608450 Sequence	c 473	103	6.2	232110	2	AC096893	AC096893 Rattus no
c 401	107	6.5	8340	11	BV178350	BV178350 sqm10003	c 474	103	6.2	267287	2	AC096702	AC096702 Rattus no
c 402	107	6.5	8426	2	AC013966	AC013966 Drosophil	475	102.5	6.2	1341	6	AX657611	AX657611 Sequence
c 403	107	6.5	2492	3	DMC5667	AL031028 Drosophil	476	102.5	6.2	1372	6	CQ596994	CQ596994 Sequence
c 404	107	6.5	54812	8	YSCCHR1RAA	L28920 Saccharomyc	477	102.5	6.2	1491	14	AF343059	AF343059 Eyach vir
c 405	107	6.5	74610	8	AP006175	AP006175 Oryza sat	478	102.5	6.2	2178	14	AF282472	AF282472 Eyach vir
c 406	107	6.5	112830	2	AC151678	AC151678 Gallus ga	479	102.5	6.2	3421	3	AY060306	AY060306 Drosophil
c 407	107	6.5	164512	9	AL365181	AL365181 Human DNA	c 480	102.5	6.2	4492	6	CQ596993	CQ596993 Sequence
c 408	107	6.5	177096	3	AC107326	AC107326 Drosophil	c 481	102.5	6.2	7868	14	HPU37537	U37537 Human papil
c 409	107	6.5	202968	2	AC137422	AE003421 Drosophil	c 482	102.5	6.2	110000	1	AE016822	Continuation (20 o
c 410	107	6.5	34820	3	AE003421	AE003421 Drosophil	c 483	102.5	6.2	174801	2	AC014376	AC014376 Drosophil
c 411	106.5	6.4	1402	6	AR269667	AR269667 Sequence	c 484	102.5	6.2	179838	3	AC091220	AC091220 Drosophil
c 412	106.5	6.4	2571	8	SCYOR383C	Z75291 S.cerevisia	c 485	102.5	6.2	181063	3	AC010107	AC010107 Drosophil
c 413	106.5	6.4	2455	3	TNAF000605	AF000605 Trichopl	c 486	102.5	6.2	285860	3	AE003551	AE003551 Drosophil
c 414	106.5	6.4	2455	6	AR129835	AR129835 Sequence	487	102	6.2	1215	14	AJ626536	AJ626536 Human her
c 415	106.5	6.4	2455	6	AR565046	AR565046 Sequence	488	102	6.2	1215	14	AJ626549	AJ626549 Human her
c 416	106.5	6.4	2821	3	TNAF000606	AF000606 Trichopl	489	102	6.2	1458	3	AF167710	AF167710 Toxocara
c 417	106.5	6.4	2821	6	AR129836	AR129836 Sequence	490	102	6.2	8246	1	AE014770	AE014770 Bifidobac
c 418	106.5	6.4	2821	6	AR565047	AR565047 Sequence	491	102	6.2	26339	3	CBRG17K04	AC084514 Caenorhab
c 419	106.5	6.4	163528	10	AC121951	AC121951 Mus muscu	c 492	102	6.2	110000	1	AF006618	Continuation (50 o
c 420	106	6.4	203159	10	AC137525	AC137525 Mus muscu	c 493	101.5	6.2	110000	2	LMFLCHR36	Continuation (22 o
c 421	106	6.4	346406	10	BX883045	BX883045 Rattus no	c 494	102	6.2	110000	8	AE016819	Continuation (11 o
c 422	105.5	6.4	614	9	AB049062S7	AB049061 Homo sapi	c 495	102	6.2	170450	2	AC105379	AC105379 Trypanoso
c 423	105.5	6.4	1720	10	AB094071	AB094071 Rattus no	c 496	102	6.2	216015	2	AC113751	AC113751 Rattus no
c 424	105.5	6.4	1747	10	AF093673	AF093673 Cricetulu	c 497	102	6.2	272147	2	AC095648	AC095648 Rattus no
c 425	105.5	6.4	144588	2	AC121239	AC121239 Homo sapi	498	102	6.2	349980	6	AX492786	AX492786 Sequence
c 426	105.5	6.4	257513	2	AC127093	AC127093 Rattus no	499	102	6.2	349980	6	AX553953	AX553953 Sequence
c 427	105	6.3	723	4	AY226865TS10	AY226866 Bos tauru	500	101.5	6.1	1144	8	TTU537508	TTU537508 Tricium
c 428	105	6.3	1941	4	BTU02292	U02292 Bos taurus	c 501	101.5	6.1	1378	1	AY127885	AY127885 Anaplasma
c 429	105	6.3	36004	14	AY530877	AY530877 Simian ad	502	101.5	6.1	2407	8	LTES32549	AY52549 Lolium te
c 430	105	6.3	36800	9	AC003110	AC003110 Human DNA	503	101.5	6.1	2586	10	MUSEGFRPDD	B0274942 POLYNUCLE
c 431	105	6.3	43185	9	AC138430	AC138430 Homo sapi	504	101.5	6.1	2607	6	BD274942	BD274942 Sequence
c 432	105	6.3	110000	8	CR382129_05	Continuation (6 Of	505	101.5	6.1	2607	6	AR474071	AR474071 Sequence
c 433	105	6.3	194459	8	AP003335	AP003335 Oryza sat	506	101.5	6.1	3319	8	AK119879	AK119879 Oryza sat
c 434	105	6.3	247266	2	AC110520	AC110520 Mus muscu	507	101.5	6.1	5005	9	AB011099	AB011099 Homo sapi
c 435	105	6.3	248017	2	AC096230	AC096230 Rattus no	c 508	101.5	6.1	6112	6	AX347419	AX347419 Sequence
c 436	104.5	6.3	35424	3	LMFL2185	AL358712 Leighmani	c 509	101.5	6.1	6112	6	AX349140	AX349140 Sequence
c 437	104.5	6.3	106586	2	AC127426	AC127426 Magnaport	c 510	101.5	6.1	6112	6	AX657789	AX657789 Sequence
c 438	104	6.3	231	10	S737719S2	S73720 aggreca=ag	c 511	101.5	6.1	39737	2	AY714855	AY714855 Unculture
c 439	104	6.3	231	10	S737721S2	S73722 aggreca=ag	c 512	101.5	6.1	39737	2	AY714855	AY714855 Unculture
c 440	104	6.3	484	9	AF098641	AF098641 Homo sapi	513	101.5	6.1	53178	6	CQ363755	CQ363755 Sequence
c 441	104	6.3	3014	9	BC008735	BC008735 Homo sapi	c 514	101.5	6.1	117099	8	AF003572	AF003572 Oryza sat
c 442	104	6.3	5916	3	AY051490	AY051490 Drosophil	c 515	101.5	6.1	146874	8	AP004868	AP004868 Oryza sat

516	101.5	6.1	147640	2	AP003542	AP003542	Oryza sat	589	100	6.0	110000	8	CR382132_06	Continuation (7 of
c 517	101.5	6.1	176022	1	SC294110	AX294110	Danio rer	c 590	100	6.0	135850	2	AC135931	AC135931 Rattus no
c 518	101.5	6.1	290850	2	SC0939127	AX939127	Streptomy	c 591	100	6.0	180995	2	AC117500	AC117500 Homo sapi
519	101	6.1	2421	8	CQ722898	CQ722898	Sequence	c 592	100	6.0	184091	2	AX294393	AX294393 Mus muscu
520	101	6.1	2493	8	AB055432	AB055432	Aspergill	c 593	100	6.0	195246	10	AC122266	AC122266 Mus muscu
521	101	6.1	3118	6	BD156554	BD156554	Primer fo	c 594	100	6.0	218311	2	CR749741	CR749741 Danio rer
522	101	6.1	3118	6	AX877234	AX877234	Sequence	c 595	100	6.0	230817	2	AC106909	AC106909 Rattus no
523	101	6.1	3118	9	AK027692	AK027692	Homo sapi	c 596	100	6.0	239696	2	AC097086	AC097086 Rattus no
524	101	6.1	3175	6	AX747807	AX747807	Sequence	597	100	6.0	254278	2	AC023836	AC023836 Mus muscu
525	101	6.1	3175	9	AK092919	AK092919	Homo sapi	598	100	6.0	308750	1	AP005216	AP005216 Corynebac
526	101	6.1	3499	6	BD156602	BD156602	Primer fo	c 599	100	6.0	349028	1	AX640413	AX640413 Bordetell
527	101	6.1	3499	6	AX876196	AX876196	Sequence	600	99.5	6.0	1008	5	AB167511	AB167511 Danio rer
528	101	6.1	3499	9	AK027440	AK027440	Homo sapi	601	99.5	6.0	1434	6	AR552751	AR552751 Sequence
529	101	6.1	4098	9	HS459424	AX59424	Homo sapi	602	99.5	6.0	3814	5	XEUNCAWA	XEUNCAWA Xenopus lae
530	101	6.1	5131	6	CQ850217	CQ850217	Sequence	603	99.5	6.0	13684	1	AE014787	AE014787 Bifidobac
531	101	6.1	5131	9	AK127328	AK127328	Homo sapi	604	99.5	6.0	16114	3	AB062881	AB062881 Mytilus g
c 532	101	6.1	24413	3	AC117272	AC117272	Leishmani	c 605	99.5	6.0	162296	9	AL616174	AL616174 Human DNA
c 533	101	6.1	72675	9	AX322573	AX322573	Human DNA	c 606	99.5	6.0	197404	10	AL672124	AL672124 Mouse DNA
534	101	6.1	79748	2	AC044890	AC044890	Homo sapi	607	99.5	6.0	202314	2	AC132694	AC132694 Rattus no
535	101	6.1	96560	9	AC090582	AC090582	Homo sapi	608	99.5	6.0	220851	5	AX649335	AX649335 Zebrafish
536	101	6.1	110000	8	AE016819_02	Continuation (3 of	609	99.5	6.0	225000	2	AC129674	AC129674 Rattus no	
537	101	6.1	112830	2	AC151678	AC151678	Gallus ga	610	99.5	6.0	263891	2	AC096166	AC096166 Rattus no
c 538	101	6.1	125623	3	AC115599	AC115599	Dictyoste	611	99.5	6.0	268651	2	AX005198	AX005198 Danio rer
c 539	101	6.1	147024	2	AC093739	AC093739	Homo sapi	612	99.5	6.0	322497	2	AC112109	AC112109 Rattus no
540	101	6.1	154612	2	AC093739	AC093739	Homo sapi	613	99.5	6.0	349980	6	AX492787	AX492787 Sequence
541	101	6.1	160625	9	AC093111	AC093111	Homo sapi	614	99.5	6.0	349980	6	AX553954	AX553954 Sequence
542	101	6.1	168624	9	AC092131	AC092131	Homo sapi	615	99	6.0	438	6	CQ662211	CQ662211 Sequence
543	101	6.1	173189	9	AC092323	AC092323	Homo sapi	616	99	6.0	1374	6	AD01700	AD01700 Sequence 4
c 544	101	6.1	178400	5	AX294376	AX294376	Zebrafish	617	99	6.0	1374	6	BD023443	BD023443 Junction
545	101	6.1	183556	2	AC019059	AC019059	Homo sapi	618	99	6.0	2029	10	MMU89915	MMU89915 Mus musculu
546	101	6.1	192177	5	AX005242	AX005242	Zebrafish	619	99	6.0	2899	10	BC020004	BC020004 Mus muscu
c 547	101	6.1	197461	2	AC134814	AC134814	Rattus no	620	99	6.0	4287	6	CQ610164	CQ610164 Sequence
548	100.5	6.1	1161	10	MMOTA	X682788	M.musculus	621	99	6.0	4488	10	AF378831	AF378831 Mus muscu
549	100.5	6.1	1209	9	AB107883	AB107883	Homo sapi	622	99	6.0	8546	1	AY512465	AY512465 Listeria
550	100.5	6.1	1236	14	AX626540	AX626540	Human her	623	99	6.0	16381	10	MMU97068	MMU97068 Mus musculu
551	100.5	6.1	1475	6	AX392229	AX392229	Sequence	624	99	6.0	110000	6	BD430793_01	BD430793_01 Continuation (2 of
552	100.5	6.1	1712	8	AK120901	AK120901	Oryza sat	625	99	6.0	110000	8	CR382128_25	CR382128_25 Continuation (26 o
553	100.5	6.1	1714	8	AK119612	AK119612	Oryza sat	626	99	6.0	110000	8	CR382129_11	CR382129_11 Continuation (12 o
554	100.5	6.1	1780	8	AK103182	AK103182	Oryza sat	627	99	6.0	143089	5	CR388386	CR388386 Zebrafish
555	100.5	6.1	1881	8	AK061650	AK061650	Oryza sat	c 628	99	6.0	153749	5	AX649585	AX649585 Zebrafish
556	100.5	6.1	1904	8	AK101618	AK101618	Oryza sat	c 629	99	6.0	166165	8	AP004753	AP004753 Oryza sat
557	100.5	6.1	1944	3	AY061148	AY061148	Drosophil	c 630	99	6.0	175124	2	AC135035	AC135035 Rattus no
558	100.5	6.1	3383	9	AY262756	AY262756	Homo sapi	c 631	99	6.0	176113	2	AC132574	AC132574 Mus muscu
559	100.5	6.1	3677	8	AF414112	AF414112	Candida a	632	99	6.0	184357	2	AC073728	AC073728 Mus muscu
560	100.5	6.1	4140	6	CQ605953	CQ605953	Sequence	633	99	6.0	207161	2	AC120651	AC120651 Rattus no
561	100.5	6.1	5409	6	BD183451	BD183451	Novel gen	634	99	6.0	224197	2	AC144404	AC144404 Medicago
562	100.5	6.1	5409	9	AB067513	AB067513	Homo sapi	635	99	6.0	240525	2	AC096895	AC096895 Rattus no
563	100.5	6.1	7596	6	AX695382	AX695382	Sequence	c 636	99	6.0	242063	2	AC126964	AC126964 Rattus no
564	100.5	6.1	8064	6	AX695381	AX695381	Sequence	c 637	99	6.0	307150	1	CNSPAX01	AX248283 Pyrococcu
565	100.5	6.1	9193	10	MMNORTA	Z11886	M.musculus	638	99	6.0	349980	6	AX041106	AX041106 Sequence
c 566	100.5	6.1	9193	10	AF508809	AF508809	Mus muscu	639	98.5	5.9	1194	14	AX626548	AX626548 Human her
c 567	100.5	6.1	15900	2	AC017311	AC017311	Drosophil	640	98.5	5.9	1194	14	AX626552	AX626552 Human her
568	100.5	6.1	16256	1	AF289050	AF289050	Bacteroid	641	98.5	5.9	1278	14	AX626556	AX626556 Human her
c 569	100.5	6.1	22029	9	AC003967	AC003967	Homo sapi	c 642	98.5	5.9	1719	8	AK176661	AK176661 Arabidops
570	100.5	6.1	43185	9	AC138430	AC138430	Homo sapi	643	98.5	5.9	1898	3	AB092978	AB092978 Haliotis
571	100.5	6.1	94779	2	AC151672	AC151672	Gallus ga	644	98.5	5.9	2039	10	BC082777	BC082777 Mus muscu
c 572	100.5	6.1	110000	2	LMFLCHR31_02	Continuation (3 of	645	98.5	5.9	2790	3	DD1301670	DD1301670 Dictyoste	
573	100.5	6.1	137033	8	AC107224	AC107224	Oryza sat	646	98.5	5.9	3381	6	CQ608193	CQ608193 Sequence
574	100.5	6.1	154865	8	OSJN00071	AL606640	Oryza sat	647	98.5	5.9	5152	5	AY144591	AY144591 Cyprinur
575	100.5	6.1	232749	2	CR354535	CR354535	Danio rer	c 648	98.5	5.9	5283	1	AF373807	AF373807 Sinorhizo
576	100.5	6.1	236907	2	AC103254	AC103254	Rattus no	649	98.5	5.9	5381	6	CQ608192	CQ608192 Sequence
c 577	100.5	6.1	300330	1	AP005222	AP005222	Corynebac	650	98.5	5.9	6141	1	MELOSX11	MELOSX11 Sequence
c 578	100.5	6.1	300950	1	AP005940	AP005940	Bradyrhiz	651	98.5	5.9	79116	8	AP006373	AP006373 Lotus cor
c 579	100.5	6.1	316050	1	BC321859	BC321859	Nitrosomo	c 652	98.5	5.9	82972	8	NCB24417	NCB24417 Neurospor
580	100	6.0	983	5	AX061275	AX061275	Xenopus t	c 653	98.5	5.9	99967	8	NCB23B10	NCB23B10 Continuation (2 of
581	100	6.0	1214	14	AX626551	AX626551	Human her	c 654	98.5	5.9	110000	8	CR382125_01	CR382125_01 of
582	100	6.0	1215	14	AJ626527	AJ626527	Human her	655	98.5	5.9	117273	2	AC015138	AC015138 Drosophil
583	100	6.0	1215	14	AJ626539	AJ626539	Human her	656	98.5	5.9	124191	9	AC005153	AC005153 Homo sapi
584	100	6.0	1215	14	AJ626553	AJ626553	Human her	657	98.5	5.9	146137	2	AC148795	AC148795 Otollemur
585	100	6.0	33706	3	CEC2564	Z70680	Caenorhabd	658	98.5	5.9	150050	1	MLQ672112	MLQ672112 Mesorhizo
c 586	100	6.0	93889	2	AC105432	AC105432	Magnapor	659	98.5	5.9	170324	3	AC007805	AC007805 Drosophil
c 587	100	6.0	100984	10	AL929138	AL929138	Mouse DNA	c 660	98.5	5.9	174527	9	AP001183	AP001183 Homo sapi
c 588	100	6.0	107352	9	HS474414	AL023285	Human DNA	661	98.5	5.9	182736	2	AC021672	AC021672 Homo sapi

c 662	98.5	5.9 190314	9	AC019227	AC019227 Homo sapi	c 735	97.5	5.9 170475	10	AL844546	AL844546 Mouse DNA
663	98.5	5.9 191041	9	AC091742	AC091742 Homo sapi	c 736	97.5	5.9 175152	2	AC074195	AC074195 Homo sapi
664	98.5	5.9 202555	5	AC148141	AC148141 Bos tauru	c 737	97.5	5.9 185553	2	AC151534	AC151534 Mus muscu
c 665	98.5	5.9 204018	2	AC116890	AC116890 Mus muscu	738	97.5	5.9 225989	2	AC135294	AC135294 Rattus no
666	98.5	5.9 227847	3	AE003692	AE003692 Drosophil	739	97.5	5.9 227555	10	AC108416	AC108416 Mus muscu
667	98.5	5.9 243185	2	AC094948	AC094948 Rattus no	c 740	97.5	5.9 243299	2	AC133800	AC133800 Rattus no
668	98.5	5.9 243899	5	BX510919	BX510919 Zebrafish	c 741	97.5	5.9 304500	1	AP005953	AP005953 Bradyrhiz
669	98.5	5.9 267156	6	AX336388	AX336388 Sequence	c 742	97.5	5.9 349980	6	AX044030	AX044030 Sequence
670	98.5	5.9 267156	6	AX336388	AX336388 Sequence	c 742	97.5	5.9 349980	6	AX044030	AX044030 Sequence
c 671	98.5	5.9 293350	1	SME591786	U66059 Human germ	c 743	97.5	5.9 349980	6	AX044031	AX044031 Sequence
672	98	5.9 1173	14	AJ626537	AL951786 Sinorhizo	744	97	5.9 304	6	CQ673468	CQ673468 Sequence
673	98	5.9 1173	14	AJ626555	AJ626537 Human her	745	97	5.9 789	6	CQ749879	CQ749879 Sequence
674	98	5.9 1815	1	AF497174	AJ626555 Human her	746	97	5.9 1035	10	BC042902	BC042902 Mus muscu
c 675	98	5.9 1815	1	AF497174	AF497174 Listeria	747	97	5.9 1215	14	AJ626533	AJ626533 Human her
676	98	5.9 2346	3	TCCP69GNA	AF497181 Listeria	748	97	5.9 1231	6	AR508054	AR508054 Sequence
c 677	98	5.9 2717	8	YLTSR1	Z2557 T.congolens	c 749	97	5.9 2293	6	AX102226	AX102226 Oryza sat
678	98	5.9 6353	6	CQ580242	Z69781 Y.lipolytic	750	97	5.9 2751	6	AX713940	AX713940 Sequence
679	98	5.9 8429	6	CQ580241	CQ580242 Sequence	751	97	5.9 2751	9	AK055882	AK055882 Homo sapi
680	98	5.9 8546	1	AY512394	CQ580241 Sequence	752	97	5.9 2901	3	BT014661	BT014661 Drosophil
681	98	5.9 8546	1	AY512394	AY512394 Listeria	c 753	97	5.9 2908	10	BC021506	BC021506 Mus muscu
682	98	5.9 8546	1	AY512406	AY512406 Listeria	c 754	97	5.9 3058	10	BC027844	BC027844 Mus muscu
683	98	5.9 8546	1	AY512408	AY512408 Listeria	c 755	97	5.9 3374	10	BC078642	BC078642 Mus muscu
684	98	5.9 8546	1	AY512414	AY512414 Listeria	c 756	97	5.9 3629	8	AK069483	AK069483 Oryza sat
685	98	5.9 8546	1	AY512416	AY512416 Listeria	757	97	5.9 3720	5	XELNCAM	M25696 X.laevlis ne
686	98	5.9 8546	1	AY512420	AY512420 Listeria	758	97	5.9 8546	1	AY512395	AY512395 Listeria
687	98	5.9 8546	1	AY512423	AY512423 Listeria	759	97	5.9 8546	1	AY512429	AY512429 Listeria
688	98	5.9 8546	1	AY512424	AY512424 Listeria	760	97	5.9 8546	1	AY512431	AY512431 Listeria
689	98	5.9 8546	1	AY512435	AY512435 Listeria	761	97	5.9 8546	1	AY512432	AY512432 Listeria
690	98	5.9 8546	1	AY512437	AY512437 Listeria	762	97	5.9 8546	1	AY512450	AY512450 Listeria
691	98	5.9 8546	1	AY512445	AY512445 Listeria	763	97	5.9 11083	1	AE001680	AE001680 Chlamydia
692	98	5.9 8546	1	AY512449	AY512449 Listeria	c 764	97	5.9 11322	1	AE002244	AE002244 Chlamydia
693	98	5.9 8546	1	AY512455	AY512455 Listeria	765	97	5.9 110000	6	CR310754_11	Continuation (12 o
694	98	5.9 8546	1	AY512461	AY512461 Listeria	766	97	5.9 110000	8	CR382123_11	Continuation (12 o
695	98	5.9 8546	1	AY512463	AY512463 Listeria	767	97	5.9 171307	9	AC104020	Homo sapi
696	98	5.9 8546	1	AY512466	AY512466 Listeria	c 768	97	5.9 176099	9	AC108201	Homo sapi
c 697	98	5.9 8546	1	AY512491	AY512491 Listeria	769	97	5.9 190790	8	AP005802	Oryza sat
c 698	98	5.9 13443	2	AC013070	AC013070 Drosophil	c 770	97	5.9 191462	2	AP005781	Oryza sat
c 699	98	5.9 98521	10	AC094507	AC094507 Rattus no	c 771	97	5.9 195859	14	AF281817	AF281817 Tupaia he
700	98	5.9 103362	8	CR382132_39	Continuation (40 o	772	97	5.9 324746	1	AE017160	Chlamydia
c 701	98	5.9 103809	1	AE008921	AE008921 Uncultu	773	97	5.9 325865	1	AP002548	Chlamydia
c 702	98	5.9 103995	2	AC096695	AC096695 Rattus no	774	97	5.9 349442	1	EX640447	Bordetell
703	98	5.9 110000	8	CR380947_0	CR380947 Candida g	775	96.5	5.8 840	8	WHITGGMPA	D78183 Triticum ae
704	98	5.9 110000	8	CR382129_28	Continuation (29 o	776	96.5	5.8 900	6	BD023445	BD023445 Junctio
705	98	5.9 119743	2	AC134515	AC134515 Rattus no	777	96.5	5.8 1194	14	AJ626531	Human her
c 706	98	5.9 120000	2	AC127673	AC127673 Leishmani	778	96.5	5.8 1194	14	AJ626534	Human her
707	98	5.9 121478	9	AL3655229	AL3655229 Human DNA	779	96.5	5.8 1194	14	AJ626538	Human her
c 708	98	5.9 141167	2	AC148140	AC148140 Bos tauru	780	96.5	5.8 1492	10	BC024403	BC024403 Mus muscu
c 709	98	5.9 152177	5	AL9355114	AL9355114 Zebrafish	781	96.5	5.8 1815	1	AF497170	AF497170 Listeria
710	98	5.9 159547	2	AC073674	AC073674 Mus muscu	c 782	96.5	5.8 1859	8	AK106807	AK106807 Oryza sat
711	98	5.9 161264	1	AY456696	AY456696 Arthrobac	c 783	96.5	5.8 3161	6	CQ611375	CQ611375 Sequence
c 712	98	5.9 172674	3	AC007807	AC007807 Drosophil	c 784	96.5	5.8 3491	10	AF319949	AF319949 Mus muscu
713	98	5.9 174108	5	BX323078	BX323078 Zebrafish	785	96.5	5.8 3628	8	AK110169	AK110169 Oryza sat
c 714	98	5.9 190866	3	AC007824	AC007824 Drosophil	786	96.5	5.8 3691	8	D87895	Aspergillus
c 715	98	5.9 215436	3	AC123337	AC123337 Rattus no	787	96.5	5.8 3959	10	BC050817	BC050817 Mus muscu
c 716	98	5.9 220035	3	AE003716	AE003716 Drosophil	788	96.5	5.8 4501	1	ATU39263	ATU39263 Agrobacteri
717	98	5.9 220710	1	AC125304	AC125304 Rattus no	789	96.5	5.8 17317	8	AY421966	AY421966 Cryptococ
c 718	98	5.9 230138	14	AF2332689	AF2332689 Rat cytOm	790	96.5	5.8 39057	8	YSC93666	YSC93666 Saccharomyc
c 719	98	5.9 256879	3	AC116982	AC116982 Dictyoste	791	96.5	5.8 40287	2	AC013199	AC013199 Phaseodact
720	98	5.9 260771	1	AE017258	AE017258 Wolbachia	792	96.5	5.8 48626	2	AC013119	AC013119 Drosophil
721	98	5.9 305225	2	AC130763	AC130763 Rattus no	793	96.5	5.8 110000	8	AE016818_09	Continuation (10 o
722	97.5	5.9 1200	10	RNO010750	AJ010750 Rattus no	794	96.5	5.8 125673	9	AL356796	Human DNA
723	97.5	5.9 1767	6	AX000158	AX000158 Sequence	c 795	96.5	5.8 154365	2	AC091753	AC091753 Rattus no
724	97.5	5.9 1767	6	AX000158	AX000158 Sequence	c 796	96.5	5.8 160986	3	AC108481	AC108481 Drosophil
725	97.5	5.9 2110	4	BTU10039	BTU10039 Bos tauru	c 797	96.5	5.8 162520	2	AC150711	AC150711 Bos tauru
726	97.5	5.9 2603	8	AF156269	AF156269 Aspergill	798	96.5	5.8 167333	2	AC147856	AC147856 Atelerix
727	97.5	5.9 2884	5	XELLDUR1A	M62976 X.laevlis lo	799	96.5	5.8 173740	2	AC020964	AC020964 Mus muscu
c 728	97.5	5.9 56374	9	AC074092	AC074092 Homo sapi	800	96.5	5.8 181179	9	AL161725	AL161725 Human DNA
c 729	97.5	5.9 109672	8	AP004119	AP004119 Oryza sat	801	96.5	5.8 186055	4	AC150569	AC150569 Bos tauru
730	97.5	5.9 110000	3	AC116957_2	Continuation (3 of	802	96.5	5.8 192662	10	AC134397	AC134397 Mus muscu
731	97.5	5.9 110000	8	CR382132_35	Continuation (36 o	803	96.5	5.8 211664	8	AF521177	Hordeum v
732	97.5	5.9 110000	8	CR382132_36	Continuation (37 o	804	96.5	5.8 232049	2	AC127108	Rattus no
733	97.5	5.9 130451	10	AC121877	AC121877 Mus muscu	c 805	96.5	5.8 242121	1	SC096371	Rattus no
c 734	97.5	5.9 150401	2	AC079980	AC079980 Homo sapi	c 806	96.5	5.8 248550	1	SC0939120	Streptomy

C 808	96.5	5.8	272888	2	AC139198	Mus muscu	C 881	95.5	5.8	12781	6	AX825931	Sequence
C 809	96.5	5.8	295177	3	AE003430	Drosophill	882	95.5	5.8	37728	8	YSL8543	U20618 Saccharomyc
C 810	96.5	5.8	297050	1	AP006569	Gloeobact	C 883	95.5	5.8	53957	8	NCB2G14	BX284753 Neurospor
C 811	96.5	5.8	348050	1	AP003581	Nostoc sp	884	95.5	5.8	65140	6	AX211705	AX211705 Sequence
C 812	96	5.8	206	9	HUMSCG02	Human cell	885	95.5	5.8	104241	10	AY046056	AY046056 Mus muscu
C 813	96	5.8	1436	9	HSW804685	AL833372 Homo sapi	886	95.5	5.8	123580	1	AF263912	AF263912 Streptomy
C 814	96	5.8	1455	5	AY288986	Gallus ga	C 887	95.5	5.8	124505	6	CNS071PW	AL731762 Oryza sat
C 815	96	5.8	1851	10	BC021876	BC021876 Mus muscu	888	95.5	5.8	125401	6	AX211739	AX211739 Sequence
C 816	96	5.8	1395	6	CQ782648	Sequence	889	95.5	5.8	126544	8	AP005106	AP005106 Oryza sat
C 817	96	5.8	1895	6	BD127244	BD127244 Primer fo	890	95.5	5.8	140414	2	AC136548	AC136548 Rattus no
C 818	96	5.8	1895	9	AK074718	Homo sapi	891	95.5	5.8	140475	8	AP005558	AP005558 Oryza sat
C 819	96	5.8	2610	5	BC077104	BC077104 Danio rer	892	95.5	5.8	143668	8	AP004268	AP004268 Oryza sat
C 820	96	5.8	4562	6	AX416781	AX416781 Sequence	893	95.5	5.8	145590	8	AC109601	AC109601 Oryza sat
C 821	96	5.8	5789	3	D82024	D82024 Dictyosteli	C 894	95.5	5.8	157397	8	AC133860	AC133860 Oryza sat
C 822	96	5.8	7137	6	CQ726893	CQ726893 Sequence	C 895	95.5	5.8	166126	2	AC149096	AC149096 Mus muscu
C 823	96	5.8	8533	1	AY512399	AY512399 Listeria	896	95.5	5.8	169184	2	AC144112	AC144112 Macaca mu
C 824	96	5.8	8542	1	AY512500	AY512500 Listeria	897	95.5	5.8	174893	3	AC104608	AC104608 Drosophill
C 825	96	5.8	8543	1	AY512393	AY512393 Listeria	C 898	95.5	5.8	176502	2	AC134706	AC134706 Rattus no
C 826	96	5.8	8543	1	AY512400	AY512400 Listeria	899	95.5	5.8	204404	2	AC113679	AC113679 Rattus no
C 827	96	5.8	8543	1	AY512425	AY512425 Listeria	C 900	95.5	5.8	203595	2	CR385054	CR385054 Danio rer
C 828	96	5.8	8543	1	AY512427	AY512427 Listeria	C 901	95.5	5.8	234922	2	AC107585	AC107585 Rattus no
C 829	96	5.8	8543	1	AY512434	AY512434 Listeria	C 902	95.5	5.8	255745	2	AC148018	AC148018 Mus muscu
C 830	96	5.8	8543	1	AY512440	AY512440 Listeria	C 903	95.5	5.8	285950	3	AE003441	AE003441 Drosophill
C 831	96	5.8	8543	1	AY512447	AY512447 Listeria	C 904	95.5	5.8	296820	10	AF312033	AF312033 Mus muscu
C 832	96	5.8	8543	1	AY512448	AY512448 Listeria	905	95.5	5.8	349061	1	NMA222491	AL162753 Neisseria
C 833	96	5.8	8543	1	AY512451	AY512451 Listeria	906	95.5	5.8	349535	1	BX248357	BX248357 Corynebact
C 834	96	5.8	8543	1	AY512456	AY512456 Listeria	907	95	5.7	623	4	AY226857S08	AY226854 Bos tauru
C 835	96	5.8	8543	1	AY512458	AY512458 Listeria	908	95	5.7	1173	14	AJ626550	AJ626550 Human her
C 836	96	5.8	8543	1	AY512464	AY512464 Listeria	909	95	5.7	1440	9	AF043724	AF043724 Homo sapi
C 837	96	5.8	8546	1	AY512436	AY512436 Listeria	910	95	5.7	1574	8	TDY14104	Y14104 Triticum du
C 838	96	5.8	8546	1	AY512441	AY512441 Listeria	911	95	5.7	1613	1	D88257	D88257 Listeria mo
C 839	96	5.8	8546	1	AY512467	AY512467 Listeria	912	95	5.7	1920	1	AF497180	AF497180 Listeria
C 840	96	5.8	8546	1	AY512492	AY512492 Listeria	913	95	5.7	2041	1	AF103807	AF103807 Listeria
C 841	96	5.8	11106	1	AE005891	AE005891 Caulobact	C 914	95	5.7	2211	6	C0588543	C0588543 Sequence
C 842	96	5.8	11297	1	AE230750	AE230750 Photorhab	915	95	5.7	2304	6	AX748227	AX748227 Sequence
C 843	96	5.8	11659	1	AE005131	AE005131 Halobacte	916	95	5.7	2304	9	AK093619	AK093619 Homo sapi
C 844	96	5.8	99890	3	AC084464	AC084464 Caenorhab	917	95	5.7	2373	5	BC057473	BC057473 Danio rer
C 845	96	5.8	110000	1	AP017283_17	Continuation (18 o	C 918	95	5.7	2803	6	AX714680	AX714680 Sequence
C 846	96	5.8	110000	1	AE006840_31	Continuation (32 o	C 919	95	5.7	2803	9	AK057241	AK057241 Homo sapi
C 847	96	5.8	168365	10	AC131653	Continuation (16 o	C 920	95	5.7	2810	3	BT010024	BT010024 Drosophill
C 848	96	5.8	110000	8	CR380953_00	CR380953 Candida g	921	95	5.7	3331	10	MMU70674	MMU70674 Mus musculu
C 849	96	5.8	137297	2	AC090714	Oryza sat	922	95	5.7	3495	10	BC033459	BC033459 Mus musculu
C 850	96	5.8	155548	2	CR484807	CR484807 Danio rer	923	95	5.7	3813	5	AJ720073	AJ720073 Gallus ga
C 851	96	5.8	163380	8	AC084767	AC084767 Oryza sat	C 924	95	5.7	4498	10	MMU91922	MMU91922 Mus musculu
C 852	96	5.8	168365	10	AC131653	AC131653 Mus muscu	C 925	95	5.7	4678	6	C0588542	C0588542 Sequence
C 853	96	5.8	179737	2	AC121552	AC121552 Mus muscu	C 926	95	5.7	5018	3	AC006797	AC006797 Caenorhab
C 854	96	5.8	189286	9	AC008125	AC008125 Homo sapi	C 927	95	5.7	5018	8	AS023040	AS023040 Arabidops
C 855	96	5.8	197845	2	BX950198	BX950198 Danio rer	C 928	95	5.7	8504	1	AY512403	AY512403 Listeria
C 856	96	5.8	211720	2	AC121145	AC121145 Mus muscu	929	95	5.7	8643	1	AY512442	AY512442 Listeria
C 857	96	5.8	239030	10	AC131323	AC131323 Mus muscu	930	95	5.7	8644	1	AY512484	AY512484 Listeria
C 858	96	5.8	251756	10	AC119801	AC119801 Mus muscu	931	95	5.7	8650	1	AY512452	AY512452 Listeria
C 859	96	5.8	290841	1	AE017322	AE017322 Listeria	932	95	5.7	8650	1	AY512471	AY512471 Listeria
C 860	96	5.8	300800	1	AP005036	AP005036 Streptomy	C 933	95	5.7	8650	1	AY512473	AY512473 Listeria
C 861	96	5.8	311000	1	SC0939122	AL939122 Streptomy	C 934	95	5.7	10101	1	AE012376	AE012376 Xanthomon
C 862	95.5	5.8	1173	8	PR3A315701	PR3A315701 Phlebia r	C 935	95	5.7	33359	3	CEF55B11	CEF55B11 Caenorhab
C 863	95.5	5.8	1434	8	YSCSM61	D29964 Saccharomyc	C 936	95	5.7	89992	9	AL135794	AL135794 Human DNA
C 864	95.5	5.8	1491	14	AF343058	AF343058 Eyaach vir	C 937	95	5.7	109519	6	AX195929	AX195929 Sequence
C 865	95.5	5.8	1693	8	AK061142	AK061142 Oryza sat	C 938	95	5.7	114020	10	AC127596	AC127596 Mus muscu
C 866	95.5	5.8	1706	9	AK075503	AK075503 Homo sapi	C 939	95	5.7	136955	2	AC011910	AC011910 Drosophill
C 867	95.5	5.8	1853	8	AK109612	AK109612 Oryza sat	C 940	95	5.7	144263	2	AP005054	AP005054 Oryza sat
C 868	95.5	5.8	2012	8	AK071956	AK071956 Oryza sat	C 941	95	5.7	149505	2	AC126927	AC126927 Felis cat
C 869	95.5	5.8	2220	8	YSCMID2P	D29945 Yeast MID2	942	95	5.7	160118	10	AC132954	AC132954 Mus muscu
C 870	95.5	5.8	2246	3	AY113653	AY113653 Drosophill	943	95	5.7	162929	5	BX323842	BX323842 Zebrafish
C 871	95.5	5.8	2517	8	AK105749	AK105749 Oryza sat	C 944	95	5.7	167475	10	AC090881	AC090881 Mus Muscu
C 872	95.5	5.8	2947	1	SLI18818	Y18818 Streptomyce	C 945	95	5.7	169427	3	AC007416	AC007416 Drosophill
C 873	95.5	5.8	3005	8	AK111157	AK111157 Oryza sat	C 946	95	5.7	173369	10	AL928966	AL928966 Mouse DNA
C 874	95.5	5.8	4435	6	AR428567	AR428567 Sequence	C 947	95	5.7	195349	2	AC006705	AC006705 Caenorhab
C 875	95.5	5.8	4435	6	BD078018	BD078018 Chlamydia	948	95	5.7	197913	2	BX572087	BX572087 Danio rer
C 876	95.5	5.8	5894	3	ACMHC	Y00624 Acanthamoeb	949	95	5.7	199152	2	CR382297	CR382297 Rattus no
C 877	95.5	5.8	11422	3	AF190405	AF190405 Drosophill	C 950	95	5.7	217807	2	AC117034	AC117034 Dictyoste
C 878	95.5	5.8	12781	6	AX251139	AX251139 Sequence	951	95	5.7	254733	3	AC117075	AC117075 Dictyoste
C 879	95.5	5.8	12781	6	AX356403	AX356403 Sequence	952	95	5.7	256307	2	AC130125	AC130125 Rattus no
C 880	95.5	5.8	12781	6	AX822291	AX822291 Sequence	953	95	5.7	258181	2	AC096936	AC096936 Rattus no

954	95	5.7	263879	2	AC096060	1027	94.5	5.7	159802	8	AP005447	AP005447	Oryza sat
955	95	5.7	268333	3	AC098998	1028	94.5	5.7	160738	5	AC073556	AC073556	Oryza sat
c 956	95	5.7	289516	3	AE003619	c1029	94.5	5.7	160871	8	AL954145	AL954145	Zebrafish
957	95	5.7	302550	1	AP006581	c1030	94.5	5.7	164223	10	AC127228	Mus muscu	
958	95	5.7	348006	1	NWA122491	c1031	94.5	5.7	166138	9	AC099684	Homo sapi	
c 959	95	5.7	341553	1	BX248355	c1032	94.5	5.7	168131	2	AC135937	Rattus no	
c 960	95	5.7	349607	1	EX957222	c1033	94.5	5.7	182122	2	AC104194	Homo sapi	
961	94.5	5.7	907	1	GV17274	c1034	94.5	5.7	198222	2	AC092429	Homo sapi	
962	94.5	5.7	948	1	AV331318	c1035	94.5	5.7	202269	9	AC130689	Homo sapi	
963	94.5	5.7	948	1	AV331321	c1036	94.5	5.7	216860	10	AC134793	Mus muscu	
964	94.5	5.7	948	1	AV331322	c1037	94.5	5.7	226307	10	AC119851	Mus muscu	
965	94.5	5.7	948	1	AV331323	c1038	94.5	5.7	232292	2	AC126517	Rattus no	
966	94.5	5.7	948	1	AV331324	c1039	94.5	5.7	242875	2	AC096494	Rattus no	
967	94.5	5.7	1152	14	AJ626535	c1040	94.5	5.7	246913	10	AC109542	Rattus no	
968	94.5	5.7	1152	14	AJ626544	c1041	94.5	5.7	247306	2	AC131445	Rattus no	
969	94.5	5.7	1188	14	AJ626529	c1042	94.5	5.7	252509	2	AC098338	Rattus no	
970	94.5	5.7	1203	6	CQ751744	c1043	94.5	5.7	252509	2	AC098943	Rattus no	
971	94.5	5.7	1507	9	BC013325	c1044	94.5	5.7	289816	1	AE016992	Shigella	
972	94.5	5.7	1608	6	BD228728	c1045	94.5	5.7	292550	1	AP001513	Bacillus	
c 973	94.5	5.7	1608	6	BD228729	c1046	94.5	5.7	349751	3	PFMAL4P3	Plasmodiu	
974	94.5	5.7	1608	6	AR232707	c1047	94	5.7	700	9	S72412	S72412	proteoglyca
c 975	94.5	5.7	1608	6	AR232708	c1048	94	5.7	942	8	AK060999	Oryza sat	
976	94.5	5.7	1608	6	AX411859	c1049	94	5.7	1566	6	CQ716121	Sequence	
c 977	94.5	5.7	1608	6	AX411861	c1050	94	5.7	1810	5	CR761800	Xenopus t	
978	94.5	5.7	1665	6	BD228726	c1051	94	5.7	1920	1	AF497173	Listeria	
c 979	94.5	5.7	1665	6	BD228726	c1052	94	5.7	1946	6	CQ588132	Sequence	
980	94.5	5.7	1665	6	AR232705	c1053	94	5.7	1946	6	AX254510	Sequence	
c 981	94.5	5.7	1665	6	AR232706	c1054	94	5.7	2023	8	CSMCPN601	X70867 Cucurbita s	
982	94.5	5.7	1665	6	AX411856	c1055	94	5.7	2398	8	AF190462	Phaseolus	
c 983	94.5	5.7	1665	6	AX411858	c1056	94	5.7	2461	8	AF190462	Phaseolus	
984	94.5	5.7	1752	3	AF178772	c1057	94	5.7	2713	10	MM2EFY	Mouse zinc	
985	94.5	5.7	1752	6	BD228724	c1058	94	5.7	2990	3	AY122212	Drosophil	
c 986	94.5	5.7	1752	6	BD228725	c1059	94	5.7	3774	2	AC019365	Drosophil	
c 987	94.5	5.7	1752	6	AR232703	c1060	94	5.7	3946	6	CQ588131	Sequence	
c 988	94.5	5.7	1752	6	AR232704	c1061	94	5.7	3946	6	AX254509	Sequence	
989	94.5	5.7	1752	6	AX411853	c1062	94	5.7	4849	3	AK113070	Ciona int	
c 990	94.5	5.7	1752	6	AX411855	c1063	94	5.7	6047	6	AX346361	Sequence	
991	94.5	5.7	1994	5	BC059200	c1064	94	5.7	6313	6	CQ604274	Sequence	
992	94.5	5.7	2155	9	S52488	c1065	94	5.7	6530	1	AB017438	Streptomy	
993	94.5	5.7	2438	6	CQ843471	c1066	94	5.7	7055	1	AF042494	Sulfolobu	
994	94.5	5.7	2438	9	AK126455	c1067	94	5.7	7823	14	HPV27	X74473 Human papil	
995	94.5	5.7	2690	3	DP020332	c1068	94	5.7	8643	1	AY512405	Listeria	
c 996	94.5	5.7	2784	6	AX654208	c1069	94	5.7	8643	1	AY512421	Listeria	
997	94.5	5.7	2967	1	AY184164	c1070	94	5.7	8643	1	AY512422	Listeria	
998	94.5	5.7	2967	1	AY184165	c1071	94	5.7	8643	1	AY512444	Listeria	
999	94.5	5.7	2967	1	AY184166	c1072	94	5.7	8643	1	AY512468	Listeria	
1000	94.5	5.7	3401	6	AX536450	c1073	94	5.7	8643	1	AY512469	Listeria	
1001	94.5	5.7	3958	8	YSCSSN6A	c1074	94	5.7	8643	1	AY512490	Listeria	
1002	94.5	5.7	4041	5	GNCEUPASC	c1075	94	5.7	8649	1	AY512481	Listeria	
1003	94.5	5.7	4866	8	YSCCYC8	c1076	94	5.7	8651	1	AY512391	Listeria	
c1004	94.5	5.7	5374	8	SCYBR112C	c1077	94	5.7	8651	1	AY512398	Listeria	
1005	94.5	5.7	6674	1	LD5E12946	c1078	94	5.7	8651	1	AY512401	Listeria	
c1006	94.5	5.7	8664	3	LMFL6823	c1079	94	5.7	8651	1	AY512415	Listeria	
c1007	94.5	5.7	8949	8	SCCMDLYS	c1080	94	5.7	8651	1	AY512426	Listeria	
c1008	94.5	5.7	11509	3	AE015347	c1081	94	5.7	8651	1	AY512457	Listeria	
c1009	94.5	5.7	15613	1	CEC03306	c1082	94	5.7	8651	1	AY512459	Listeria	
1010	94.5	5.7	26356	3	AF077538	c1083	94	5.7	8651	1	AY512460	Listeria	
1011	94.5	5.7	50709	1	AY034092	c1084	94	5.7	9642	10	AF187873	AF187873 Cavia por	
1012	94.5	5.7	68702	9	AL445193	c1085	94	5.7	10029	1	AE011851	Xanthomon	
c1013	94.5	5.7	69748	8	SCRACII	c1086	94	5.7	11085	1	AE006896	Sulfolobu	
c1014	94.5	5.7	67768	10	AL663044	c1087	94	5.7	11106	1	AE001283	Xanthomon	
c1015	94.5	5.7	92294	1	AY117439	c1088	94	5.7	14198	1	AE011967	Xanthomon	
1016	94.5	5.7	102311	9	AC005377	c1089	94	5.7	80167	2	AC020038	Drosophil	
1017	94.5	5.7	103419	2	AL133921	c1090	94	5.7	110000	1	AP006618_28	Continuation (29 o	
1018	94.5	5.7	107379	1	SHGCPJR	c1091	94	5.7	121377	8	AP004038	Oryza sat	
1019	94.5	5.7	110000	2	AC102349_1	c1092	94	5.7	123010	2	AC009746	Drosophil	
1020	94.5	5.7	110000	2	AC102349_2	c1093	94	5.7	127405	10	AL645599	Mouse DNA	
c1021	94.5	5.7	110000	2	LMFLCHR36_01	c1094	94	5.7	137046	8	AP004775	Oryza sat	
1022	94.5	5.7	121705	9	AC006452	c1095	94	5.7	138994	2	AC141046	Rattus no	
1023	94.5	5.7	125862	9	AC026696	c1096	94	5.7	146123	2	AC147458	Felis cat	
c1024	94.5	5.7	132151	8	AC144491	c1097	94	5.7	169138	3	AC010571	Rosophil	
1025	94.5	5.7	139275	2	BX323887	c1098	94	5.7	184887	3	AC008207	Drosophil	
1026	94.5	5.7	144695	8	AP005451	c1099	94	5.7	192187	3	AC117072	Dictyosce	

c1100	94	5.7	199271	2	AC142243	AC142243 Mus muscu	c1173	93.5	5.6	349980	6	AX492786	AX492786 Sequence
c1101	94	5.7	212459	2	AC113023	AC113023 Mus muscu	c1174	93.5	5.6	349980	6	AX553953	AX553953 Sequence
c1102	94	5.7	214256	10	AC118007	AC118007 Mus muscu	c1175	93	5.6	712	3	AK174897	AK174897 Ciona int
c1103	94	5.7	227219	3	AE003750	AE003750 Drosophill	c1176	93	5.6	786	3	AJ586552	AJ586552 Eimeria t
c1104	94	5.7	241592	2	AC111683	AC111683 Rattus no	c1177	93	5.6	1050	3	AY466439	AY466439 Caenorhab
c1105	94	5.7	246566	2	AC097926	AC097926 Rattus no	c1178	93	5.6	1095	9	CR457114	CR457114 Homo sapi
c1106	94	5.7	263297	2	AC127631	AC127631 Rattus no	c1179	93	5.6	1200	14	AF395734	AF395734 Human sat
c1107	94	5.7	292100	1	SC0939121	AL939121 Streptomy	c1180	93	5.6	1268	3	AF250045	AF250045 Caenorhab
c1108	94	5.7	294272	3	AE003595	AE003595 Drosophill	c1181	93	5.6	1321	6	AR097540	AR097540 Mus muscu
c1109	94	5.7	297950	1	AP006582	AP006582 Gloebact	c1182	93	5.6	1815	10	AF170709	AF170709 Mus muscu
c1110	94	5.7	302040	1	AE017317	AE017317 Desulfovi	c1183	93	5.6	1920	1	AF497175	AF497175 Listeria
c1111	94	5.7	303550	1	SC0939131	AL939131 Streptomy	c1184	93	5.6	1920	1	AF497177	AF497177 Listeria
c1112	94	5.7	329861	1	NW4523491	AL162756 Neisseria	c1185	93	5.6	1929	10	AF169191	AF169191 Mus muscu
c1113	93.5	5.6	757	10	BC021401	BC021401 Mus muscu	c1186	93	5.6	1929	10	AF169191	AF169191 Mus muscu
c1114	93.5	5.6	826	5	CHLNKPA4	M35038 Chicken car	c1187	93	5.6	1962	10	AF169192	AF169192 Mus muscu
c1115	93.5	5.6	981	9	BC0411179	BC0411179 Homo sapi	c1188	93	5.6	2032	3	DMU17693	DMU17693 Sequence
c1116	93.5	5.6	1070	8	AK0611303	AK0611303 Oryza sat	c1189	93	5.6	2032	6	AR195309	AR195309 Sequence
c1117	93.5	5.6	1152	14	AJ626554	AJ626554 Human her	c1190	93	5.6	2032	6	AR222274	AR222274 Sequence
c1118	93.5	5.6	1172	8	AK104138	AK104138 Oryza sat	c1191	93	5.6	2051	4	CFGPCR1	CFGPCR1
c1119	93.5	5.6	1175	8	AK104400	AK104400 Oryza sat	c1192	93	5.6	2105	5	BC081615	BC081615 Danio rer
c1120	93.5	5.6	1216	10	BC060539	BC060539 Rattus no	c1193	93	5.6	2806	10	AF299345	AF299345 Mus muscu
c1121	93.5	5.6	1245	8	AK073355	AK073355 Oryza sat	c1194	93	5.6	2833	10	BC005414	BC005414 Mus muscu
c1122	93.5	5.6	1785	3	AB162804	AB162804 Haliotis	c1195	93	5.6	2841	10	AB028895	AB028895 Mus muscu
c1123	93.5	5.6	1824	1	AF497171	AF497171 Listeria	c1196	93	5.6	3004	6	CQ593711	CQ593711 Sequence
c1124	93.5	5.6	1881	3	AF164027	AF164027 Leishmani	c1197	93	5.6	3036	3	AY245772	AY245772 Neosiga
c1125	93.5	5.6	1943	3	AK116624	AK116624 Ciona int	c1198	93	5.6	4047	9	HS2298318	HS2298318 Homo sapi
c1126	93.5	5.6	2176	6	CQ841674	CQ841674 Sequence	c1199	93	5.6	4977	1	CDCMANA	CDCMANA
c1127	93.5	5.6	2176	9	AK123334	AK123334 Homo sapi	c1200	93	5.6	5931	6	CQ607290	CQ607290 Sequence
c1128	93.5	5.6	2900	8	HVB1HORG	X03103 Barley gene	c1201	93	5.6	7396	3	TG062660	TG062660 Toxoplasma
c1129	93.5	5.6	6108	3	CETRA351	U12516 Caenorhabdi	c1202	93	5.6	7931	6	CQ607289	CQ607289 Sequence
c1130	93.5	5.6	6166	6	AX699575	AX699575 Sequence	c1203	93	5.6	8651	1	AY512410	AY512410 Listeria
c1131	93.5	5.6	7348	6	AX251090	AX251090 Sequence	c1204	93	5.6	8651	1	AY512489	AY512489 Listeria
c1132	93.5	5.6	8146	6	AR448064	AR448064 Sequence	c1205	93	5.6	8651	1	AY512489	AY512489 Listeria
c1133	93.5	5.6	9169	6	CQ413012	CQ413012 Sequence	c1206	93	5.6	8651	1	AY512489	AY512489 Listeria
c1134	93.5	5.6	9220	6	CQ492536	CQ492536 Sequence	c1207	93	5.6	8651	1	AY512489	AY512489 Listeria
c1135	93.5	5.6	9416	9	HUNSEXQ	L06237 Human micro	c1208	93	5.6	8651	1	AY512489	AY512489 Listeria
c1136	93.5	5.6	9416	9	HUNSEXQ	L06237 Human micro	c1209	93	5.6	8651	1	AY512489	AY512489 Listeria
c1137	93.5	5.6	1474	1	AE014763	AE014763 Bifidobac	c1210	93	5.6	8651	1	AY512489	AY512489 Listeria
c1138	93.5	5.6	1917	6	AR454559	AR454559 Sequence	c1211	93	5.6	8651	1	AY512489	AY512489 Listeria
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: EP 1067182-A 149 10-JAN-2001;
Helix Research Institute (JP)
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Alignment Scores:
Pred. No.: 4,17e-127 Length: 1755
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-063-670-6 (1-322) x AX136227 (1-1755)

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QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTPIIysValProVal	120
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QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
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QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
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QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu	240
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QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
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QY	281	LysValValLysGluLysAlaAenAspSerAsnProAsnGluGluSerLysLysThr	300
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DEFINITION	Secretory protein or membrane protein.	1755 bp	DNA linear PAT 18-SEP-2002
ACCESSION	BD123566		
VERSION	BD123566.1	GI:23218511	
KEYWORDS	JP 2002017376-A/75.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 1755)
AUTHORS	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
TITLE	Secretory protein or membrane protein
JOURNAL	HELIX RESEARCH INSTITUTE
COMMENT	OS Homo sapiens (human) PN JP 2002017376-A/75 PD 22-JAN-2002 PF 07-JUL-2000 JP 2000253173 PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA, YURI KAWAI, TOMOYASU SUGIYAMA, PI KOJI HAYASHI PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/PC 10, PC C12P21/02,C12Q1/68//C12P21/08,C12N15/00,C12N5/00 CC Secretory protein or membrane protein FH Key Location/Qualifiers FT CDS Location/Qualifiers FEATURES source 1..1755 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" ORIGIN Alignment Scores: Pred. No.: 4.17e-127 Length: 1755 Score: 1657.00 Matches: 322 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 6 Gaps: 0 US-10-063-670-6 (1-322) x BD123566 (1-1755) QY 1 MetaAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20 Db 201 ATGGCCAGGTGCTTCAGCTGGTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCCTG 260 QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40 Db 261 GTCCAAAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGCTATGCAGAAATTTAGGG 320 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60 Db 321 ATCACCTTGTGAGCAAAAGCGCAACAGCAGCTGAATTTACAGAGAGCTAAGGAGGCC 380 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80 Db 381 TGTAGGCTGCTGGAGCTTAAGTTTGGCCGCGCAAGACCACCAAGTTGAAACAGCTTTGAAAGCT 440 QY 81 SerPheGluThrCysSerTyrGlyTTPValGlyAspGlyPheValValIleSerArgIle 100 Db 441 AGCTTTGAAACTTGCAGCTATGCGTGGGTGGAGATGGATTCGTGTCATCTCTAGGATT 500 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120 Db 501 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTCTCTGATTTGGAAGGTTTCCAGTG 560 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140 Db 561 AGCCGACAGTTTGAGCGCTATTGTTTACAACCTCATCTGATACTTTGGACTTAACTCGTGCATT 620 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160 Db 621 CCAGAAATATTACACCAACAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 680 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

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Db      1161  GAAGTT 1166

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DEFINITION Homo sapiens cDNA PSEC0135 fis, clone P1ACE1004850, highly similar to Homo sapiens lymphatic endothelium-specific hyaluronan receptor LYVE-1 mRNA.
ACCESSION AK075443
VERSION   AK075443.1  GI:22761535
KEYWORDS  oligo capping; fis (full insert sequence).
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Ota, T., Nishikawa, T., Suzuki, Y., Kawai-Hio, Y., Hayashi, K., Ishii, S., Saito, K., Yamamoto, J., Wakamatsu, A., Nagai, T., Nakamura, Y., Nagahara, K., Sugano, S. and Isogai, T.
TITLE     HRI human cDNA sequencing project
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 1755)
AUTHORS   Isogai, T. and Yamamoto, J.
TITLE     Direct Submission
JOURNAL   Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT   HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing; Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction; Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center.
FEATURES             Location/Qualifiers
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ORIGIN
Alignment Scores: 4.17e-127 Length: 1755
Pred. No.: 1657.00 Matches: 322
Score: 100.00% Conservative: 0
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Best Local Similarity: 100.00% Indels: 0
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Qy      181  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuLeu 200
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Db      861  GAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 920
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LOCUS Human signal peptide-containing protein. 2029 bp DNA linear PAT 17-JUL-2003  
DEFINITION  
ACCESSION BD222718  
VERSION BD222718.1 GI:33032488  
KEYWORDS JP 2002519030-A/64.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2029)  
AUTHORS Lal,P., Tang,Y.T., Gorgone,G.A., Corley,N.C., Guegler,K.J.,  
Baughn,M.R., Akerblom,I.E., Young,J.A., Yue,H., Patterson,C.,  
Reddy,R., Hillman,J.L. and Bandman,O.  
TITLE Human signal peptide-containing protein  
JOURNAL Patent: JP 2002519030-A 64 02-JUL-2002;  
INCYTE PHARMACEUTICALS INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002519030-A/64  
PD 02-JUL-2002  
PF 25-JUN-1999 JP 2000557363  
PR 26-JUN-1998 US 60/090762,31-JUL-1998 US 60/094983 PR  
01-OCT-1998 US 60/102686,11-DEC-1998 US 60/112129 PI PREETI  
LAL,Y TOM TANG,GINA A GORGONE,NEIL C CORLEY,KARL J PI GUEGLER,  
PI MARIAN R BAUGHN,INGRID E AKERBLUM,JANICE AU YOUNG,HENRY YUE,  
PI CHANDRA PATTERSON,ROOPA REDDY,JENNIFER L HILLMAN,OLGA BANDMAN  
PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61P9/00,A61P15/00,  
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ORIGIN  
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Score: 1657.00 Matches: 322  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
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DEFINITION Sequence 13 from patent US 6388794.  
ACCESSION AR204700  
VERSION AR204700.1 GI:21502094  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2029)  
AUTHORS Daniel,S., Gilmore,J., Stuart,S.G. and Stuve,L.L.  
TITLE Detection of altered expression of genes regulating cell proliferation  
JOURNAL Patent: US 6368794-A 13 09-APR-2002;  
FEATURES Location/Qualifiers

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ACCESSION BD172392  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2372)  
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and  
Yuan,J.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
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JOURNAL Patent: JP 2002223786-A 165 13-AUG-2002;  
GENENTECH INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002223786-A/165  
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PF 18-DEC-2001 JP 2001385135  
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24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR  
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WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI  
JIAN ZHENG,  
PI JEAN YUAN  
PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC  
C12N5/10,  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL patent: JP 2002238586-A 165 27-AUG-2002;
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PN JP 2002238586-A/165
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JIAN ZHENG,
PI JEAN YUAN
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ACCESSION BD173349
VERSION BD173349.1 GI:28414660
KEYWORDS JP 2002238588-A/165.
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Wood, W. I., Gurney, A. L., Goddard, A., Pennica, D., Zheng, J. and
Yuan, J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: JP 2002238588-A 165 27-AUG-2002;
GENENTECH INC
COMMENT OS Homo sapiens (human)
PN JP 2002238588-A/165
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385315
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18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR
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24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/435, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC
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PC C12P21/02/C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19),
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

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Searched: 4708233 seqs, 24227607955 residues

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- 11: gb.sts.\*
- 12: gb.sv.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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53	211	18.8	1072	5	AF332869	Anas plat
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88	197	17.5	1483	6	AX060538	AX060538 Sequence	161	127.5	11.3	1985	6	BD175393	BD175393 Secretory
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91	197	17.5	1794	9	HUMCD44B	M59040 Human cell	164	127.5	11.3	1985	6	AR439135	AR439135 Sequence
92	197	17.5	2035	5	AF153205	AF153205 Gallus ga	165	127.5	11.3	1985	6	AR473155	AR473155 Sequence
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101	196	17.4	1083	6	AX824985	AX824985 Sequence	174	127.5	11.3	2558	9	AF229053	AF229053 Homo sapi
102	196	17.4	1339	9	AY101193	AY101193 Homo sapi	175	127.5	11.3	2868	10	RNALPBRE	X79881 R.norvegicu
103	196	17.4	1356	9	BC067348	BC067348 Homo sapi	176	127.5	11.3	2878	9	AF228710	AF228710 Homo sapi
104	196	17.4	1823	9	HUMKCAA	M25078 Human Herm	177	127.5	11.3	3077	10	RNU37142	U37142 Rattus norv
105	196	17.4	4606	9	HSMB03952	AL832642 Homo sapi	178	127.5	11.3	3245	9	BC010571	BC010571 Homo sapi
106	196	17.4	5165	6	CQ413028	CQ413028 Sequence	179	127.5	11.3	3275	9	BC009117	BC009117 Homo sapi
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112	183.5	16.3	1338	4	ECCD44	X66862 Equus cabal	185	127.5	11.3	3476	9	AX358372	AX358372 Homo sapi
113	175.5	15.6	1697	6	CQ723838	CQ723838 Sequence	186	127.5	11.3	168751	2	AC068969	AC068969 Homo sapi
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118	153.5	13.6	270	6	AX033418	AX033418 Sequence	191	127	11.3	79444	2	AC150153	AC150153 Gallus ga
119	150	13.3	2863	6	AX747085	AX747085 Sequence	192	127	11.3	143178	2	AC150117	AC150117 Gallus ga
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121	146	13.0	7447	4	BTU76615	U76615 Bos taurus	194	126	11.2	8157	10	AF364951	AF364951 Mus muscu
122	145.5	12.9	769	9	HUMZD93D04	AF086484 Homo sapi	195	126	11.2	199942	2	AC150038	AC150038 Gallus ga
123	145.5	12.9	781	6	CQ730585	CQ730585 Sequence	196	125.5	11.2	2160	6	AX748299	AX748299 Sequence
124	145.5	12.9	834	9	HSAA19936	AX419936 Homo sapi	197	125.5	11.2	2160	9	AK093774	AK093774 Homo sapi
125	145.5	12.9	1430	9	BC030205	BC030205 Homo sapi	198	125.5	11.2	2780	10	AF098460	AF098460 Mus muscu
126	145.5	12.9	1481	4	AF314813	AF314813 Sus scrof	199	125.5	11.2	4738	10	BC066853	BC066853 Mus muscu
127	145.5	12.9	12307	5	CHKPRL	DI3542 Chicken mRN	200	125.5	11.2	7870	9	BSA275213	AJ275213 Homo sapi
128	145	12.9	466	6	CQ713460	CQ713460 Sequence	201	125	11.1	201	11	BV206501	BV206501 sqnm22108
129	145	12.9	834	9	HSAA21518	AJ421518 Homo sapi	202	125	11.1	1414	6	AX336169	AX336169 Sequence
130	145	12.9	1414	6	AR063905	AR063905 Sequence	203	125	11.1	1414	9	HUMTSG6A	M31165 Human tumor
131	145	12.9	1414	6	AR144434	AR144434 Sequence	204	124.5	11.1	2430	10	AF139572	AF139572 Mus muscu
132	145	12.9	1414	6	AR281307	AR281307 Sequence	205	124.5	11.1	7136	6	CQ716466	BC716466 Sequence
133	144	12.8	1616	10	MMU83903	U83903 Mus musculu	206	124.5	11.1	7909	9	D87433	D87433 Homo sapien
134	144	12.8	1616	10	BC021155	BC021155 Mus muscu	207	124.5	11.1	7916	9	AB052956	AB052956 Homo sapi
135	143	12.7	6452	5	CHKSPGCP	L21913 Chicken cho	208	124	11.0	1682	5	CR762351	CR762351 Xenopus t
136	143	12.7	6477	5	CHKAGRECA	M88101 White legno	209	124	11.0	24541	2	AC095672	AC095672 Rattus no
137	140	12.4	3911	10	BC031166	BC031166 Mus muscu	210	124	11.0	249774	2	AC126196	AC126196 Rattus no
138	140	12.4	7931	10	AF290914	AF290914 Mus muscu	211	123	10.9	2116	4	AF060459	AF060459 Bos tauru
139	140	12.4	208621	2	AC150078	AC150078 Gallus ga	212	123	10.9	4040	5	AF325324	AF325324 Xenopus l
140	139.5	12.4	7104	4	CFU65589	U65589 Canis fami	213	123	10.9	5077	4	AF060458	AF060458 Bos tauru
141	139	12.4	1608	9	AK129808	AK129808 Homo sapi	214	123	10.9	7330	4	AF060457	AF060457 Bos tauru
142	139	12.4	6597	5	GGU78555	U78555 Gallus gall	215	123	10.9	10291	4	AF060456	AF060456 Bos tauru
143	138.5	12.3	1411	6	AX202114	AX202114 Sequence	216	122	10.8	1183	4	RABAGRECA	L38480 Oryctolagus
144	137	12.2	1406	4	RABPS4EA	M86381 Oryctolagus	217	121.5	10.8	959	6	CQ723845	CQ723845 Sequence
145	137	12.2	6939	10	RATPGCA	J03485 Rat alterna	218	121	10.8	1587	6	AR432563	AR432563 Sequence
146	135.5	12.0	3076	10	BC052032	BC052032 Mus muscu	219	121	10.8	1587	6	BD078622	BD078622 Human pro
147	135.5	12.0	3153	10	MMBRVGEN	X87096 M.musculus	220	121	10.8	1704	9	AY007241	AY007241 Homo sapi
148	135	12.0	7382	10	MUSAGGRECA	L07049 Mus musculu	c 221	121	10.8	15548	2	CR484047	CR484047 Danio rer
149	133.5	11.9	1734	6	AR220822	AR220822 Sequence	222	120.5	10.7	3259	4	BTBREV	X75687 B.taurus Br
150	133	11.8	1683	10	RNU46958	U46958 Rattus norv	223	120.5	10.7	5614	5	AB119257	AB119257 Danio rer



224	120	10.7	2554	5	BC046259	BC046259 Xenopus l	c 297	110	9.8	271812	2	BX530095	BX530095	Danio rer
225	120	10.7	4069	5	BC078043	BC078043 Xenopus l	c 298	110	9.8	292007	2	AC128762	AC128762	Rattus no
c 226	119.5	10.6	221762	2	BX308731	BX308731 Danio rer	299	109.5	9.7	1406	10	AB049056	AB049056	Rattus no
227	119	10.6	480	10	MMLINK4	AF137277 Mus muscu	300	109.5	9.7	5191	6	I56080	I56080	Sequence 1
228	118.5	10.5	5923	9	HSU26555	U26555 Human versu	301	109.5	9.7	5191	10	RATNCAN	RATNCAN	M97161 Rattus norv
229	118.5	10.5	11185	6	CQ776629	CQ776629 Sequence	302	109	9.7	6310	9	AF026547	AF026547	Homo sapi
230	118.5	10.5	11185	6	AX330530	AX330530 Sequence	303	109	9.7	6312	6	CQ727544	CQ727544	Sequence
231	118.5	10.5	11185	6	AX410665	AX410665 Sequence	304	109	9.7	110000	2	AC096220	AC096220	Rattus no
232	118.5	10.5	11185	9	HSU16306	U16306 Human chond	c 305	109	9.7	183682	9	AL133330	AL133330	Human DNA
233	118.5	10.5	12319	6	AX281831	AX281831 Sequence	c 306	109	9.7	232127	2	AC113724	AC113724	Rattus no
234	118.5	10.5	164846	2	AC107727	AC107727 Mus muscu	307	109	9.7	235684	2	AC129422	AC129422	Rattus no
235	118	10.5	2318	10	MUSPGM3B	D32040 Mouse pgk3	308	109	9.7	273258	2	AC123370	AC123370	Rattus no
236	118	10.5	7375	6	CQ777492	CQ777492 Sequence	309	108.5	9.6	103201	2	AC149525	AC149525	Xenopus t
237	118	10.5	7375	10	MUSPGMV	D16263 Mus musculus	310	108	9.6	317	10	RATLNKP4	RATLNKP4	M22339 Rat link pr
238	118	10.5	10427	10	MUSPGM	D28599 Mouse mRNA	311	108	9.6	685	4	AY226857	AY226857	Bos tauru
239	117	10.4	209852	10	AC151363	AC151363 Gasterost	312	108	9.6	1319	10	AY269788	AY269788	Mus muscu
240	116	10.3	1910	5	CHLNKPA2	M13212 Chicken car	c 313	108	9.6	1320	4	AF529268	AF529268	Ovis arie
241	116	10.3	8444	6	AX686192	AX686192 Sequence	314	108	9.6	1433	10	AY262757	AY262757	Mus muscu
242	115.5	10.3	1626	9	AK090712	AK090712 Homo sapi	315	108	9.6	1492	9	HSCLTK115	HSCLTK115	H.sapiens C
243	115.5	10.3	1630	9	BC029864	BC029864 Homo sapi	316	108	9.6	1492	9	HSCLTK115	HSCLTK115	Human mRNA
244	115.5	10.3	8069	9	AK160380	AK160380 Homo sapi	317	108	9.6	1493	6	CQ728128	CQ728128	Sequence
245	115.5	10.3	197370	9	AC1033982	AC1033982 Homo sapi	318	108	9.6	1721	9	BC057808	BC057808	Homo sapi
246	115	10.2	1249	10	BC022136	BC022136 Mus muscu	319	108	9.6	1759	9	HSU43328	HSU43328	Human link
247	114.5	10.2	1736	10	AB049055	AB049055 Mus muscu	320	108	9.6	68574	2	AC113212	AC113212	Homo sapi
248	114	10.1	1794	9	AB049054	AB049054 Homo sapi	c 321	108	9.6	164286	9	AC020899	AC020899	Homo sapi
c 249	114	10.1	192862	10	AC134397	AC134397 Mus muscu	322	108	9.6	167872	2	AC007554	AC007554	Homo sapi
250	114	10.1	272888	2	AC139198	AC139198 Mus muscu	323	108	9.6	226416	2	AC103519	AC103519	Rattus no
c 251	113.5	10.1	64675	2	BX322628_3	Continuation (1 of	324	108	9.6	247266	2	AC110520	AC110520	Mus muscu
c 252	113.5	10.1	110000	2	BX322628_2	Continuation (3 of	325	107.5	9.6	1335	4	SSLINK	SSLINK	Sus scrofa
253	113.5	10.1	170883	9	AC067805	AC067805 Homo sapi	326	107	9.5	427	5	CHLNKPA3	CHLNKPA3	Chicken car
254	113.5	10.1	218103	5	BX465199	BX465199 Zebrafish	327	107	9.5	427	5	CHLNKPA3	CHLNKPA3	Sequence
255	113.5	10.1	271812	2	BS300095	BS300095 Danio rer	328	107	9.5	1400	6	AR036272	AR036272	Sequence
256	113	10.0	1925	9	BC050524	BC050524 Homo sapi	329	107	9.5	1400	6	AR036272	AR036272	Sequence
257	113	10.0	2087	6	AX338947	AX338947 Sequence	330	107	9.5	1520	6	I44674	I44674	Sequence 1
258	113	10.0	2087	9	HUMPGRH3A	D32039 Human pgH3	331	107	9.5	1851	6	AX302626	AX302626	R.norvegicu
259	113	10.0	8224	6	CQ728127	CQ728127 Sequence	332	107	9.5	2011	6	AX149447	AX149447	Sequence
260	113	10.0	8224	6	AR362654	AR362654 Sequence	333	107	9.5	5259	10	MMNEUROCM	MMNEUROCM	Sequence
261	113	10.0	8224	9	AX582877	AX582877 Sequence	334	107	9.5	7147	10	BC065118	BC065118	Mus muscu
262	113	10.0	8224	9	HSVERS	X15998 H.sapiens m	c 335	107	9.5	8340	11	BV178350	BV178350	sqmm10003
263	113	10.0	136886	2	AC149262	AC149262 Spherooid	c 336	107	9.5	112830	2	AC151678	AC151678	Gallus ga
264	113	10.0	138091	2	AC113583	AC113583 Tetraooid	c 337	107	9.5	164512	9	AL365181	AL365181	Human DNA
c 265	113	10.0	19942	2	AC150038	AC150038 Gallus ga	338	106.5	9.5	2447	10	AF060879	AF060879	Rattus no
266	112.5	10.0	3260	6	AX586401	AX586401 Sequence	339	106.5	9.5	77928	2	AC149263	AC149263	Spherooid
267	112.5	10.0	3260	9	AF160476	AF160476 Homo sapi	c 340	106.5	9.5	150209	2	CR759744	CR759744	Danio rer
268	112.5	10.0	3591	6	CQ719622	CQ719622 Sequence	c 341	106	9.4	203159	10	AC137525	AC137525	Mus muscu
269	112.5	10.0	4492	9	AY227444	AY227444 Homo sapi	c 342	106	9.4	346406	10	BX883045	BX883045	Rattus no
270	112.5	10.0	4575	9	AK024503	AK024503 Homo sapi	343	105.5	9.4	614	9	AB049062	AB049062	Homo sapi
271	112.5	10.0	5604	9	AK074051	AK074051 Homo sapi	344	105.5	9.4	1308	6	BD231671	BD231671	31 human
272	112.5	10.0	8214	9	AB052958	AB052958 Homo sapi	c 345	105.5	9.4	193188	10	AL844155	AL844155	Mouse DNA
273	112.5	10.0	8251	9	AY311388	AY311388 Homo sapi	c 346	105.5	9.4	229628	2	BX908768	BX908768	Mus muscu
274	112.5	10.0	8266	6	CQ704239	CQ704239 Sequence	347	105	9.3	723	4	AY226857	AY226857	Bos tauru
275	112	10.0	340	6	HS295695	HS295695 Sequence	348	105	9.3	1941	4	BTU02292	BTU02292	Bos tauru
276	112	10.0	2026	5	BC068325	BC068325 Danio rer	349	105	9.3	36800	9	AC003110	AC003110	Human DNA
c 277	112	10.0	79444	2	AC150153	AC150153 Gallus ga	c 350	105	9.3	43185	9	AC138430	AC138430	Homo sapi
c 278	112	10.0	143178	2	AC150117	AC150117 Gallus ga	c 351	105	9.3	247266	2	AC110520	AC110520	Mus muscu
279	112	10.0	166863	2	AC150140	AC150140 Gallus ga	352	105	9.3	248817	2	AC096230	AC096230	Rattus no
280	112	10.0	176022	2	BX294110	BX294110 Danio rer	353	104.5	9.2	189608	5	AL929208	AL929208	Zebrafish
281	112	10.0	208621	2	AC150078	AC150078 Gallus ga	354	104	9.2	231	10	S73719S2	S73719S2	aggregran-ag
c 282	112	10.0	232749	2	CR354535	CR354535 Danio rer	355	104	9.2	231	10	S73721S2	S73721S2	aggregran-ag
c 283	111.5	9.9	226416	2	AC103519	AC103519 Rattus no	356	104	9.2	484	9	AF098641	AF098641	Homo sapi
c 284	111.5	9.9	230817	2	AC106909	AC106909 Rattus no	357	104	9.2	5580	5	AC096866	AC096866	Takifugu
285	111	9.9	1478	4	ECRTTLIG	X78077 Equus cabal	c 358	103.5	9.2	1310	3	AK173360	AK173360	Ciona inc
286	111	9.9	1720	6	BD195591	BD195591 70 human	c 359	103.5	9.2	8433	6	CQ610163	CQ610163	Sequence
287	111	9.9	1720	6	CQ775636	CQ775636 Sequence	360	103.5	9.2	54309	2	AC017353	AC017353	Drosophil
288	111	9.9	1720	6	AR352646	AR352646 Sequence	361	103.5	9.2	157482	3	AC092227	AC092227	Sphosphil
289	111	9.9	3625	6	AX149461	AX149461 Sequence	c 362	103.5	9.2	177426	2	CR339044	CR339044	Danio rer
290	111	9.9	8495	6	AX686194	AX686194 Sequence	363	103.5	9.2	186803	3	AC092225	AC092225	Drosophil
c 291	111	9.9	184365	2	AC079639	AC079639 Mus muscu	c 364	103.5	9.2	278521	3	AE003642	AE003642	Drosophil
c 292	110.5	9.8	207418	2	AC109112	AC109112 Rattus no	c 365	103.5	9.2	305502	3	DROSADH03	DROSADH03	Sequence
293	110.5	9.8	246369	2	AC125707	AC125707 Rattus no	c 366	103	9.2	402	6	AX785805	AX785805	Sequence
294	110	9.8	4634	5	AF116856	AF116856 Gallus ga	367	103	9.2	1099	3	AF436624	AF436624	Macronema
295	110	9.8	110000	2	BX322628_0	BX322628 Danio rer	368	103	9.2	1519	4	FOBEHAB	FOBEHAB	F.domesticu
c 296	110	9.8	110000	2	BX322628_1	Continuation (2 of	369	103	9.2	1519	6	I44675	I44675	Sequence 2

370	103	9.2	1785	9	BC052287	Homo sapi	BC052287 Homo sapi	C 443	98.5	8.8	82972	8	NCB24H17	ALJ356815	Neutrosopor
C 371	103	9.2	267287	2	AC096702	Rattus no	AC096702 Rattus no	444	98.5	8.8	124191	9	AC005153	AC005153	Homo sapi
372	102.5	9.1	1482	6	AR269667	Sequence	AR269667 Sequence	445	98.5	8.8	146137	2	AC148795	AC148795	Otolemur
C 373	102.5	9.1	1962	6	BD195649	70 human	BD195649 70 human	446	98.5	8.8	184357	2	AC073728	AC073728	Mus muscu
C 374	102.5	9.1	1962	6	CQ775694	Sequence	CQ775694 Sequence	C 447	98.5	8.8	299350	1	SME591786	AL591786	Sinorhizo
C 375	102.5	9.1	1962	6	AR352704	Sequence	AR352704 Sequence	448	98	8.7	1341	6	AX657611	AX657611	Sequence
C 376	102.5	9.1	198756	2	AC135657	Rattus no	AC135657 Rattus no	C 449	98	8.7	1378	1	AY127887	AY127887	Anaplasma
C 377	102	9.1	216015	2	AC113751	Rattus no	AC113751 Rattus no	450	98	8.7	2421	6	C0722898	C0722898	Sequence
C 378	102	9.1	272147	2	AC095648	Rattus no	AC095648 Rattus no	451	98	8.7	3118	6	BD156554	BD156554	Primer fo
379	101.5	9.0	1236	14	AJ626545	Human her	AJ626545 Human her	452	98	8.7	3118	6	AX877234	AX877234	Sequence
380	101.5	9.0	2586	10	MUSEGFRP	Mus musculu	L02613 Mus musculu	453	98	8.7	3118	9	AX027692	AX027692	Homo sapi
381	101.5	9.0	3319	8	AK119879	Oryza sat	AK119879 Oryza sat	454	98	8.7	3499	6	BD156002	BD156002	Primer fo
C 382	101.5	9.0	110000	1	AP006618	49	Continuation (50 o	455	98	8.7	3499	6	AX876196	AX876196	Sequence
C 383	101.5	9.0	202968	2	AC137422	Rattus no	AC137422 Rattus no	456	98	8.7	3499	6	AX876196	AX876196	Sequence
384	101	9.0	3014	9	BC008735	Homo sapi	BC008735 Homo sapi	457	98	8.7	3499	9	AK027440	AK027440	Homo sapi
C 385	101	9.0	72675	9	EX322573	Human DNA	EX322573 Human DNA	C 458	98	8.7	4098	9	HGA459424	AJ459424	Homo sapi
386	101	9.0	79748	2	AC044890	Homo sapi	AC044890 Homo sapi	C 459	98	8.7	4128	1	AF527423	AF527423	Anaplasma
387	101	9.0	110000	8	AE016819	02	Continuation (3 of	C 460	98	8.7	4185	1	AMU60779	U60779	Anaplasma m
388	101	9.0	154612	2	AC093739	Homo sapi	AC093739 Homo sapi	461	98	8.7	5131	6	CQ850217	CQ850217	Sequence
389	101	9.0	160625	9	AC009311	Homo sapi	AC009311 Homo sapi	462	98	8.7	5131	6	CQ580242	CQ580242	Sequence
C 390	101	9.0	178400	5	BX294376	Zebrafish	BX294376 Zebrafish	463	98	8.7	8429	6	CQ580241	CQ580241	Sequence
C 391	101	9.0	192177	5	EX005242	Sequence	EX005242 Sequence	C 464	98	8.7	13443	2	AC013070	AC013070	Drosophil
392	100.5	8.9	1161	10	MNMTA	M. musculus	X68278 M. musculus	C 465	98	8.7	103995	2	AC096695	AC096695	Rattus no
393	100.5	8.9	1209	9	AB107883	Homo sapi	AB107883 Homo sapi	C 466	98	8.7	121478	9	ALJ35229	ALJ35229	Human DNA
394	100.5	8.9	1475	6	AX392229	Sequence	AX392229 Sequence	C 467	98	8.7	144588	2	AC012239	AC012239	Homo sapi
395	100.5	8.9	1712	8	AK120901	Oryza sat	AK120901 Oryza sat	C 468	98	8.7	172674	3	AC007807	AC007807	Drosophil
396	100.5	8.9	1714	8	AK119612	Oryza sat	AK119612 Oryza sat	C 469	98	8.7	172674	3	AC007807	AC007807	Drosophil
397	100.5	8.9	1780	8	AK103182	Oryza sat	AK103182 Oryza sat	C 470	98	8.7	190866	3	AC007824	AC007824	Drosophil
398	100.5	8.9	1881	8	AK061650	Oryza sat	AK061650 Oryza sat	C 471	98	8.7	220035	3	AE003716	AE003716	Drosophil
399	100.5	8.9	1904	8	AK101618	Oryza sat	AK101618 Oryza sat	472	98	8.7	220710	2	AC125304	AC125304	Rattus no
400	100.5	8.9	3383	9	AY262756	Homo sapi	AY262756 Homo sapi	473	98	8.7	305225	2	AC130763	AC130763	Rattus no
401	100.5	8.9	5409	6	BD183451	Novel gen	BD183451 Novel gen	474	97.5	8.7	1144	8	TTU537508	TTU537508	Bordetell
402	100.5	8.9	5409	9	AB067513	Homo sapi	AB067513 Homo sapi	C 475	97.5	8.7	1144	8	TTU537508	TTU537508	Bordetell
403	100.5	8.9	7596	6	AX695382	Sequence	AX695382 Sequence	C 476	97.5	8.7	1144	8	TTU537508	TTU537508	Bordetell
404	100.5	8.9	8064	6	AX695381	Sequence	AX695381 Sequence	C 477	97.5	8.7	1144	8	TTU537508	TTU537508	Bordetell
405	100.5	8.9	8064	10	MNMTA	M. musculus	Z11886 M. musculus	C 478	97.5	8.7	56374	9	AC074092	AC074092	Homo sapi
406	100.5	8.9	9193	10	AF508809	Mus muscu	AF508809 Mus muscu	C 479	97.5	8.7	56374	9	AC074092	AC074092	Homo sapi
C 407	100.5	8.9	22029	9	AC003967	Homo sapi	AC003967 Homo sapi	C 480	97.5	8.7	150401	2	AC079980	AC079980	Homo sapi
408	100.5	8.9	43185	9	AC138430	Homo sapi	AC138430 Homo sapi	C 481	97.5	8.7	174527	9	AP001183	AP001183	Homo sapi
409	100.5	8.9	112830	2	AC151678	Gallus ga	AC151678 Gallus ga	C 482	97.5	8.7	182736	2	AC021672	AC021672	Homo sapi
C 410	100.5	8.9	154865	8	OSN00071	Oryza sat	AL060640 Oryza sat	C 483	97.5	8.7	190314	9	AC019327	AC019327	Homo sapi
C 411	100.5	8.9	300330	1	AP005222	Corynebac	AP005222 Corynebac	C 484	97	8.6	202555	2	AC148141	AC148141	Bos tauru
412	100	8.9	33706	3	C6C25G4	Caenorhabdi	Z70680 Caenorhabdi	485	97	8.6	304	6	CQ673468	AP005953	Bradyrhiz
413	100	8.9	100984	10	AL929138	Mouse DNA	AL929138 Mouse DNA	486	97	8.6	304	6	CQ673468	AP005953	Bradyrhiz
C 414	100	8.9	107352	9	HS474A14	Human DNA	AL023285 Human DNA	487	97	8.6	789	6	CQ749879	CQ749879	Sequence
C 415	100	8.9	135850	2	AC135931	Rattus no	AC135931 Rattus no	488	97	8.6	789	6	CQ749879	CQ749879	Sequence
C 416	100	8.9	180995	9	AC117500	Homo sapi	AC117500 Homo sapi	489	97	8.6	1173	14	AJ626547	AJ626547	Human her
C 417	100	8.9	184091	2	BR294393	Mus muscu	BX294393 Mus muscu	C 490	97	8.6	1173	14	AJ626547	AJ626547	Human her
C 418	100	8.9	218311	2	CR749741	Danio rer	CR749741 Danio rer	491	97	8.6	1173	14	AJ626547	AJ626547	Human her
419	100	8.9	230817	2	AC106909	Rattus no	AC106909 Rattus no	C 492	97	8.6	12979	14	HEHSV1SU	X02138	Herpes simp
C 420	100	8.9	239696	2	AC097086	Rattus no	AC097086 Rattus no	C 493	97	8.6	26245	14	HS1US	L00036	Human herpe
421	99.5	8.8	1008	5	AB167511	Danio rer	AB167511 Danio rer	494	97	8.6	26245	14	HS1US	L00036	Human herpe
422	99.5	8.8	1194	14	AJ626546	Human her	AJ626546 Human her	495	97	8.6	152261	14	HE1CG	X14112	Human herpe
423	99.5	8.8	37711	3	C6ZK996	Caenorhabdi	Z82288 Caenorhabdi	496	97	8.6	171307	9	AC104020	AC104020	Homo sapi
C 424	99.5	8.8	162296	9	AL161774	Human DNA	AL161774 Human DNA	497	96.5	8.6	263891	2	AC096166	AC096166	Rattus no
C 425	99.5	8.8	176022	2	BX294110	Danio rer	BX294110 Danio rer	C 498	96.5	8.6	349442	1	EX640447	EX640447	Bordetell
426	99.5	8.8	225000	2	AC129674	Rattus no	AC129674 Rattus no	C 499	96.5	8.6	840	8	WHTGMPA	D78183	Triticum ae
427	99.5	8.8	232749	2	CR354535	Danio rer	CR354535 Danio rer	C 500	96.5	8.6	1859	8	AK106807	AK106807	Oryza sat
428	99.5	8.8	236907	2	AC103254	Rattus no	AC103254 Rattus no	C 501	96.5	8.6	4501	1	ATU39263	U39263	Agrobacteri
429	99	8.8	438	6	CQ662211	Sequence	AC103254 Rattus no	C 502	96.5	8.6	24413	3	AC117272	AC117272	Leishmani
430	99	8.8	4287	6	CQ610164	Sequence	CQ610164 Sequence	C 503	96.5	8.6	110000	1	AE016822	Continuation (20 o	
C 431	99	8.8	110000	2	LMFLCHR36	21	Continuation (22 o	504	96.5	8.6	125673	9	ALJ356796	ALJ356796	Human DNA
432	99	8.8	110000	6	BD430793	01	Continuation (2 of	505	96.5	8.6	181179	9	ALJ161725	ALJ161725	Human DNA
433	99	8.8	143089	5	CR388386	Zebrafish	CR388386 Zebrafish	506	96.5	8.6	192662	10	AC134397	AC134397	Mus muscu
C 434	99	8.8	153749	5	EX649585	Zebrafish	BX649585 Zebrafish	C 507	96.5	8.6	224197	2	AC144404	AC144404	Medicago
435	99	8.8	307150	1	CNSPAX01	Pyrococcu	AJ248283 Pyrococcu	508	96	8.6	225989	2	AC135294	AC135294	Rattus no
436	99	8.8	349980	6	AX041106	Arabidops	AK176661 Arabidops	509	96	8.5	272888	2	AC139198	AC139198	Mus muscu
C 437	98.5	8.8	1719	8	AK176661	Rattus no	AB094071 Rattus no	510	96	8.5	206	9	HUMSCG02	L05407	Human cell
438	98.5	8.8	1720	10	AB094071	Haliotis	AB092978 Haliotis	511	96	8.5	1458	3	AF167710	AF167710	Toxocara
439	98.5	8.8	1898	3	AB092978	Cyprinus	AY144591 Cyprinus	512	96	8.5	1767	6	AR310497	AR310497	Sequence
440	98.5	8.8	5152	5	AY144591	Sinorhizo	AF373807 Sinorhizo	513	96	8.5	2603	8	AX000158	AX000158	Sequence
C 441	98.5	8.8	5283	1	AF373807	Human papil	U37537 Human papil	514	96	8.5	11659	1	AE005131	AE005131	Halobacte
442	98.5	8.8	7868	14	HPU37537			515	96	8.5	110000	2	LMFLCHR31	Continuation (16 o	

c 516	96	8.5	174108	5	BX323078	589	93.5	8.3	1231	6	AR508054	AR508054 Sequence
c 517	96	8.5	300800	1	AP005036	590	93.5	8.3	1245	8	AK073355	AK073355 Oryza sat
c 518	95.5	8.5	1693	8	AK061142	591	93.5	8.3	1574	8	TDY14104	Y14104 Triticum du
c 519	95.5	8.5	2012	8	AK071956	592	93.5	8.3	1785	3	AB162804	AB162804 Halio
c 520	95.5	8.5	2517	8	AK105749	593	93.5	8.3	1943	3	AK116624	AK116624 Ciona int
c 521	95.5	8.5	5894	3	ACWHC	594	93.5	8.3	7137	6	C0726893	C0726893 Sequence
c 522	95.5	8.5	65140	6	AX211705	595	93.5	8.3	8146	6	AR448064	AR448064 Sequence
c 523	95.5	8.5	123580	1	AF263912	596	93.5	8.3	9169	6	CQ413012	CQ413012 Sequence
c 524	95.5	8.5	125401	6	AX211739	597	93.5	8.3	9220	6	CQ492536	CQ492536 Sequence
c 525	95.5	8.5	140475	8	AP005558	598	93.5	8.3	9220	6	CQ493387	CQ493387 Sequence
c 526	95.5	8.5	145590	8	AC109601	599	93.5	8.3	9416	9	HUMSEQ	HUMSEQ Human micro
c 527	95.5	8.5	157397	8	AC133860	600	93.5	8.3	11474	1	AE014763	AE014763 Bifidobac
c 528	95.5	8.5	169184	2	AC144112	601	93.5	8.3	11917	6	AR454559	AR454559 Sequence
c 529	95.5	8.5	243899	5	AX510919	602	93.5	8.3	138994	2	AC141046	AC141046 Rattus no
c 530	95	8.4	623	4	BY226857S08	603	93.5	8.3	148433	9	AC012609	AC012609 Homo sapi
c 531	95	8.4	4498	10	MMU91922	604	93.5	8.3	152177	5	AL935114	AL935114 Zebrafish
c 532	95	8.4	5018	3	AC006797	605	93.5	8.3	166138	9	AC099684	AC099684 Homo sapi
c 533	95	8.4	6478	8	AB023040	606	93.5	8.3	202269	9	AC130689	AC130689 Homo sapi
c 534	95	8.4	10101	1	AE012376	607	93.5	8.3	214146	2	AC096822	AC096822 Rattus no
c 535	95	8.4	114020	10	AC127596	608	93.5	8.3	246566	2	AC097926	AC097926 Rattus no
c 536	95	8.4	159547	2	AC073674	609	93.5	8.3	254733	3	AC117075	AC117075 Dictyoste
c 537	95	8.4	173369	10	AL928966	610	93.5	8.3	263297	2	AC127631	AC127631 Rattus no
c 538	95	8.4	258181	2	AC096936	611	93.5	8.3	313800	1	SCO939114	SCO939114 Streptomy
c 539	95	8.4	302550	1	AP006581	612	93.5	8.3	321250	1	SCO939111	SCO939111 Streptomy
c 540	95	8.4	349607	1	BX957222	613	93.5	8.3	349980	6	AX492786	AX492786 Sequence
c 541	94.5	8.4	907	1	GV17274	614	93.5	8.3	349980	6	AX553953	AX553953 Sequence
c 542	94.5	8.4	948	1	AV331318	615	93	8.3	1321	6	AR097540	AR097540 Sequence
c 543	94.5	8.4	948	1	AV331321	616	93	8.3	1378	1	AY127885	AY127885 Anaplasma
c 544	94.5	8.4	948	1	AV331322	617	93	8.3	1995	6	C0782648	C0782648 Sequence
c 545	94.5	8.4	948	1	AV331323	618	93	8.3	1995	6	BD127244	BD127244 Primer fo
c 546	94.5	8.4	948	1	AV331324	619	93	8.3	1995	9	AK074718	AK074718 Homo sapi
c 547	94.5	8.4	1372	6	CQ596994	620	93	8.3	2105	5	BC081615	BC081615 Danio rer
c 548	94.5	8.4	2155	9	S52488	621	93	8.3	3036	3	AY245772	AY245772 Monosiga
c 549	94.5	8.4	2168	3	BT001711	622	93	8.3	4849	3	AK113070	AK113070 Ciona int
c 550	94.5	8.4	2407	8	LTE532549	623	93	8.3	4977	1	CDCMANA	CDCMANA Caldocellum
c 551	94.5	8.4	2690	3	DPU20332	624	93	8.3	5931	6	C0607290	C0607290 Sequence
c 552	94.5	8.4	3421	3	AY060306	625	93	8.3	7931	6	C0607289	C0607289 Sequence
c 553	94.5	8.4	4492	6	CQ596993	626	93	8.3	15900	2	AC017311	AC017311 Drosophil
c 554	94.5	8.4	5388	6	CQ608451	627	93	8.3	35307	2	AC014905	AC014905 Drosophil
c 555	94.5	8.4	7782	6	CQ608450	628	93	8.3	107480	9	AL596094	AL596094 Human DNA
c 556	94.5	8.4	8426	2	AC013966	629	93	8.3	110000	2	AL732359_06	AL732359_06 Continuation (7 of
c 557	94.5	8.4	8664	3	LMFL6823	630	93	8.3	162329	2	CR381583	CR381583 Danio rer
c 558	94.5	8.4	24492	3	DMC5667	631	93	8.3	164223	10	AC127228	AC127228 Mus muscu
c 559	94.5	8.4	110000	2	LMFLCHR36_01	632	93	8.3	180498	3	AC009847	AC009847 Drosophil
c 560	94.5	8.4	121705	9	AC006452	633	93	8.3	198162	5	BX323985	BX323985 Zebrafish
c 561	94.5	8.4	125862	9	AC026696	634	93	8.3	208145	2	AC053504	AC053504 Homo sapi
c 562	94.5	8.4	132151	8	AC144491	635	93	8.3	226307	10	AC119851	AC119851 Mus muscu
c 563	94.5	8.4	160738	8	AC073556	636	93	8.3	244978	2	AC128734	AC128734 Rattus no
c 564	94.5	8.4	174801	2	AC014376	637	93	8.3	260091	2	AC134021	AC134021 Rattus no
c 565	94.5	8.4	177096	3	AC107326	638	93	8.3	265602	2	AC107184	AC107184 Rattus no
c 566	94.5	8.4	179838	3	AC091220	639	93	8.3	301129	3	AE003785	AE003785 Drosophil
c 567	94.5	8.4	181063	3	AC010107	640	92.5	8.2	1247	10	AY262758	AY262758 Mus muscu
c 568	94.5	8.4	198222	2	AC092429	641	92.5	8.2	2556	10	AY269789	AY269789 Mus muscu
c 569	94.5	8.4	216860	10	AC134793	642	92.5	8.2	2589	6	I32212	I32212 Sequence 3
c 570	94.5	8.4	285860	3	AE003551	643	92.5	8.2	2685	6	A39780	A39780 Sequence 14
c 571	94.5	8.4	297050	1	AP006569	644	92.5	8.2	2685	6	A74265	A74265 Sequence 21
c 572	94.5	8.4	304204	3	AE003421	645	92.5	8.2	2967	1	AY184164	AY184164 Chlamydia
c 573	94	8.4	700	9	S72412	646	92.5	8.2	2967	1	AY184165	AY184165 Chlamydia
c 574	94	8.4	2346	3	TCCP69GNA	647	92.5	8.2	2967	1	AY184166	AY184166 Chlamydia
c 575	94	8.4	110000	1	AP006618_28	648	92.5	8.2	3606	10	AB107882	AB107882 Mus muscu
c 576	94	8.4	121377	8	AP004038	649	92.5	8.2	4614	6	BD271910	BD271910 Process f
c 577	94	8.4	137046	8	AP004775	650	92.5	8.2	4614	6	I32211	I32211 Sequence 1
c 578	94	8.4	212159	2	AC113023	651	92.5	8.2	5500	4	AY212921	AY212921 Oryctolag
c 579	94	8.4	292100	1	SC0939121	652	92.5	8.2	5743	8	SGFL01	SGFL01 S.cerevisia
c 580	94	8.4	297950	1	AP006582	653	92.5	8.2	2753	2	AC017598	AC017598 Drosophil
c 581	94	8.4	302040	1	AE017317	654	92.5	8.2	32481	3	U21310	U21310 Caenorhabdi
c 582	94	8.4	349028	1	EX640413	655	92.5	8.2	3359	3	CEP55B11	CEP55B11 Caenorhabdi
c 583	93.5	8.3	757	10	BC021401	656	92.5	8.2	36604	14	AY530877	AY530877 Simian ad
c 584	93.5	8.3	826	5	CHKLNRP4	657	92.5	8.2	38573	2	AC017717	AC017717 Drosophil
c 585	93.5	8.3	1070	8	AK061303	658	92.5	8.2	54812	8	YSCCHR1RAA	YSCCHR1RAA Saccharomyc
c 586	93.5	8.3	1172	8	AK104138	659	92.5	8.2	82064	2	AC006937	AC006937 Drosophil
c 587	93.5	8.3	1175	8	AK104400	660	92.5	8.2	93134	8	BX908807	BX908807 Neurospor
c 588	93.5	8.3	1194	14	AU626543	661	92.5	8.2	134511	2	AC149927	AC149927 Strongylo



[illegible]

954	89	7.9	1640	8	DI7320	D17320 Candida tro	1027	89	7.9	298900	1	AP005937	AP005937 Bradyrhiz
955	89	7.9	1789	10	BC034162	BC034162 Mus muscu	c1028	89	7.9	300217	1	AE016922	AE016922 Chromobac
c 956	89	7.9	2090	4	AF529269	AF529269 Ovis arie	1029	89	7.9	341346	1	AC146873	AC146873 Xenopus t
957	89	7.9	2298	3	AF317090	AF317090 Drosophil	c1030	88.5	7.9	300	8	CR377485	CR377485 Pinus pin
958	89	7.9	2339	9	BC021288	BC021288 Homo sapi	c1031	88.5	7.9	651	3	AY515020	AY515020 Eulimnadi
959	89	7.9	2409	6	E11341	E11341 Cellulase g	1032	88.5	7.9	948	1	AY331337	AY331337 Pseudomon
960	89	7.9	2409	6	AR213262	AR213262 Sequence	1033	88.5	7.9	1216	8	AY667097	AY667097 Aegilops
961	89	7.9	2416	9	AK092398	AK092398 Homo sapi	1034	88.5	7.9	1799	5	GGNEU27	Y14350 Gallus gall
962	89	7.9	2455	6	I55036	I55036 Sequence 1	1035	88.5	7.9	1962	3	DOAMY1	X76240 D. pseudoob
963	89	7.9	2455	9	HUM1A	J04182 Homo sapien	1036	88.5	7.9	2310	6	BD263729	BD263729 Modified
964	89	7.9	2649	8	AB048710	AB048710 Humicola	1037	88.5	7.9	2310	6	AR474254	AR474254 Sequence
965	89	7.9	2712	6	E01813	E01813 cDNA encodi	1038	88.5	7.9	2535	6	BD263721	BD263721 Modified
966	89	7.9	2716	6	E02135	E02135 cDNA encodi	1039	88.5	7.9	2535	6	AR474246	AR474246 Sequence
967	89	7.9	3177	8	AB001030	AB001030 Humicola	c1040	88.5	7.9	2665	6	CQ611648	CQ611648 Sequence
c 968	89	7.9	3183	6	C0596669	C0596669 Sequence	1041	88.5	7.9	4068	3	AY582941	AY582941 Litomosoi
969	89	7.9	3762	3	AX052017	AX052017 Drosophil	1042	88.5	7.9	9031	9	HSR291390	AJ291390 Homo sapi
970	89	7.9	4736	2	AC014951	AC014951 Drosophil	c1043	88.5	7.9	10481	1	AE012541	AE012541 Xanthomon
971	89	7.9	5162	1	AF151965	AF151965 Pseudomon	c1044	88.5	7.9	18088	1	AE004447	AE004447 Pseudomon
c 972	89	7.9	5618	1	ECNIRBC	X14202 E. coli nir	1045	88.5	7.9	26449	3	U23449	U23449 Caenorhabdi
973	89	7.9	6751	3	DMSG8378	X01918 Drosophila	c1046	88.5	7.9	73005	1	EX571966	EX571966 31
c 974	89	7.9	8660	1	AF153207	AF153207 Pseudomon	c1047	88.5	7.9	110000	1	AP006618	AP006618 57
c 975	89	7.9	9677	8	AY495602	AY495602 Gibberell	c1048	88.5	7.9	110000	2	AC095208	AC095208 70
c 976	89	7.9	11449	1	AB005078	AB005078 Halobacte	1049	88.5	7.9	110000	2	AC095248	AC095248 3
977	89	7.9	13496	3	DAU53698	US3698 Drosophila	1050	88.5	7.9	110000	2	AP006501	AP006501 08
c 978	89	7.9	14782	1	AY118081	AY118081 Streptomy	1051	88.5	7.9	110000	2	LMFLCHR36	LMFLCHR36 02
c 979	89	7.9	54695	2	AC010004	AC010004 Drosophil	1052	88.5	7.9	110000	8	CR382129	CR382129 25
980	89	7.9	56127	2	AC100393	AC100393 Mus muscu	1053	88.5	7.9	110000	8	CR382132	CR382132 24
c 981	89	7.9	83340	3	AC004438	AC004438 Drosophil	c1054	88.5	7.9	133894	6	A48542	A48542 Sequence 1
982	89	7.9	98832	9	AL137127	AL137127 Human DNA	c1055	88.5	7.9	133894	14	L22858	L22858 Autographa
983	89	7.9	99890	3	AC084464	AC084464 Caenorhab	c1056	88.5	7.9	148481	2	CR548627	CR548627 Danio rer
984	89	7.9	101762	5	AL928854	AL928854 Zebrafish	c1057	88.5	7.9	151449	9	AL954244	AL954244 Pan trogl
c 985	89	7.9	110000	1	U00096 34	Continuation (35 o	1058	88.5	7.9	160173	2	AC141008	AC141008 Rattus no
c 986	89	7.9	110000	1	EC0W67 2	Continuation (3 of	c1059	88.5	7.9	162180	9	AC124287	AC124287 Homo sapi
987	89	7.9	110000	8	CR382128	Continuation (25 o	c1060	88.5	7.9	166000	3	AC104511	AC104511 Drosophil
988	89	7.9	110000	8	CR382132	Continuation (7 of	1061	88.5	7.9	167131	8	CNS08C8L	AL733881 Oryza sat
989	89	7.9	110000	8	CR382136	Continuation (4 of	c1062	88.5	7.9	173299	2	AC120815	AC120815 Rattus no
990	89	7.9	125623	3	AC115599	AC115599 Dictyoste	1063	88.5	7.9	187712	2	AC120815	AC120815 Rattus no
991	89	7.9	132891	2	EX088564	EX088564 Danio rer	1064	88.5	7.9	190676	2	AC084747	AC084747 Mus muscu
c 992	89	7.9	136171	2	AC141946	AC141946 Rattus no	1065	88.5	7.9	199152	2	CR382297	CR382297 Danio rer
c 993	89	7.9	137477	5	BX004882	BX004882 Zebrafish	c1066	88.5	7.9	199916	3	AC008099	AC008099 Drosophil
c 994	89	7.9	140327	2	AF003938	AF003938 Oryza sat	c1067	88.5	7.9	206851	2	AC094583	AC094583 Rattus no
c 995	89	7.9	142000	9	AC095353	AC095353 Homo sapi	c1068	88.5	7.9	214332	2	AC120945	AC120945 Rattus no
c 996	89	7.9	150695	2	AC023576	AC023576 Homo sapi	1069	88.5	7.9	214911	2	AC098924	AC098924 Rattus no
c 997	89	7.9	157947	8	OSJN00260	AL731614 Oryza sat	1070	88.5	7.9	215566	10	AC119805	AC119805 Mus muscu
c 998	89	7.9	160982	2	CR786564	CR786564 Danio rer	c1071	88.5	7.9	216379	9	AL954243	AL954243 Pan trogl
999	89	7.9	163063	10	BX813333	BX813333 Mouse DNA	c1072	88.5	7.9	220742	2	AC105644	AC105644 Rattus no
1000	89	7.9	167076	2	AC128174	AC128174 Rattus no	1073	88.5	7.9	224500	2	AC136530	AC136530 Rattus no
1001	89	7.9	167333	8	AC147856	AC147856 Ateleleix	c1074	88.5	7.9	227442	2	AC111515	AC111515 Rattus no
c1002	89	7.9	173301	8	AF003539	AF003539 Oryza sat	c1075	88.5	7.9	227769	2	AC112437	AC112437 Rattus no
1003	89	7.9	173570	2	CR457484	CR457484 Danio rer	c1076	88.5	7.9	231008	2	AC129166	AC129166 Rattus no
1004	89	7.9	174773	5	CR383662	CR383662 Zebrafish	c1077	88.5	7.9	241974	2	AC095601	AC095601 Rattus no
c1005	89	7.9	185249	2	OSJN00223	AL731585 Oryza sat	c1078	88.5	7.9	242139	2	AC095431	AC095431 Rattus no
1006	89	7.9	186474	2	AL831728	AL831728 Mus muscu	c1079	88.5	7.9	242463	2	AC095409	AC095409 Rattus no
1007	89	7.9	188653	3	AC010033	AC010033 Drosophil	c1080	88.5	7.9	246199	2	AC119558	AC119558 Rattus no
c1008	89	7.9	190948	2	AC036131	AC036131 Homo sapi	c1081	88.5	7.9	253567	2	AC113827	AC113827 Rattus no
1009	89	7.9	191512	2	BX914207	BX914207 Danio rer	1082	88.5	7.9	254175	2	AC096015	AC096015 Rattus no
1010	89	7.9	193552	2	AC068463	AC068463 Homo sapi	1083	88.5	7.9	257028	2	AC129248	AC129248 Rattus no
1011	89	7.9	195252	9	AC097511	AC097511 Homo sapi	1084	88.5	7.9	283883	2	AC126084	AC126084 Rattus no
c1012	89	7.9	211118	2	AC073752	AC073752 Mus muscu	1085	88.5	7.9	301399	1	AE017233	AE017233 Mycobacte
1013	89	7.9	218243	2	AC141505	AC141505 Rattus no	c1086	88.5	7.9	308750	1	AP005216	AP005216 Corynebac
c1014	89	7.9	228855	2	AC096703	AC096703 Rattus no	1087	88.5	7.9	313096	2	AC131879	AC131879 Rattus no
c1015	89	7.9	235435	2	AC094124	AC094124 Rattus no	1088	88.5	7.9	330401	3	AE003575	AE003575 Drosophil
c1016	89	7.9	235468	10	AC105586	AC105586 Rattus no	1089	88.5	7.9	332029	3	AE003491	AE003491 Drosophil
1017	89	7.9	237423	2	AC149593	AC149593 Mus muscu	c1090	88.5	7.9	346357	1	EX842647	EX842647 Bdellovib
1018	89	7.9	240691	2	AC115178	AC115178 Rattus no	1091	88	7.8	310	4	AF159384	AF159384 Sus scrofa
c1019	89	7.9	244742	2	AC125663	AC125663 Rattus no	1092	88	7.8	1017	11	CNS06EFT	ALJ395055 T7 end of
c1020	89	7.9	246143	2	AC127063	AC127063 Rattus no	1093	88	7.8	1618	8	CRECPN1C	L27473 Chlamydomon
1021	89	7.9	249691	2	AC096154	AC096154 Rattus no	1094	88	7.8	1662	6	CQ733018	CQ733018 Sequence
1022	89	7.9	249994	2	AC103191	AC103191 Rattus no	1095	88	7.8	1701	6	CQ829353	CQ829353 Sequence
1023	89	7.9	261278	2	AC130742	AC130742 Rattus no	1096	88	7.8	1738	9	HS272L161	AL049588 Human gen
1024	89	7.9	267459	2	AC118927	AC118927 Mus muscu	c1097	88	7.8	1804	8	AK073372	AK073372 Oryza sat
1025	89	7.9	269572	2	AC108552	AC108552 Rattus no	c1098	88	7.8	1852	9	AK129672	AK129672 Homo sapi
1026	89	7.9	280394	3	AE003544	AE003544 Drosophil	c1099	88	7.8	1917	9	AK093489	AK093489 Homo sapi

1100	88	7.8	1946	6	CQ588132	Sequence	1173	88	7.8	34866	1	BX640426
1101	88	7.8	1946	6	AX254510	Sequence	1174	88	7.8	34980	6	AX492783
c1102	88	7.8	1955	6	AX833072	Sequence	1175	88	7.8	34980	6	AX53950
c1103	88	7.8	1955	9	AK094497	Homo sapi	1176	87.5	7.8	543	3	AF457962
1104	88	7.8	2148	9	AF253321	Homo sapi	1177	87.5	7.8	712	3	AK174897
1105	88	7.8	2165	6	AR339318	Sequence	1178	87.5	7.8	759	6	AB7197
1106	88	7.8	2198	6	CQ723340	Sequence	1179	87.5	7.8	759	6	AB7580
1107	88	7.8	2447	6	AX399682	Sequence	1180	87.5	7.8	770	6	AB7196
1108	88	7.8	2456	8	AK107164	Oryza sat	1181	87.5	7.8	770	6	AB7579
1109	88	7.8	2474	9	BC032787	Homo sapi	1182	87.5	7.8	823	8	AK062502
1110	88	7.8	2580	8	ATH011641	Arabidops	1183	87.5	7.8	834	8	TA6133613
1111	88	7.8	2612	9	AK095713	Homo sapi	1184	87.5	7.8	914	8	AK102186
1112	88	7.8	2717	8	YL7SR1	Y. lipolytic	1185	87.5	7.8	1358	8	AY197773
1113	88	7.8	2821	8	AK099800	Oryza sat	1186	87.5	7.8	1449	3	AK116662
1114	88	7.8	2890	3	AY122212	Drosophil	1187	87.5	7.8	1539	8	AB018537
1115	88	7.8	3153	8	AK066544	Oryza sat	1188	87.5	7.8	1611	10	NMU70651
1116	88	7.8	3227	3	AB095267	AB095267 Babesia c	1189	87.5	7.8	2036	8	AF465468
c1117	88	7.8	3946	6	CQ588131	Sequence	1190	87.5	7.8	2298	8	AF356870
c1118	88	7.8	3946	6	AX254509	Sequence	1191	87.5	7.8	2484	9	BC021557
c1119	88	7.8	4338	10	RNCNG41	AJ000496 Rattus no	c1192	87.5	7.8	2525	1	SCDNAFABD
1120	88	7.8	4971	8	AF201084	AF201084 Secale ce	1193	87.5	7.8	2561	9	AB045292
c1121	88	7.8	10006	1	AE009473	AE009473 Brucella	1194	87.5	7.8	2578	6	BD134612
1122	88	7.8	10626	1	AE014464	AE014464 Brucella	c1195	87.5	7.8	2589	3	AK115983
1123	88	7.8	11106	1	AE012183	AE012183 Xanthomon	c1196	87.5	7.8	2713	10	MMZFV
1124	88	7.8	12829	1	AE014692	AE014692 Bifidobac	c1197	87.5	7.8	3306	1	CFCENC
1125	88	7.8	16114	3	AB062881	AB062881 Mytilus g	1198	87.5	7.8	3671	14	ADEPP
c1126	88	7.8	28291	3	CEP5689	274473 Caenorhabdi	1199	87.5	7.8	5249	4	S67307
c1127	88	7.8	31685	3	U67956	U67956 Caenorhabdi	1200	87.5	7.8	5275	6	AR012622
c1128	88	7.8	51531	2	AC017444	AC017444 Drosophil	1201	87.5	7.8	5275	6	AR028465
c1129	88	7.8	69644	1	AY179507	AY179507 Streptomy	1202	87.5	7.8	5275	6	AR078217
c1130	88	7.8	80167	2	AC1020038	AC1020038 Drosophil	1203	87.5	7.8	5275	6	AR177781
1131	88	7.8	92770	8	AC138854	AC138854 Magnapor	1204	87.5	7.8	5275	6	I75051
1132	88	7.8	106973	8	UR9959	UR9959 Arabidopsis	c1205	87.5	7.8	10280	1	AE004808
1133	88	7.8	110000	8	CR382128_04	Continuation (5 of	1206	87.5	7.8	10643	1	AE011581
1134	88	7.8	110000	8	CR382128_05	Continuation (6 of	c1207	87.5	7.8	11712	1	AE011976
1135	88	7.8	12820	8	CR382130_16	Continuation (17 of	c1208	87.5	7.8	14198	1	AE011967
c1136	88	7.8	143561	2	AP004123	AP004123 Oryza sat	1209	87.5	7.8	14568	1	AE004453
c1137	88	7.8	153749	2	CR318598	CR318598 Danio rer	c1210	87.5	7.8	25821	2	AC013226
c1138	88	7.8	153749	8	AP003019	AP003019 Oryza sat	c1211	87.5	7.8	92294	1	AY117439
1139	88	7.8	155366	5	BX294662	BX294662 Zebrafish	c1212	87.5	7.8	94287	1	AP005645
c1140	88	7.8	166093	10	AL714011	AL714011 Mouse DNA	1213	87.5	7.8	106859	9	AL512626
1141	88	7.8	167475	10	AC090881	AC090881 Mus muscu	1214	87.5	7.8	110000	1	AE017282_23
c1142	88	7.8	168339	5	BX004999	BX004999 Zebrafish	c1215	87.5	7.8	110000	2	AC138524_0
c1143	88	7.8	168949	9	AC046134	AC046134 Homo sapi	1216	87.5	7.8	110000	2	LMFLCHR12_12
c1144	88	7.8	169138	3	AC010571	AC010571 Drosophil	1217	87.5	7.8	110000	2	LMFLCHR12_13
1145	88	7.8	170240	8	AP005869	AP005869 Oryza sat	1218	87.5	7.8	110000	8	CR382128_25
c1146	88	7.8	171329	2	AC147785	AC147785 Pan trogl	c1219	87.5	7.8	110000	9	AY528719_1
c1147	88	7.8	179661	2	CR318647	CR318647 Danio rer	1220	87.5	7.8	113212	9	AL513355
1148	88	7.8	184321	2	AC025890	AC025890 Homo sapi	c1221	87.5	7.8	117099	8	AP003572
c1149	88	7.8	186939	2	CR450728	CR450728 Danio rer	c1222	87.5	7.8	120138	2	AC024624
1150	88	7.8	194785	2	AC136047	AC136047 Rattus no	1223	87.5	7.8	127643	5	BX321877
c1151	88	7.8	200906	2	BX649457	BX649457 Danio rer	1224	87.5	7.8	143178	2	BX005034
1152	88	7.8	204579	2	CR354552	CR354552 Danio rer	c1225	87.5	7.8	144386	8	AP003538
c1153	88	7.8	207091	10	AC079443	AC079443 Mus muscu	c1226	87.5	7.8	145524	2	AC016777
c1154	88	7.8	208564	2	AC093936	AC093936 Rattus no	1227	87.5	7.8	147640	2	AP003542
1155	88	7.8	209797	5	AC146541	AC146541 Gasterost	c1228	87.5	7.8	152668	9	AC142291
c1156	88	7.8	214819	2	AC145079	AC145079 Mus muscu	1229	87.5	7.8	154153	9	AL445933
1157	88	7.8	227319	10	AC119894	AC119894 Mus muscu	1230	87.5	7.8	156102	7	AY129337
c1158	88	7.8	227781	2	BX649554	BX649554 Rattus no	c1231	87.5	7.8	157141	3	AC016445
1159	88	7.8	237193	2	AC108555	AC108555 Rattus no	1232	87.5	7.8	163432	2	AC073982
1160	88	7.8	238090	2	AC135202	AC135202 Rattus no	c1233	87.5	7.8	169247	9	AL669970
c1161	88	7.8	248550	2	SC0939120	AC139120 Streptomy	1234	87.5	7.8	170507	9	AC087530
c1162	88	7.8	252352	1	BX545917	BX545917 Danio rer	c1235	87.5	7.8	173639	10	AL606921
c1163	88	7.8	258158	2	BX957297	BX957297 Danio rer	c1236	87.5	7.8	176349	2	AC122679
1164	88	7.8	262812	2	BX510345	BX510345 Danio rer	1237	87.5	7.8	176918	2	AC109613
c1165	88	7.8	294272	3	AE003595	AE003595 Drosophil	c1238	87.5	7.8	177855	3	AC010211
1166	88	7.8	300150	1	AP004598	AP004598 Oceanobac	c1239	87.5	7.8	182041	2	AC023025
c1167	88	7.8	300425	1	AP005041	AP005041 Streptomy	c1240	87.5	7.8	182916	9	AC112482
1168	88	7.8	304985	2	CR385070	CR385070 Danio rer	1241	87.5	7.8	190563	2	BX927257
c1169	88	7.8	309904	1	AE016865	AE016865 Pseudomon	1242	87.5	7.8	192096	2	AC126838
c1170	88	7.8	329861	1	NMA522491	AL162756 Neisseria	c1243	87.5	7.8	192410	2	AC135831
1171	88	7.8	334520	1	AP003588	AP003588 Nostoc sp	1244	87.5	7.8	207439	14	AY509253
1172	88	7.8	348624	1	BX640441	BX640441 Bordetell	c1245	87.5	7.8	208978	2	AC101932

c1246	87.5	7.8	209844	9	AC011495	AC011495 Homo sapi	1319	87	7.7	176231	3	AC008367	AC008367 Drosophil
1247	87.5	7.8	219254	2	AC122677	AC122677 Rattus no	1320	87	7.7	180139	10	AC012297	AC012297 Mus muscu
c1248	87.5	7.8	230278	14	MCU68299	U68299 Mouse cytom	c1321	87	7.7	183914	2	AC069331	AC069331 Homo sapi
1249	87.5	7.8	234684	10	AC1133618	AC1133618 Rattus no	1322	87	7.7	185644	9	AC087455	AC087455 Homo sapi
1250	87.5	7.8	235095	10	AC115361	AC115361 Mus muscu	1323	87	7.7	192540	3	AC010846	AC010846 Drosophil
c1251	87.5	7.8	243351	2	AC119616	AC119616 Rattus no	1324	87	7.7	193273	2	AC012054	AC012054 Homo sapi
1252	87.5	7.8	244813	2	AC097868	AC097868 Rattus no	c1325	87	7.7	198318	2	EX957253	EX957253 Danio rer
c1253	87.5	7.8	251269	2	AC119030	AC119030 Rattus no	c1326	87	7.7	200274	9	AC115088	AC115088 Homo sapi
c1254	87.5	7.8	253611	2	AC111473	AC111473 Rattus no	1327	87	7.7	200771	2	AC133587	AC133587 Homo sapi
1255	87.5	7.8	292641	3	AE003600	AE003600 Drosophil	c1328	87	7.7	205825	2	AP000881	AP000881 Homo sapi
1256	87.5	7.8	299950	1	AP005963	AP005963 Bradyrhiz	1329	87	7.7	210719	2	AC087646	AC087646 Homo sapi
c1257	87.5	7.8	300800	1	SC0939112	AP0939112 Streptomy	1330	87	7.7	213217	2	CR356230	CR356230 Danio rer
c1258	87.5	7.8	301925	1	AP005046	AP005046 Streptomy	c1331	87	7.7	213359	2	AC069006	AC069006 Homo sapi
c1259	87.5	7.8	343504	2	AL158031	AL158031 Homo sapi	c1332	87	7.7	218631	2	AC109532	AC109532 Rattus no
1260	87	7.7	705	10	RNMUC1NR	Z29072 R.norvegicu	1333	87	7.7	219180	2	AC092251	AC092251 Mus muscu
1261	87	7.7	765	10	BC021158	BC021158 Mus muscu	c1334	87	7.7	221911	2	AC114095	AC114095 Rattus no
1262	87	7.7	790	6	AR560749	AR560749 Sequence	c1335	87	7.7	231001	2	AC130981	AC130981 Rattus no
1263	87	7.7	840	8	TA6416337	TA6416337 Triticum	c1336	87	7.7	233804	10	AC130831	AC130831 Mus muscu
1264	87	7.7	867	6	AR279196	AR279196 Sequence	c1337	87	7.7	235050	2	AC106979	AC106979 Rattus no
1265	87	7.7	867	6	AR279197	AR279197 Sequence	c1338	87	7.7	241420	2	AC094501	AC094501 Rattus no
1266	87	7.7	901	8	ALO389713	AJ389713 Aegilops	1339	87	7.7	284274	2	AC117062	AC117062 Escherich
1267	87	7.7	902	8	ABI389711	AJ389711 Aegilops	c1340	87	7.7	300359	1	AE016767	AE016767 Escherich
1268	87	7.7	902	8	ABI389712	AJ389712 Aegilops	c1341	87	7.7	302070	1	AP005223	AP005223 Corynebac
1269	87	7.7	927	8	ABI75312	AF175312 Triticum	1342	87	7.7	304713	3	AE003502	AE003502 Drosophil
1270	87	7.7	936	8	AY338388	AY338388 Triticum	1343	86.5	7.7	515	3	LM1251079	LM1251079 Locusta m
1271	87	7.7	1030	10	BC042902	BC042902 Mus muscu	1344	86.5	7.7	813	6	AX587914	AX587914 Sequence
1272	87	7.7	1178	8	AF234650	AF234650 Triticum	1345	86.5	7.7	948	1	AY331329	AY331329 Pseudomon
1273	87	7.7	1397	6	AR279198	AR279198 Sequence	c1346	86.5	7.7	1008	12	AY659220	AY659220 Synthetic
c1274	87	7.7	1397	6	AR279199	AR279199 Sequence	1347	86.5	7.7	1052	3	AF167708	AF167708 Toxocara
1275	87	7.7	1397	8	WHITGLIG	ML6064 Wheat (T. ae	1348	86.5	7.7	1100	3	DNUS1236	US1236 Drosophila
1276	87	7.7	1658	8	D17321	D17321 Candida tro	c1349	86.5	7.7	1145	8	TATFTIID	Y59874 T.aestivum
1277	87	7.7	1990	8	AK107421	AK107421 Oryza sat	1350	86.5	7.7	1239	3	DNAMY3	Y15605 Drosophila
1278	87	7.7	2167	8	CFPS17	Y14554 Cladoeporiu	1351	86.5	7.7	1297	6	C0859343	C0859343 Sequence
1279	87	7.7	2464	9	AF428261	AF428261 Homo sapi	1352	86.5	7.7	1368	6	A10377	A10377 Artificial
1280	87	7.7	3393	6	C0794770	C0794770 Sequence	1353	86.5	7.7	1378	5	XELSPA	M19971 X.laevis sp
1281	87	7.7	4569	5	XUIMB1	Y08296 X.laevis mR	c1354	86.5	7.7	1815	6	AX654840	AX654840 Sequence
1282	87	7.7	7056	1	AF042494	AF042494 Sulfolobu	1355	86.5	7.7	1910	8	AK100984	AK100984 Oryza sat
c1283	87	7.7	7417	6	C0594035	C0594035 Sequence	c1356	86.5	7.7	2015	6	AX660204	AX660204 Sequence
1284	87	7.7	7921	3	AF153362	AF153362 Dictyoste	c1357	86.5	7.7	2067	8	AK061588	AK061588 Oryza sat
c1285	87	7.7	8778	10	MMU27268	U27268 Mus musculu	c1358	86.5	7.7	2113	8	AK099094	AK099094 Oryza sat
1286	87	7.7	10177	1	AE004977	AE004977 Halobacte	1359	86.5	7.7	2322	6	BD263727	BD263727 Modified
c1287	87	7.7	10885	1	AE006896	AE006896 Sulfolobu	1360	86.5	7.7	2322	6	AR474252	AR474252 Sequence
1288	87	7.7	11279	1	AE009940	AE009940 Pyrobacul	1361	86.5	7.7	2335	1	SSU46156	U46156 Synchrococc
c1289	87	7.7	11361	1	AE011741	AE011741 Xanthomon	1362	86.5	7.7	2541	6	BD263720	BD263720 Modified
1290	87	7.7	11434	1	AE001097	AE001097 Archaeogl	1363	86.5	7.7	2541	6	AR474245	AR474245 Sequence
1291	87	7.7	12713	6	C0580895	C0580895 Sequence	1364	86.5	7.7	2607	6	C0594036	C0594036 Sequence
c1292	87	7.7	16377	3	AP202180	AP202180 Plasmodi	1365	86.5	7.7	2940	1	AY184167	AY184167 Chlamydia
c1293	87	7.7	60101	9	AL672207	AL672207 Human DNA	1366	86.5	7.7	2940	1	AY184169	AY184169 Chlamydia
c1294	87	7.7	73424	2	AC129508	AC129508 Homo sapi	1367	86.5	7.7	2943	1	AY184168	AY184168 Chlamydia
1295	87	7.7	85740	2	AC014942	AC014942 Drosophil	1368	86.5	7.7	3079	9	HUMHGX13G	M26679 Homo sapien
c1296	87	7.7	92113	9	AC108070	AC108070 Homo sapi	1369	86.5	7.7	3079	11	HUMSW1229	G18274 human chrom
c1297	87	7.7	93381	2	HSDJ766D4	AL118504 Homo sapi	1370	86.5	7.7	3623	8	AK107281	AK107281 Oryza sat
c1298	87	7.7	103320	3	AC116920	AC116920 Dictyoste	1371	86.5	7.7	4435	6	AR428567	AR428567 Sequence
c1299	87	7.7	110000	2	AP006495	Continuation (8 of	1372	86.5	7.7	4435	6	BD078018	BD078018 Chlamydia
1300	87	7.7	110000	8	CR380957	Continuation (10 o	1373	86.5	7.7	5005	9	AE011099	AE011099 Homo sapi
1301	87	7.7	110000	8	CR380957	Continuation (11 o	1374	86.5	7.7	6658	6	AX427788	AX427788 Sequence
1302	87	7.7	110000	8	AP016919	Continuation (11 o	1375	86.5	7.7	6730	6	AX427823	AX427823 Sequence
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c1309	87	7.7	154080	5	AL953855	AL953855 Zebrafish	1382	86.5	7.7	10944	1	AE004771	AE004771 Pseudomon
1310	87	7.7	153472	9	AC026591	AC026591 Homo sapi	1383	86.5	7.7	33482	3	CEFT07C12	Z73976 Caenorhabdi
c1311	87	7.7	157011	2	AC140115	AC140115 Rattus no	c1384	86.5	7.7	42416	9	AC005551	AC005551 Homo sapi
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1318	87	7.7	174621	2	AC026968	AC026968 Homo sapi	1391	86.5	7.7	110000	1	EX571965	EX571965 Burkholdre



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1403	86.5	7.7	151806	8	AP002093	AP002093 Oryza sat	c1475	86	7.6	24232	3	CFC03E10	Z81458 Caenorhabdi
c1404	86.5	7.7	165571	2	CR450795	CR450795 Danio rer	c1476	86	7.6	32058	2	AC019925	Drosophil
1405	86.5	7.7	168788	2	CR318610	CR318610 Danio rer	c1477	86	7.6	33529	6	AR166425	Sequence
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c1407	86.5	7.7	171272	2	CR450726	CR450726 Danio rer	c1479	86	7.6	44266	1	AB047548	Pseudomon
c1408	86.5	7.7	172295	2	AC012268	AC012268 Homo sapi	c1480	86	7.6	52158	2	AC013185	AC013185 Drosophil
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## ALIGNMENTS

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LOCUS	AF127670	Homo sapiens	hyaluronic acid receptor (HAR)	mrna, complete cds.	
DEFINITION	AF127670				
ACCESSION	AF127670				
VERSION	AF127670.2	GI:10800121			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
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AUTHORS					
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REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
REMARK					
COMMENT					
FEATURES					
source					



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QY 141 ThrGlnThrThrGluPheIleValSerAspSerThrThrSerValAlaSerProTyrSer 160
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QY 201 GluProPheValGluAsnLysAlaPheLysAsnGluAlaAlaGlyPheGly 218
DB 849 GAACCATTTGTTGAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGA 902

RESULT 3
BD123566
LOCUS BD123566 1755 bp DNA linear PAT 18-SEP-2002
DEFINITION Secretory protein or membrane protein.
ACCESSION BD123566
VERSION BD123566.1 GI:23218511
KEYWORDS JP 2002017376-A/75.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1755)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: JP 2002017376-A 75 22-JAN-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002017376-A/75
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253173
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU
PI SUGIYAMA,
PI KOJI HAYASHI
PC
C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10,
PC C12P21/02,C12Q1/68//C12P21/08,C12N15/00,C12N5/00 CC
Secretory protein or membrane protein
FH Key Location/Qualifiers
FT CDS (201)..(1166).
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ORIGIN
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Pred. No.: 1125.00 Matches: 218
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Percent Similarity: 100.00% Mismatches: 0
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US-10-063-670-6_COPY_17_234 (1-218) x BD123566 (1-1755)

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QY 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40
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QY 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60

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DB 429 GCTTGAAGAGTAGCTTTGAAACTTGCAGCTATGCTGGTGGAGATGGATTGCTGGTC 488
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DB 849 GAACCATTTGTTGAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGA 902

RESULT 4
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LOCUS AK075443
DEFINITION Homo sapiens cDNA PSEC0135 fis, clone PLACE1004850, highly similar
to Homo sapiens lymphatic endothelium-specific hyaluronan receptor
LYVE-1 mRNA.
ACCESSION AK075443
VERSION AK075443.1 GI:22761535
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K.,
Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T.,
Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.
TITLE HRI human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1755)
AUTHORS Isogai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
sequencing, clone selection and full insert sequencing; Helix
Research Institute (supported by Japan Key Technology Center etc.);
cDNA library construction; Institute of Medical Science, University
of Tokyo, Laboratory of Genome Structure, Human Genome Center.
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/note="cloning vector: pME18SFL3"

ORIGIN

Alignment Scores: 6.08e-83 Length: 1755  
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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-063-670-6\_COPY\_17\_234 (1-218) x AK075443 (1-1755)

Qy 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20  
Db 249 ACGAGGCTCTTGTCCTCAAGGCTCTTTGGTCGACAGAGAGCTTTTCATCCAGGTGTCAATGC 308  
Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40  
Db 309 AGAATTATGGGGATCACCCCTTTGTGAGCAAAAAGGCGAACCCAGCAGCTGAATTTTCACAGAA 368  
Qy 41 AlalysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60  
Db 369 GCTAAGGAGGCTGTAGGCTCTGGAGCTTAAGTTGGCCGCAAGGACCAAGTTGAAACA 428  
Qy 61 AlaleuLysAlaSerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValVal 80  
Db 429 GCCTTGAAGGCTAGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGCTGTGGTC 488  
Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100  
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Qy 101 LysValProValSerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThr 120  
Db 549 AAGGTTCCAGTGAGCGGACAGTTTGCAGCCCTATTGTTACAACTCATCTGATCTGGACT 608  
Qy 121 AsnSerCysIleProGluIleThrThrLysAspProIlePheAsnThrGlnThrAla 140  
Db 609 AACTCGTGATCCAGAAATTTATCCACCAAGATCCCATATTTCAACACTCAAACTGCA 668  
Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160  
Db 669 ACACAAACACAGAAATTTATTGTGTCAGTCACAGTACCTACTCGGTGGCATCCCTTACTCT 728  
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RESULT 5

BD222718 2029 bp DNA linear PAT 17-JUL-2003  
LOCUS Human signal peptide-containing protein.  
DEFINITION BD222718  
ACCESSION BD222718.1 GI:33032488  
VERSION JP 2002519030-A/64.  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 2029)  
REFERENCE Lal, P., Tang, Y. T., Gorgone, G. A., Corley, N. C., Guegler, K. J.,  
AUTHORS Baughn, M. R., Akerblom, I. E., Young, J. A., Yue, H., Patterson, C.,  
Reddy, R., Hillman, J. L. and Bandman, O.  
Human signal peptide-containing protein

JOURNAL

Patent: JP 2002519030-A 64 02-JUL-2002;

COMMENT

OS Homo sapiens (human)  
PN JP 2002519030-A/64  
PD 02-JUL-2002  
PF 25-JUN-1999 JP 2000557363  
PR 26-JUN-1998 US 60/090762,31-JUL-1998 US 60/094983 PR  
01-OCT-1998 US 60/102686,11-DEC-1998 US 60/112129 PI PREETI  
LAL, Y. TOM TANG GINA A GORGONE, NEIL C CORLEY, KARL J PI GUEGLER,  
PI MARIAH R BAUGHN, INGRID E AKERBLOM, JANICE AU YOUNG, HENRY YUE,  
PI CHANDRA PATTERSON, ROOPA REDDY, JENNIFER L HILLMAN, OLGA BANDMAN  
PC C12N15/09, A61K38/00, A61K39/395, A61K45/00, A61P9/00, A61P15/00,  
PC A61P25/00,  
PC A61P29/00, A61P35/00, A61P43/00, C07K14/47, C07K16/18, C12N1/15, PC  
C12N1/19,  
PC C12N1/21, C12N5/10, C12P21/02, C12Q1/68, G01N33/68//C12P21/08, PC  
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PC A61K37/02, C12N5/00  
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FEATURES

source

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Query Match: 100.00% Indels: 0  
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Qy 61 AlaleuLysAlaSerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValVal 80  
Db 411 GCCTTGAAGCTAGCTTTGAAACTTGCAGCTATCGCTGGGTGGAGATGGAATTCGTGGTC 470  
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Qy 101 LysValProValSerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThr 120  
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Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160  
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Qy 161 ThrIleProAlaProThrThrThrProAlaProAlaSerThrSerIleProArgArg 180

Db 711 ACAATACCTGCCCTACTACTCTCTCTGCTCCAGCTTCCACTTCTACTTCCACGGAGA 770  
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Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218  
Db 831 GAACCATTTGTTGAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGA 884

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DEFINITION Sequence 13 from patent US 6368794.  
ACCESSION AR204700  
VERSION AR204700.1 GI:21502094  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2029)  
AUTHORS Daniel S., Gilmore, J., Stuart, S.G. and Stuve, L.L.  
TITLE Detection of altered expression of genes regulating cell proliferation  
JOURNAL Patent: US 6368794-A 13 09-APR-2002;  
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Best Local Similarity: 100.00% Mismatches: 0  
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US-10-063-670-6\_COPY\_17\_234 (1-218) x AR204700 (1-2029)

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Qy 101 LysValProValSerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThr 120  
Db 531 AAGGTTCCAGTGAGCGCAGTTTGCAGCTATTGTGTAACAATCATCTGATACCTGGACT 590

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Db 771 AAAAAATTGATTGTGTGCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAACT 830

Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218  
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DEFINITION Sequence 6722 from Patent WO2068579.  
ACCESSION CQ720788  
VERSION CQ720788.1 GI:42281645  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof  
JOURNAL Patent: WO 02068579-A 6722 06-SEP-2002;  
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Best Local Similarity: 100.00% Mismatches: 0  
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Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40  
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Qy 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValVal 80  
Db 320 GCCTTGAAGAGCTAGCTTTGAAACTTGCAGCTATAGCTGGTGGAGATGGATTCGTGTC 379

Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValIleuIleTrp 100  
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Qy 101 LysValProValSerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThr 120  
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Qy 121 AsnSerCysIleProGluIleThrThrLysAspProIlePheAsnThrGlnThrAla 140

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DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding the same.  
ACCESSION BD172392  
VERSION BD172392.1 GI:28413692  
KEYWORDS JP 2002223786-A/165.  
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ORGANISM Homo sapiens  
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1 (bases 1 to 2372)  
AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: JP 2002223786-A 165 13-AUG-2002;  
COMMENT GENENTECH INC  
OS Homo sapiens (human)  
PN JP 2002223786-A/165  
PD 13-AUG-2002  
PF 18-DEC-2001 JP 2001385135  
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR  
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24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066511 PR  
24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI  
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI  
JIAN ZHENG,  
PI JEAN YUAN  
PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC  
C12N5/10,  
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(C12P21/02, C12R1:645), C12N15/00, C12N5/00  
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encoding the same  
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Qy 41 AlalysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60  
Db 328 GCTAAGAGGCTGTAGGCTGCTGGAGTAAGTTTGGCCGCAAGGACCAAGTTGAAACA 387  
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Db 388 GCCTTGAAAGCTAGCTTTTGAACCTTGACAGCTATGCTGGGTGGAGATGGATTCTGTGTC 447  
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DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding the same.  
ACCESSION BD172711

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VERSION BD172711.1 GI:28414015
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SOURCE Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
Yuan, J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: JP 2002238586-A 165 27-AUG-2002;
GENENTECH INC
COMMENT OS Homo sapiens (human)
PN JP 2002238586-A/165
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385205
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24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066511 PR
24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
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PC C12P21/02//C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19),
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encoding the same
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Alignment Scores:
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-063-670-6_COPY_17_234 (1-218) x BD172711 (1-2372)
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DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding  
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ACCESSION BD173030  
VERSION BD173030.1 GI:28414336  
KEYWORDS JP 2002238587-A/165.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2372)  
AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and  
Yuan, J.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: JP 2002238587-A 165 27-AUG-2002;  
GENENTECH INC  
COMMENT OS Homo sapiens (human)  
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24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
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REFERENCE  1 (bases 1 to 2372)
AUTHORS   Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
            Yuan, J.
TITLE      Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL    Patent: JP 2002238588-A 165 27-AUG-2002;
            GENENTECH INC
COMMENT    OS Homo sapiens (human)
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            PD 27-AUG-2002
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            WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
            JIAN ZHENG,
            PI JEAN YUAN
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REFERENCE 1 (Bases 1 to 2372)  
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and  
Yuan,J.  
TITLE Secretory and transmembrane polypeptide and nucleic acid encoding  
the same  
JOURNAL Patent: JP 2002253280-A 165 10-SEP-2002;  
COMMENT GENENTECH INC  
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PN JP 2002253280-A/165  
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VERSION	AR410761.1 GI:40162261		
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ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2372)		
	Ashkenazi, A., Botstein, D., Desnovers, L., Eaton, D.L., Ferrara, N.,		
	Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E.,		
	Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J.,		
	KlJavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A.,		
	Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
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Db	328	GCTAAGGAGGCTGTAGGCTGTGGACTAAGTTTGGCCGCGCAAGGACCAAGTTGAACA	387		
Qy	61	AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal	80		
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	Ashkenazi, A., Botstein, D., Desnovers, L., Eaton, D.L., Ferrara, N.,				
	Filvaroff, E., Fong, S., Gao, W.-O., Gerber, H., Gerritsen, M.E.,				
	Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J.,				
	KlJavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A.,				
	Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.				
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same				
JOURNAL	Patent: US 6635468-A 200 21-OCT-2003;				
FEATURES	Location/Qualifiers				
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ORIGIN	.				
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Alignment Scores:

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Percent Similarity: 100.00% Conservatives: 0  
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DB: 6 Gaps: 0

US-10-063-670-6\_COPY\_17\_234 (1-218) x AR410761 (1-2372)

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Qy	21	ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu	40
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Qy	41	AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr	60
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Qy	61	AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal	80
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Qy	81	IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp	100
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Qy	101	LysValProValSerArgGlnPheAlaTyrCysTyrAsnSerSerAspThrTrpThr	120
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Db	628	ACACAAACACAGAAATTTATTGTGACGACAGTACCTACTCGGTGGCATCCCTTACTCT	687
Qy	161	ThrIleProAlaProThrThrProProAlaProAlaSerThrSerIleProArgArg	180
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DEFINITION	Sequence 200 from patent US 6664376.		
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VERSION	AR439125.1 GI:42664974		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2372)		
	Ashkenazi, A., Botstein, D., Desnovers, L., Eaton, D.L., Ferrara, N.,		
	Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E.,		
	Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J.,		
	KlJavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A.,		
	Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		

JOURNAL Patent: US 6664376-A 200 16-DEC-2003;  
FEATURES Location/Qualifiers  
source 1..2372  
/organism="unknown"  
/mol\_type="genomic DNA"

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Alignment Scores:  
Pred. No.: 8,756-83 Length: 2372  
Score: 1125.00 Matches: 218  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-063-670-6\_COPY\_17\_234 (1-218) x AR439125 (1-2372)

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Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40  
Db 268 AGAATTATGGGATCACCTTGTGAGCAAAAGGCGAACACGACCTGAATTTACAGAA 327

Qy 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60  
Db 328 GCTAAGGAGGCTGTAGGCTGTGGGACTAAGTTTGGCGCGCAAGGACCAAGTTGAAACA 387

Qy 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTyrValGlyValGlyValVal 80  
Db 388 GCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCTGGTGC 447

Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValGlyVal 100  
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Qy 121 AsnSerCysIleProGluIleThrThrLysAspProIlePheAsnThrGlnThrAla 140  
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DEFINITION Sequence 200 from patent US 6686451.  
ACCESSION AR473145  
VERSION AR473145.1 GI:42708520  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2372)  
AUTHORS Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L., Mather,J.P.,

Search completed: October 9, 2005, 01:20:55  
Job time : 3815.72 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 8, 2005, 16:31:30 ; Search time 2812.6 Seconds  
(without alignments)  
2950.295 Million cell updates/sec

Title: US-10-063-670-6\_COPY\_17\_234

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Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Maximum Match 100%

Listing first 1500 summaries

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2: gb\_est2:\*  
3: gb\_htc:\*  
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9: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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89	359.5	32.0	569	2	BE627175	BE627175	uu16h04.y	162	198.5	17.6	666	6	BY731449	BY731449	BY731449
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91	355.5	31.6	437	1	AJ686473	AJ686473	AJ686473	164	198.5	17.6	749	6	CD470595	CD470595	Leuk0S4_5
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93	349.5	31.1	479	2	BE847124	BE847124	uw22b07.y	166	198.5	17.6	2851	3	AK045226	AK045226	Mus muscu
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101	277.5	24.7	449	2	BF041814	BF041814	BP250014B	174	196.5	17.5	810	6	CB314546	CB314546	AGENCOURT
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108	246.5	21.9	895	6	CA474635	CA474635	AGENCOURT	181	196	17.4	698	7	CN347073	CN347073	170005325
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110	243.5	21.6	354	5	BY107653	BY107653	BY107653	183	196	17.4	728	4	BI769128	BI769128	603053720
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112	240	21.3	242	2	AW318386	AW318386	um96a08.y	185	196	17.4	764	4	BG759720	BG759720	602711117
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123	216	19.2	905	5	BP166057	BP166057	BP166057	196	196	17.4	906	5	BUI49945	BUI49945	AGENCOURT
124	215.5	19.2	766	5	BP167565	BP167565	BP167565	197	196	17.4	916	5	BUI66171	BUI66171	AGENCOURT
125	215	19.1	599	6	CB515759	CB515759	sealrqb51	198	196	17.4	923	5	BQ946450	BQ946450	AGENCOURT
126	215	19.1	825	5	BP157524	BP157524	BP157524	199	196	17.4	940	4	BI747697	BI747697	602705169
127	214.5	19.1	423	2	AW419846	AW419846	fj84c10.y	200	196	17.4	985	5	BUI68480	BUI68480	AGENCOURT
128	213.5	19.0	800	9	AY411059	AY411059	Mus muscu	201	196	17.4	985	5	BI585671	BI585671	602705169
129	213	18.9	974	7	CK404422	CK404422	AUF_IHdk	202	196	17.4	985	5	BI585671	BI585671	602705169
130	212	18.8	913	7	CK410366	CK410366	AUF_IHdk	203	196	17.4	1004	5	BI585671	BI585671	602705169
131	211.5	18.8	599	6	CB582683	CB582683	AMGNNUC:N	204	196	17.4	1010	1	AL552534	AL552534	AGENCOURT
132	211.5	18.8	763	7	CO570158	CO570158	AGENCOURT	205	196	17.4	1085	5	BM913991	BM913991	AGENCOURT
133	211.5	18.8	810	7	CK476032	CK476032	AGENCOURT	206	196	17.4	1876	3	CR596847	CR596847	full-leng
134	209.5	18.6	563	5	BQ566621	BQ566621	g164e12.y	207	196	17.4	1955	3	CR621045	CR621045	full-leng
135	209	18.6	721	7	CF763972	CF763972	CS004694	208	195.5	17.4	832	4	BG114530	BG114530	602284857
136	208	18.5	793	7	CN823883	CN823883	Oa.sp1bn	209	195.5	17.4	984	5	BQ677018	BQ677018	AGENCOURT
137	205.5	18.3	824	7	CK791054	CK791054	AGENCOURT	210	195.5	17.4	1054	5	BM918483	BM918483	AGENCOURT
138	203.5	18.1	598	6	CA367101	CA367101	642837.NC	211	195	17.3	476	2	AW501445	AW501445	UI-HF-BP0
139	203	18.0	705	7	CN823877	CN823877	Oa.sp1bn	212	195	17.3	579	5	BP268197	BP268197	BP268197
140	202.5	18.0	619	5	BQ393883	BQ393883	NISC_rg06	213	195	17.3	738	5	BUI95946	BUI95946	AGENCOURT
141	202.5	18.0	838	7	CF727499	CF727499	UI-M-HB0-	214	195	17.3	801	2	BE570280	BE570280	601332944
142	202	18.0	828	4	BG170766	BG170766	602323885	215	195	17.3	928	5	BQ683148	BQ683148	AGENCOURT
143	201	17.9	821	6	CA846294	CA846294	haa12a06.	216	195	17.3	1067	1	AL544334	AL544334	AL544334
144	201	17.9	867	5	BUI84888	BUI84888	AGENCOURT	217	194	17.2	574	4	BM742230	BM742230	K-EST0015
145	201	17.9	1085	4	BM550721	BM550721	AGENCOURT	218	194	17.2	583	5	BP280870	BP280870	BP280870
146	200.5	17.8	864	5	BQ690615	BQ690615	AGENCOURT	219	194	17.2	625	4	BG822513	BG822513	602725591
147	200	17.8	1024	5	BM904914	BM904914	AGENCOURT	220	194	17.2	660	4	BM745022	BM745022	K-EST0018
148	199.5	17.7	750	6	CD467776	CD467776	Leuk0S1_6	221	194	17.2	662	5	BQ109366	BQ109366	imageqc_6
149	199	17.7	578	4	BI008726	BI008726	QV3-RT007	222	194	17.2	667	6	CB125104	CB125104	K-EST0173
150	199	17.7	627	5	BP280494	BP280494	BP280494	223	194	17.2	668	4	BG421565	BG421565	602452141
151	199	17.7	834	5	BUI50725	BUI50725	Mus muscu	224	194	17.2	668	4	BM763472	BM763472	K-EST0044
152	199	17.7	1906	3	AK087472	AK087472	AGENCOURT	225	194	17.2	670	6	CB141293	CB141293	K-EST0194
153	198.5	17.6	592	7	CN660471	CN660471	A0705G09-	226	194	17.2	676	4	BG250321	BG250321	602362454
154	198.5	17.6	615	7	CF907877	CF907877	A0516A04-	227	194	17.2	678	6	BI36318	BI36318	K-EST0188
155	198.5	17.6	623	7	CN661635	CN661635	A0721H04-	228	194	17.2	757	4	BI821097	BI821097	603035569

229	194	17.2	796	5	BU527984	AGENCOURT	302	190	16.9	581	5	BP225898	BP225898
230	194	17.2	805	4	BG827701	AGENCOURT	303	190	16.9	581	5	BP237035	BP237035
231	194	17.2	883	5	BQ877431	AGENCOURT	304	190	16.9	581	5	BP252243	BP252243
232	194	17.2	913	4	BG327238	602426190	305	190	16.9	581	5	BP252906	BP252906
233	193.5	17.2	677	6	BY744790	BY744790	306	190	16.9	581	5	BP278646	BP278646
234	193.5	17.2	1036	5	BM908486	AGENCOURT	307	190	16.9	581	5	BP280300	BP280300
235	193	17.2	630	6	CD470529	Leukosa_5	308	190	16.9	581	5	BP280869	BP280869
236	193	17.2	635	6	CD468828	Leukosa_7	309	190	16.9	581	5	BP285640	BP285640
237	193	17.2	649	6	CD469564	Leukosa_2	310	190	16.9	581	5	BP295553	BP295553
238	193	17.2	647	6	CD469238	Leukosa_2	311	190	16.9	581	5	BP297294	BP297294
239	193	17.2	668	4	BI855939	60338313	312	190	16.9	581	5	BP323904	BP323904
240	192.5	17.1	572	6	CB016588	pgn1c_pk0	313	190	16.9	581	5	BP354214	BP354214
241	192.5	17.1	1184	5	BM908074	AGENCOURT	314	190	16.9	581	5	BP355784	BP355784
242	192	17.1	582	5	BP236685	BP236685	315	190	16.9	582	5	BP215631	BP215631
243	192	17.1	582	5	BP278321	BP278321	316	190	16.9	582	5	BP222379	BP222379
244	192	17.1	582	5	BP353372	BP353372	317	190	16.9	582	5	BP222548	BP222548
245	192	17.1	743	6	CB318661	AGENCOURT	318	190	16.9	582	5	BP223038	BP223038
246	192	17.1	959	5	BQ935522	AGENCOURT	319	190	16.9	582	5	BP225812	BP225812
247	192	17.1	976	5	BQ957776	AGENCOURT	320	190	16.9	582	5	BP230984	BP230984
248	191.5	17.0	500	6	CD734509	4048585_1	321	190	16.9	582	5	BP231716	BP231716
249	191.5	17.0	582	7	CF256984	pha005_c0	322	190	16.9	582	5	BP233787	BP233787
250	191.5	17.0	608	7	CF257313	pha009_f1	323	190	16.9	582	5	BP278171	BP278171
251	191.5	17.0	660	6	CD468968	Leuko3_8	324	190	16.9	582	5	BP278231	BP278231
252	191.5	17.0	739	1	AJ450624	AJ450624	325	190	16.9	582	5	BP278305	BP278305
253	191.5	17.0	775	7	CN218866	RJA040G05	326	190	16.9	582	5	BP278475	BP278475
254	191.5	17.0	855	7	CF257095	pha006_g0	327	190	16.9	582	5	BP278491	BP278491
255	191.5	17.0	859	7	CF257757	pha015_a1	328	190	16.9	582	5	BP279295	BP279295
256	191.5	17.0	881	7	CF251803	hdm004_e0	329	190	16.9	582	5	BP279324	BP279324
257	191	17.0	393	7	CF144025	UI-HF-Bp0	330	190	16.9	582	5	BP279363	BP279363
258	191	17.0	515	4	BM753415	K-EST0030	331	190	16.9	582	5	BP280048	BP280048
259	191	17.0	536	5	BP162646	BP162646	332	190	16.9	582	5	BP280228	BP280228
260	191	17.0	565	5	BP267691	BP267691	333	190	16.9	582	5	BP280613	BP280613
261	191	17.0	582	5	BP278066	BP278066	334	190	16.9	582	5	BP280921	BP280921
262	191	17.0	582	5	BP356315	BP356315	335	190	16.9	582	5	BP280955	BP280955
263	191	17.0	587	5	BP354072	BP354072	336	190	16.9	582	5	BP280957	BP280957
264	191	17.0	598	5	BP279982	BP279982	337	190	16.9	582	5	BP288145	BP288145
265	191	17.0	602	5	BP279073	BP279073	338	190	16.9	582	5	BP303210	BP303210
266	191	17.0	625	2	AW732339	603b02_Y	339	190	16.9	582	5	BP358311	BP358311
267	191	17.0	697	4	BG912337	602806886	340	190	16.9	582	5	BP336193	BP336193
268	190.5	16.9	503	6	CA573126	CA573126	341	190	16.9	582	5	BP352339	BP352339
269	190.5	16.9	504	5	BQ562475	H4076B11	342	190	16.9	582	5	BP353072	BP353072
270	190.5	16.9	509	2	AW761944	u51f10_Y	343	190	16.9	582	5	BP353576	BP353576
271	190.5	16.9	519	6	CA570202	K0503C08	344	190	16.9	582	5	BP355366	BP355366
272	190.5	16.9	521	6	CA570891	K0513B10	345	190	16.9	582	5	BP363182	BP363182
273	190.5	16.9	522	6	CA873377	K0924G02	346	190	16.9	582	5	BP363335	BP363335
274	190.5	16.9	546	6	CA883079	B0101A04	347	190	16.9	582	5	BP365020	BP365020
275	190.5	16.9	581	6	CA896005	B0196A07	348	190	16.9	582	5	BP365667	BP365667
276	190.5	16.9	820	4	BM051234	60363189	349	190	16.9	582	5	BP365708	BP365708
277	190.5	16.9	951	4	BG119674	602347092	350	190	16.9	582	5	BP365745	BP365745
278	190.5	16.9	973	4	BI820251	603036802	351	190	16.9	583	5	BP234498	BP234498
279	190	16.9	512	4	BM744870	K-EST0018	352	190	16.9	583	5	BP234878	BP234878
280	190	16.9	545	6	CB135807	K-EST0018	353	190	16.9	583	5	BP236879	BP236879
281	190	16.9	550	5	BP377364	BP377364	354	190	16.9	583	5	BP278008	BP278008
282	190	16.9	553	4	BM846600	K-EST0125	355	190	16.9	583	5	BP278196	BP278196
283	190	16.9	556	6	CB141325	K-EST0194	356	190	16.9	583	5	BP278366	BP278366
284	190	16.9	556	6	CB141372	K-EST0194	357	190	16.9	583	5	BP278548	BP278548
285	190	16.9	558	7	CN482614	hw22e06_Y	358	190	16.9	583	5	BP278697	BP278697
286	190	16.9	561	4	BM743702	K-EST0016	359	190	16.9	583	5	BP278792	BP278792
287	190	16.9	563	4	BM840881	K-EST0118	360	190	16.9	583	5	BP278933	BP278933
288	190	16.9	569	4	BM848299	K-EST0128	361	190	16.9	583	5	BP279202	BP279202
289	190	16.9	569	4	BM853235	K-EST0134	362	190	16.9	583	5	BP279356	BP279356
290	190	16.9	573	1	AU280746	AU280746	363	190	16.9	583	5	BP279519	BP279519
291	190	16.9	576	5	BP279188	BP279188	364	190	16.9	583	5	BP279772	BP279772
292	190	16.9	578	4	BM742678	K-EST0015	365	190	16.9	583	5	BP280081	BP280081
293	190	16.9	579	5	BP363851	BP363851	366	190	16.9	583	5	BP280334	BP280334
294	190	16.9	580	5	BP233550	BP233550	367	190	16.9	583	5	BP280604	BP280604
295	190	16.9	580	5	BP272835	BP272835	368	190	16.9	583	5	BP280708	BP280708
296	190	16.9	581	4	BI824066	603038788	369	190	16.9	583	5	BP280810	BP280810
297	190	16.9	581	5	BP206044	BP206044	370	190	16.9	583	5	BP280838	BP280838
298	190	16.9	581	5	BP221857	BP221857	371	190	16.9	583	5	BP281053	BP281053
299	190	16.9	581	5	BP221889	BP221889	372	190	16.9	583	5	BP281058	BP281058
300	190	16.9	581	5	BP222451	BP222451	373	190	16.9	583	5	BP281074	BP281074
301	190	16.9	581	5	BP222755	BP222755	374	190	16.9	583	5	BP341512	BP341512

375	190	16.9	583	5	BP352289	448	186	16.5	521	6	CD469959	Leukos4_2
376	190	16.9	583	5	BP353855	450	186	16.5	526	6	CD464259	Leukon4_2
377	190	16.9	583	5	BP354184	450	186	16.5	533	6	CD471150	Leukos5_4
378	190	16.9	584	5	BP280286	451	186	16.5	548	6	CD469967	Leukos4_2
379	190	16.9	585	5	BP253708	452	186	16.5	549	6	CD469106	Leukos2_1
380	190	16.9	585	6	CB129134	453	186	16.5	549	6	CD471912	Leukos6_2
381	190	16.9	587	5	BP278759	454	186	16.5	554	6	CD469251	Leukos2_2
382	190	16.9	587	5	BP278794	455	186	16.5	571	6	CD470950	Leukos5_3
383	190	16.9	587	5	BP279977	456	186	16.5	576	6	CD471137	Leukos5_4
384	190	16.9	587	5	BP280171	457	186	16.5	579	6	CD465192	Leukon1_2
385	190	16.9	587	5	BP365344	458	186	16.5	582	5	BP365073	BP365073
386	190	16.9	588	5	BP236489	459	186	16.5	584	6	CD468526	Leukos3_3
387	190	16.9	588	5	BP277748	460	186	16.5	596	6	CD471747	Leukos6_4
388	190	16.9	588	5	BP278268	461	186	16.5	599	6	CD471683	Leukos6_4
389	190	16.9	588	5	BP279065	462	186	16.5	602	6	CD470977	Leukos5_3
390	190	16.9	588	5	BP365173	463	186	16.5	602	6	CD535917	Leukon5_5
391	190	16.9	589	5	BP233222	464	186	16.5	607	5	BP280139	BP280139
392	190	16.9	589	6	CB130851	465	186	16.5	612	6	CD469627	Leukos2_7
393	190	16.9	592	4	BM848361	466	186	16.5	821	6	CD559300	AGENCOCURT
394	190	16.9	592	5	BP277740	467	185.5	16.5	405	6	BY766304	BY766304
395	190	16.9	593	4	BM742647	468	185.5	16.5	502	6	CA567008	K0408F05-
396	190	16.9	594	5	BP279022	469	185.5	16.5	761	1	AA637653	vu10e10.r
397	190	16.9	597	5	BP280234	470	185	16.4	488	6	CD536274	Leukon6_4
398	190	16.9	598	5	BP279140	471	185	16.4	515	6	CD464497	Leukon4_4
399	190	16.9	598	5	BP280362	472	185	16.4	516	6	CD470165	Leukos4_1
400	190	16.9	598	5	BP281033	473	185	16.4	548	4	BI960855	MONO1_1_G
401	190	16.9	598	5	BP351569	474	185	16.4	574	5	BP297283	BP297283
402	190	16.9	598	6	CB124471	475	185	16.4	592	5	BP279039	BP279039
403	190	16.9	598	6	CB132093	476	185	16.4	598	5	BP366031	BP366031
404	190	16.9	598	6	CB149427	477	185	16.4	605	6	CD471149	Leukos5_4
405	190	16.9	600	4	BM742193	478	185	16.4	941	4	BI602405	603251183
406	190	16.9	601	6	CD469117	479	184.5	16.4	590	1	AI151808	u146C06.Y
407	190	16.9	603	5	BP278981	480	184	16.4	329	7	W40206	zc83a0e.r1
408	190	16.9	608	4	BM846665	481	184	16.4	544	4	BM762984	K-EST0044
409	190	16.9	613	4	BM846787	482	184	16.4	582	5	BP254097	BP254097
410	190	16.9	617	5	BP278547	483	184	16.4	583	5	BP280763	BP280763
411	190	16.9	625	5	BP280558	484	183.5	16.3	735	7	CK364727	AGENCOCURT
412	190	16.9	626	2	AW955521	485	183	16.3	555	4	BM753425	K-EST0030
413	190	16.9	635	2	AW239286	486	183	16.3	571	4	BM846524	K-EST0125
414	190	16.9	648	4	EG548953	487	183	16.3	581	5	BP234294	BP234294
415	190	16.9	702	1	AU140087	488	183	16.3	582	5	BP235338	BP235338
416	190	16.9	706	4	EG868920	489	183	16.3	584	5	BP277956	BP277956
417	190	16.9	835	4	BI914860	490	183	16.3	584	5	BP354729	BP354729
418	190	16.9	837	4	BI161210	491	183	16.3	587	5	BP365226	BP365226
419	190	16.9	894	5	BQ880928	492	183	16.3	875	4	BI193879	602948207
420	190	16.9	925	2	BF311255	493	183	16.3	181	4	EG704723	602688330
421	190	16.9	939	5	BU501360	494	182.5	16.2	573	1	AA273296	vc01e02.r
422	190	16.9	1158	4	EG323913	495	182	16.2	511	4	BM848382	K-EST0128
423	189.5	16.8	548	2	BF039338	496	182	16.2	576	5	BP206244	BP206244
424	189.5	16.8	634	7	CN662209	497	182	16.2	579	5	BP334408	BP334408
425	189	16.8	510	4	BM836382	498	182	16.2	937	4	EG325414	602424105
426	189	16.8	582	5	BP279220	499	181	16.1	515	4	BM753439	K-EST0030
427	189	16.8	583	5	BP278114	500	181	16.1	516	2	BM867486	BM867486
428	189	16.8	583	5	BP279317	501	181	16.1	582	5	BP278478	BP278478
429	189	16.8	583	5	BP280964	502	181	16.1	604	4	BM743657	BM743657
430	189	16.8	587	5	BP277775	503	181	16.1	679	6	CB135879	K-EST0188
431	189	16.8	588	5	BP277718	504	180	16.0	541	6	CD470152	Leukos4_1
432	188.5	16.8	857	4	BI160643	505	179.5	16.0	732	4	EG615658	602643016
433	188	16.7	305	1	AV749159	506	179	15.9	534	6	CD464299	Leukon4_2
434	188	16.7	418	1	AL835535	507	179	15.9	576	6	CD472209	Leukos6_1
435	188	16.7	582	5	BP279321	508	179	15.9	582	6	BP278062	BP278062
436	188	16.7	582	5	BP353503	509	179	15.9	902	4	BM020134	603648704
437	188	16.7	584	5	BP356262	510	178	15.8	591	5	BP336010	BP336010
438	187.5	16.7	469	1	AA794029	511	178	15.8	591	5	BP363850	BP363850
439	187.5	16.7	579	5	BP339083	512	178	15.8	838	4	EG704722	602688329
440	187	16.6	557	6	CB140797	513	177.5	15.8	858	5	BY325378	BY325378
441	187	16.6	580	5	BP259795	514	177.5	15.8	503	2	BM867301	BM867301
442	187	16.6	583	5	BP277883	515	177.5	15.8	828	5	BX078167	BX078167
443	187	16.6	601	2	AW951906	516	177	15.7	570	5	BP333735	BP333735
444	187	16.6	889	4	EG679238	517	177	15.7	573	6	CB157265	K-EST0216
445	187	16.6	889	4	BI602413	518	177	15.7	580	5	BP299494	BP299494
446	186	16.5	478	6	CD465065	519	177	15.7	581	5	BP305097	BP305097
447	186	16.5	495	6	CD465358	520	177	15.7	581	5	BP324616	BP324616



521	177	15.7	581	5	B353795	B353795	B353795	594	166.5	14.8	480	6	CB139711	CB139711	K-EST0192
522	177	15.7	581	5	B354113	B354113	B354113	595	166.5	14.8	482	6	BM752546	BM752546	K-EST0029
523	177	15.7	581	5	B363831	B363831	B363831	596	166.5	14.8	476	6	BY752585	BY752585	K-EST0029
524	177	15.7	581	5	B365172	B365172	B365172	597	166	14.8	582	5	BP236892	BP236892	BP236892
525	177	15.7	582	5	B279349	B279349	B279349	598	166	14.8	669	6	CD638322	CD638322	AGENCOURT
526	177	15.7	582	5	B279398	B279398	B279398	599	166	14.8	843	4	BT868960	BT868960	601395245
527	177	15.7	582	5	B279865	B279865	B279865	600	165	14.7	550	5	BP279159	BP279159	BP279159
528	177	15.7	582	5	B279956	B279956	B279956	601	165	14.7	582	5	BP339224	BP339224	BP339224
529	177	15.7	582	5	B299760	B299760	B299760	602	165	14.7	583	5	BP255503	BP255503	BP255503
530	177	15.7	582	5	B353628	B353628	B353628	603	165	14.7	748	2	BE546472	BE546472	601077647
531	177	15.7	582	5	B366132	B366132	B366132	604	164.5	14.6	452	4	BM742492	BM742492	K-EST0015
532	177	15.7	583	5	B279259	B279259	B279259	605	164.5	14.6	457	2	BB859479	BB859479	BB859479
533	177	15.7	583	5	B279567	B279567	B279567	606	164	14.6	448	4	BM797335	BM797335	K-EST0080
534	177	15.7	583	5	B365496	B365496	B365496	607	164	14.6	737	5	BP366227	BP366227	BP366227
535	177	15.7	583	5	B279517	B279517	B279517	608	164	14.6	583	7	CF121799	CF121799	UI-HF-BP0
536	177	15.7	584	5	B226308	B226308	B226308	609	163.5	14.5	341	6	BY790717	BY790717	BY790717
537	177	15.7	592	5	B279041	B279041	B279041	610	163	14.5	548	4	BM818972	BM818972	K-EST0086
538	177	15.7	596	5	B365383	B365383	B365383	611	162.5	14.4	341	6	BY790716	BY790716	BY790716
539	177	15.7	603	5	B279828	B279828	B279828	612	162.5	14.4	446	4	BI960888	BI960888	MONOL_2_B
540	177	15.7	603	5	B280025	B280025	B280025	613	162.5	14.4	476	6	CD465241	CD465241	LeukoN1_2
541	177	15.7	607	5	B279866	B279866	B279866	614	162	14.4	477	4	BM825765	BM825765	K-EST0097
542	176	15.6	581	5	B222120	B222120	B222120	615	161.5	14.4	450	7	CK613064	CK613064	LPS1_H05
543	176	15.6	582	5	B333904	B333904	B333904	616	161	14.3	582	5	BP323917	BP323917	BP323917
544	176	15.6	592	5	B281049	B281049	B281049	617	161	14.3	869	5	BQ212256	BQ212256	AGENCOURT
545	176	15.6	696	2	B274840	B274840	B274840	618	160	14.2	770	6	CD559302	CD559302	AGENCOURT
546	176	15.6	1119	5	BQ675971	BQ675971	BQ675971	619	160	14.2	887	4	BG528427	BG528427	602579863
547	175	15.6	486	4	BM847024	BM847024	BM847024	620	159.5	14.2	420	2	BE767810	BE767810	CM3-GN004
548	175	15.6	581	5	B364418	B364418	B364418	621	159.5	14.2	459	7	CF137888	CF137888	UI-HF-BNO
549	175	15.6	582	5	B356350	B356350	B356350	622	159.5	14.2	492	4	BM824519	BM824519	K-EST0096
550	175	15.6	582	5	B365046	B365046	B365046	623	159.5	14.2	765	7	CN347077	CN347077	170004177
551	175	15.6	584	5	B343491	B343491	B343491	624	158.5	14.1	433	5	BY252039	BY252039	BY252039
552	174	15.5	577	5	B279183	B279183	B279183	625	158.5	14.1	464	2	BE127204	BE127204	DEPA0953
553	174	15.5	582	5	B281087	B281087	B281087	626	158.5	14.1	483	5	BU661013	BU661013	z16b003_z
554	174	15.5	583	5	B299450	B299450	B299450	627	158	14.0	549	1	AA282906	AA282906	ct14h05_r
555	173.5	15.4	804	2	B5618977	B5618977	B5618977	628	157	14.0	457	2	BB862318	BB862318	BB862318
556	173	15.4	588	2	B280786	B280786	B280786	629	157	14.0	570	5	BP369857	BP369857	BP369857
557	173	15.4	697	4	BM019476	BM019476	BM019476	630	157	14.0	592	5	BP280439	BP280439	BP280439
558	172.5	15.3	499	2	BB856698	BB856698	BB856698	631	157	14.0	676	6	CD528831	CD528831	LeukoN3_5
559	172.5	15.3	908	7	CF257407	CF257407	CF257407	632	156.5	13.9	628	5	BP278601	BP278601	BP278601
560	172	15.3	581	5	B355143	B355143	B355143	633	156.5	13.9	693	4	BI557680	BI557680	603237040
561	172	15.3	581	5	B208292	B208292	B208292	634	156.5	13.9	744	4	BG250382	BG250382	602362532
562	172	15.3	582	5	B215537	B215537	B215537	635	156.5	13.9	785	5	EX915863	EX915863	EX915863
563	172	15.3	583	5	BP349577	BP349577	BP349577	636	156	13.9	583	5	BP278490	BP278490	BP278490
564	172	15.3	589	5	BP354144	BP354144	BP354144	637	155.5	13.8	332	6	CD584497	CD584497	RK025A2G1
565	171.5	15.2	698	4	BG748079	BG748079	BG748079	638	155.5	13.8	449	6	CD469110	CD469110	LeukoS2_1
566	171	15.2	445	2	AW403376	AW403376	AW403376	639	155.5	13.8	459	6	CD469110	CD469110	LeukoS2_1
567	171	15.2	581	5	B362018	B362018	B362018	640	155	13.8	583	5	BP363547	BP363547	BP363547
568	171	15.2	905	4	BG251812	BG251812	BG251812	641	155	13.8	815	9	EX188005	EX188005	DanLo_rer
569	170.5	15.2	492	2	BB867185	BB867185	BB867185	642	155	13.8	915	5	BQ432026	BQ432026	AGENCOURT
570	170.5	15.2	571	4	BM764098	BM764098	BM764098	643	154.5	13.7	582	5	BP361203	BP361203	BP361203
571	170	15.1	598	5	B320978	B320978	B320978	644	153.5	13.6	432	4	BM764097	BM764097	K-EST0045
572	170	15.1	708	4	BI157374	BI157374	BI157374	645	153.5	13.6	438	4	BM785480	BM785480	K-EST0063
573	170	15.1	1336	3	CP660524	CP660524	CP660524	646	153.5	13.6	444	4	BM826025	BM826025	K-EST0097
574	169.5	15.1	598	5	B280260	B280260	B280260	647	153.5	13.6	483	4	BM739115	BM739115	K-EST0008
575	169.5	15.1	611	1	A1787649	A1787649	A1787649	648	153.5	13.6	641	6	BY726835	BY726835	BY726835
576	169.5	15.1	669	6	CB140905	CB140905	CB140905	649	153.5	13.6	879	5	BQ962151	BQ962151	AGENCOURT
577	169	15.0	582	5	B281083	B281083	B281083	650	152.5	13.6	573	6	CD535920	CD535920	LeukoN5_5
578	169	15.0	582	5	BP364971	BP364971	BP364971	651	152	13.5	3454	3	AK028441	AK028441	Mus_musCu
579	169	15.0	583	5	B3254393	B3254393	B3254393	652	151.5	13.5	422	5	BU428717	BU428717	UI-HF-BNO
580	169	15.0	811	4	BI856520	BI856520	BI856520	653	151.5	13.5	509	4	BM088473	BM088473	501959_MA
581	168	14.9	581	5	BP355480	BP355480	BP355480	654	151.5	13.5	719	7	CV221259	CV221259	Le_mxo_46
582	168	14.9	583	5	BP280217	BP280217	BP280217	655	151	13.4	758	5	BQ227807	BQ227807	AGENCOURT
583	168	14.9	930	5	BQ878706	BQ878706	BQ878706	656	150.5	13.4	539	2	AW959677	AW959677	EST371747
584	167.5	14.9	1243	5	BQ230605	BQ230605	BQ230605	657	150	13.3	828	4	BM019684	BM019684	603647966
585	167	14.8	582	5	BP315724	BP315724	BP315724	658	149.5	13.3	467	6	CB149408	CB149408	K-EST0205
586	167	14.8	582	5	BP354763	BP354763	BP354763	659	149.5	13.3	482	1	AL553043	AL553043	AL553043
587	166.5	14.8	289	5	BY145458	BY145458	BY145458	660	149.5	13.3	582	2	BB611006	BB611006	BB611006
588	166.5	14.8	442	7	CF166420	CF166420	CF166420	661	149.5	13.3	598	6	CB724514	CB724514	EST0318_R
589	166.5	14.8	443	7	CF166401	CF166401	CF166401	662	149	13.2	793	2	BF247176	BF247176	601857845
590	166.5	14.8	448	2	BB859819	BB859819	BB859819	663	149	13.2	850	2	BE735557	BE735557	601304365
591	166.5	14.8	463	6	CB120042	CB120042	CB120042	664	148.5	13.2	287	6	CB140504	CB140504	K-EST0193
592	166.5	14.8	464	1	AL048049	AL048049	AL048049	665	148.5	13.2	572	5	BP333480	BP333480	BP333480
593	166.5	14.8	465	2	BB859952	BB859952	BB859952	666	148	13.2	574	5	BP278877	BP278877	BP278877

667	147.5	13.1	514	4	BG684702	602635990	740	139	12.4	388	2	AW435659	AW435659	74622	MAR
668	147	13.1	582	5	BP215565	BP215565	741	139	12.4	561	4	BI710853	BI710853	iD92907.Y	
669	147	13.1	588	5	BP336450	BP336450	742	139	12.4	575	5	BP300359	BP300359	BP300359	
670	147	13.1	625	6	CD471271	Leuko85_1	743	139	12.4	583	5	BP304428	BP304428	BP304428	
671	147	13.1	708	7	CN347076	170004248	744	139	12.4	614	9	CG589077	CG589077	OST240788	
672	147	13.1	992	2	BE616364	601279172	745	139	12.4	674	7	CK685212	CK685212	ZF101-P00	
673	146.5	13.0	767	4	BG822533	602725618	746	138.5	12.3	451	2	BB858834	BB858834		
674	146.5	13.0	1073	2	BE904427	601496388	747	137.5	12.2	432	6	CB128106	CB128106	K-EST0177	
675	146	13.0	331	1	AA363579	EST73724	C 748	136.5	12.1	595	9	FR0016223	FR0016223		
676	146	13.0	577	9	AY421183	Pan tlogl	C 749	136	12.1	589	1	A1830544	A1830544	Fugu rubr	
677	146	13.0	1122	7	CK028027	AGENCOURT	750	136	12.1	694	4	BI771330	BI771330	wJ51a03.x	
678	145.5	12.9	418	6	CA567844	K0419D04	751	136	12.1	808	6	CD512219	CD512219	AGENCOURT	
679	145.5	12.9	468	6	CA389865	ca103f03	752	135.5	12.0	718	5	BM951526	BM951526	UI-M-EGO-	
680	145.5	12.9	582	7	BP205440	BP205440	753	135.5	12.0	2661	9	AY402614	AY402614	Mus muscu	
681	145.5	12.9	587	7	CV029518	8335 Full1	754	134.5	12.0	378	7	W68991	W68991	T2873 MVAT4	
682	145.5	12.9	751	6	CD366440	UI-H-FT1-	755	134.5	12.0	442	7	CK608407	CK608407	IFNb_B08	
683	145.5	12.9	828	7	CK795924	AGENCOURT	756	134.5	12.0	466	5	BI153109	BI153109	WJ51a03.x	
684	145.5	12.9	834	9	AY421182	Homo sapi	757	134.5	12.0	694	6	CA376384	CA376384	654727 NC	
685	145.5	12.9	1001	1	AL540999	AL540999	758	134	11.9	582	5	BP363410	BP363410	BP363410	
686	145	12.9	545	5	BX480271	DKFZp6860	759	134	11.9	3025	3	BC049247	BC049247	Mus muscu	
687	145	12.9	557	4	BI467634	389291 MA	760	133.5	11.9	729	7	CN056501	CN056501	Salamande	
688	145	12.9	582	5	BP194641	BP194641	761	133	11.8	245	1	AA360733	AA360733	EST70005	
689	145	12.9	583	5	BP204751	BP204751	762	133	11.8	291	1	AA347120	AA347120	EST53364	
690	145	12.9	691	7	CO132920	EST00003	C 763	133	11.8	669	5	BU631966	BU631966	UI-H-FE1-	
691	145	12.9	760	7	CV079185	AGENCOURT	764	132	11.7	327	7	W40210	W40210	zc83b06.r1	
692	145	12.9	806	7	CO556630	AGENCOURT	765	132	11.7	770	5	BU749989	BU749989	CH3#030 C	
693	145	12.9	866	7	CO390036	AGENCOURT	766	131.5	11.7	860	4	BG541514	BG541514	602570961	
694	145	12.9	868	5	BQ230041	AGENCOURT	767	131.5	11.7	874	2	BF582542	BF582542	602094513	
695	144.5	12.8	500	1	AL544354	AL544354	768	131	11.6	986	5	BX390379	BX390379	BX390379	
696	144.5	12.8	589	4	BI342110	369784 MA	769	130.5	11.6	358	6	BY770042	BY770042	BY770042	
697	144.5	12.8	673	6	CD772495	AGENCOURT	770	130.5	11.6	584	5	BP217677	BP217677	BP217677	
698	144.5	12.8	680	6	CD465458	LeukoN1_4	771	130.5	11.6	906	1	AA717936	AA717936	vt09f11.r	
699	144.5	12.8	831	6	CA473822	AGENCOURT	772	130	11.6	329	7	W93163	W93163	zd93a04.r1	
700	144	12.8	450	2	BE855266	ux28a10.Y	773	130	11.6	362	5	BY019901	BY019901	BY019901	
701	144	12.8	467	2	BE478431	162683 BA	774	130	11.6	582	5	BP301774	BP301774	BP301774	
702	144	12.8	467	4	BI1132408	AR030G05L	775	130	11.6	640	2	BE371133	BE371133	601218624	
703	144	12.8	476	4	BM286083	526000 MA	776	129.5	11.5	784	4	BG866546	BG866546	602785510	
704	144	12.8	516	2	BE483741	170029 BA	777	129	11.5	706	2	AW954379	AW954379	EST366449	
705	144	12.8	550	2	BE666586	150090 MA	778	128.5	11.4	931	2	CN321916	CN321916	AGENCOURT	
706	144	12.8	585	5	BP289867	BP289867	779	128.5	11.4	1110	7	CK028468	CK028468	AGENCOURT	
707	144	12.8	599	1	AV593707	AV593707	780	127.5	11.3	581	5	BP250869	BP250869	BF250869	
708	144	12.8	608	7	CF371082	TG8STzYj6	781	127.5	11.3	1832	3	CR613805	CR613805	full-Leng	
709	144	12.8	647	6	CB442528	693111 MA	782	127.5	11.3	1844	3	AY037161	AY037161	Homo sapi	
710	144	12.8	688	6	CD469382	Leuko82_3	783	127.5	11.3	2485	3	BC023209	BC023209	Homo sapi	
711	144	12.8	796	2	BF031320	601559076	784	127.5	11.3	2736	9	AY402612	AY402612	Homo sapi	
712	144	12.8	828	9	AY421184	Mus muscu	785	127.5	11.3	2759	3	BC029313	BC029313	Homo sapi	
713	144	12.8	895	6	CB250522	AGENCOURT	786	127.5	11.3	3105	3	BC053689	BC053689	Homo sapi	
714	143.5	12.8	1090	5	BM908074	AGENCOURT	787	127.5	11.3	3270	3	BC035457	BC035457	Homo sapi	
715	143.5	12.8	1090	5	BM908074	AGENCOURT	788	127.5	11.3	3295	3	BC029348	BC029348	Homo sapi	
716	143	12.7	719	6	CA342417	672284 NC	789	127	11.3	422	1	AV670072	AV670072	AV670072	
717	143	12.7	743	4	BI961594	MONO1_1 GC	790	127	11.3	642	7	CV078311	CV078311	AGENCOURT	
718	143	12.7	880	4	BI085422	602863908	791	127	11.3	732	7	CK805674	CK805674	AGENCOURT	
719	143	12.7	2368	3	BC019712	Mus muscu	792	127	11.3	938	7	CK799651	CK799651	AGENCOURT	
720	142.5	12.7	582	5	BP227819	BP227819	793	127	11.3	964	4	BI222267	BI222267	602939755	
721	142.5	12.7	606	6	CA347334	678437 NC	794	126.5	11.2	750	9	CK699945	CK699945	ZF101-P00	
722	142	12.6	559	4	BI960863	MONO1_1 GC	795	126	11.2	1079	9	CNS05DEJ	CNS05DEJ	Tetraodon	
723	142	12.6	649	7	CN980729	48731_126	C 796	126	11.2	3085	3	AK034522	AK034522	Mus muscu	
724	142	12.6	678	7	CN969354	16851_123	797	125.5	11.2	446	2	BB840038	BB840038	BB840038	
725	141.5	12.6	427	4	BM847672	K-EST0127	798	125.5	11.2	572	7	CNS32870	CNS32870	UI-M-HO0-	
726	141.5	12.6	444	2	BB860365	BB860365	799	125.5	11.2	648	5	BP765140	BP765140	BP765140	
727	140.5	12.5	359	6	BY788232	BY788232	800	125.5	11.2	765	7	CNS08989	CNS08989	AGENCOURT	
728	140.5	12.5	442	1	A1226003	uj08b06.Y	801	125.5	11.2	878	6	CD359001	CD359001	AGENCOURT	
729	140.5	12.5	879	7	CF251752	hdm003.g1	802	125.5	11.2	2189	3	AK001582	AK001582	Mus muscu	
730	140	12.4	428	5	BQ133343	fz40d02.Y	803	125.5	11.2	2194	3	AK048107	AK048107	Mus muscu	
731	140	12.4	599	1	A1934454	wp58b10.X	804	125.5	11.2	2876	3	AK032750	AK032750	Mus muscu	
732	140	12.4	603	5	BQ131025	fz47g05.Y	805	125	11.1	683	4	BJ523552	BJ523552	BJ523552	
733	140	12.4	604	2	AW595426	fK37g02.Y	806	124.5	11.1	504	7	N24337	N24337	yx24f11.r1	
734	140	12.4	689	4	BG696649	602658956	807	124	11.0	572	6	CB268774	CB268774	1007680 H	
735	140	12.4	821	7	CK697330	ZF101-P00	808	124	11.0	690	2	BF342700	BF342700	602013653	
736	140	12.4	905	7	CNS10906	AGENCOURT	809	124	11.0	915	5	BF748376	BF748376	BX748376	
737	139.5	12.4	387	6	CD471434	Leuko85_5	810	123.5	11.0	885	6	CA496501	CA496501	AGENCOURT	
738	139.5	12.4	403	5	BY160556	BY160556	811	123	10.9	524	5	BQ259314	BQ259314	fz297g05.Y	
739	139.5	12.4	617	7	CF906668	A0500B09-	812	123	10.9	562	4	BM254875	BM254875	516445 MA	

813	123	10.9	568	2	BE200989	BE200989	fk84e04.y	886	116	10.3	380	5	BY011815	BY011815
814	123	10.9	591	5	BQ093786	BQ093786	fz51h01.y	887	116	10.3	2809	5	BC021652	Mus_muscu
815	123	10.9	758	7	CF998236	CF998236	AGENCOURT	888	115.5	10.3	382	6	BY772496	BY772496
816	123	10.9	780	7	CF348306	CF348306	AGENCOURT	889	115.5	10.3	588	5	BM949590	BM949590
817	123	10.9	800	7	CK028357	CK028357	AGENCOURT	890	115.5	10.3	736	7	CF457207	CF457207
818	123	10.9	814	7	CK030082	CK030082	AGENCOURT	891	115.5	10.3	1023	1	AL526824	AL526824
819	123	10.9	822	7	CN510127	CN510127	AGENCOURT	892	115	10.2	362	6	BY766890	BY766890
820	123	10.9	840	7	CN506106	CN506106	AGENCOURT	893	115	10.2	364	5	BY171892	BY171892
821	123	10.9	868	7	CK018837	CK018837	AGENCOURT	894	115	10.2	375	4	BF175470	MYE5034.M
822	123	10.9	872	4	BG541447	BG541447	602570880	895	115	10.2	707	4	BG770063	BG770063
823	122.5	10.9	416	5	BY208234	BY208234	AGENCOURT	896	115	10.2	714	4	BG760615	BG760615
824	122.5	10.9	567	2	BZ016734	BZ016734	fk68b07.y	897	114.5	10.2	389	5	BY165009	BY165009
825	122.5	10.9	724	4	B1755270	B1755270	603022711	898	114.5	10.2	722	2	BF529219	BF529219
826	122	10.8	497	4	B1328214	B1328214	fz39d09.y	899	114.5	10.2	738	2	BF346219	BF346219
827	122	10.8	513	2	AW343039	AW343039	f172f05.y	900	114.5	10.2	819	5	EX717115	EX717115
828	122	10.8	583	5	BP230565	BP230565	BP230565	901	114	10.1	638	2	BB590171	BB590171
829	122	10.8	721	4	BG764304	BG764304	602736181	902	114	10.1	792	7	CF456942	CF456942
830	122	10.8	894	5	BX431647	BX431647	AGENCOURT	903	113.5	10.1	2143	3	AK040503	AK040503
831	122	10.8	946	5	BO720761	BO720761	AGENCOURT	904	113.5	10.1	385	6	BY770884	BY770884
832	121.5	10.8	384	5	BY172775	BY172775	BY172775	905	113.5	10.1	431	5	BY226451	BY226451
833	121.5	10.8	436	7	CF371048	CF371048	TG8ST2YJ6	906	113.5	10.1	444	5	BY155496	BY155496
834	121.5	10.8	790	1	AV704163	AV704163	AGENCOURT	907	113.5	10.1	461	2	BB58159	BB58159
835	121	10.8	377	5	BY075544	BY075544	AGENCOURT	908	113.5	10.1	584	5	BP250707	BP250707
836	121	10.8	492	1	AV671084	AV671084	YV671084	909	113	10.0	444	7	T96904	Y952909.r1
837	121	10.8	526	5	BO565916	BO565916	gi47g06.y	910	113	10.0	713	7	CN312058	CN312058
838	121	10.8	557	4	BM254894	BM254894	516470.MA	911	113	10.0	723	5	BU410657	BU410657
839	121	10.8	683	5	BM300493	BM300493	BM300493	912	113	10.0	7102	9	AY418551	AY418551
840	121	10.8	688	6	CA308497	CA308497	UI-H-F71-	913	112.5	10.0	611	2	AW593307	AW593307
841	121	10.8	703	5	BM301620	BM301620	BM301620	914	112.5	10.0	748	7	CK138733	CK138733
842	120.5	10.7	221	5	BX447415	BX447415	AGENCOURT	915	112.5	10.0	883	7	CN019296	CN019296
843	120	10.7	273	5	BO132939	BO132939	fz35g10.y	916	112	10.0	372	4	BM743705	BM743705
844	120	10.7	353	5	BY016053	BY016053	BY016053	917	112	10.0	629	7	CN412529	CN412529
845	120	10.7	534	1	AV605303	AV605303	AV605303	918	112	10.0	648	6	CB442867	CB442867
846	120	10.7	875	2	BF531009	BF531009	602072338	919	112	10.0	669	9	DR49F8T	DR49F8T
847	119.5	10.6	395	6	CB140481	CB140481	K-EST0193	920	112	10.0	721	4	B1219897	B1219897
848	119.5	10.6	398	6	CD465668	CD465668	Leukon1.6	921	112	10.0	961	6	BY171654	BY171654
849	119.5	10.6	582	5	BP289784	BP289784	BP289784	922	111.5	9.9	552	5	EQ472599	EQ472599
850	119.5	10.6	848	7	CK236600	CK236600	AGENCOURT	923	111.5	9.9	652	5	BQ211047	BQ211047
851	119	10.6	235	6	CA946461	CA946461	ni06c11.x	924	111.5	9.9	680	5	BQ211047	UI-R-DX1-
852	119	10.6	324	7	CN661075	CN661075	AO714A10-	925	111.5	9.9	776	7	CO387930	CO387930
853	119	10.6	367	5	BY330481	BY330481	BY330481	926	111.5	9.9	783	5	BU479797	BU479797
854	119	10.6	371	6	BY767768	BY767768	BY767768	927	111.5	9.9	917	2	BF339458	BF339458
855	119	10.6	377	5	BY352647	BY352647	BY352647	928	111.5	9.9	977	4	BI857845	BI857845
856	119	10.6	381	5	BY164785	BY164785	BY164785	929	111	9.9	360	6	CD471311	CD471311
857	119	10.6	654	6	CB056916	CB056916	NISC_jj22	930	111	9.9	433	1	BE233224	BE233224
858	119	10.6	841	2	BF528870	BF528870	602043330	931	111	9.9	570	2	AL589309	AL589309
859	119	10.6	931	5	BO876201	BO876201	AGENCOURT	932	111	9.9	585	4	BM812126	BM812126
860	118.5	10.5	491	6	CB153314	CB153314	K-EST0210	933	111	9.9	3642	3	HSM801377	HSM801377
861	118.5	10.5	515	6	CB153421	CB153421	K-EST0210	934	110.5	9.8	408	5	BY314612	BY314612
862	118.5	10.5	582	5	BF310145	BF310145	BF310145	935	110.5	9.8	741	4	BG966850	BG966850
863	118	10.5	290	1	AA374988	AA374988	EST87204	936	110	9.8	357	5	BY019919	BY019919
864	118	10.5	373	5	BY134672	BY134672	BY134672	937	110	9.8	630	6	CB044799	CB044799
865	118	10.5	520	4	BM798170	BM798170	K-EST0081	938	110	9.8	684	6	CA414871	CA414871
866	118	10.5	562	5	BO130854	BO130854	i188f05.y	939	110	9.8	781	9	AY418556	AY418556
867	118	10.5	788	4	BG912617	BG912617	602808055	940	109.5	9.7	697	2	BF528688	BF528688
868	118	10.5	2273	3	AK034871	AK034871	Mus_muscu	941	109.5	9.7	891	5	BU484122	BU484122
869	118	10.5	2448	3	AK014525	AK014525	Mus_muscu	942	109	9.7	358	5	BY320846	BY320846
870	118	10.5	6914	9	AY418553	AY418553	Mus_muscu	943	109	9.7	362	5	BY173073	BY173073
871	117.5	10.4	382	7	CN484304	CN484304	hw45d01.y	944	109	9.7	491	6	CA353467	CA353467
872	117.5	10.4	592	5	BP235883	BP235883	BP235883	945	109	9.7	589	4	BM769767	BM769767
873	117.5	10.4	932	5	BU438823	BU438823	603202928	946	109	9.7	759	5	BQ5474012	BQ5474012
874	117	10.4	361	9	CQ502350	CQ502350	OST47179	947	109	9.7	783	5	BU479065	BU479065
875	117	10.4	457	1	AA305495	AA305495	EST176742	948	109	9.7	825	6	CA317002	CA317002
876	117	10.4	624	5	BX390371	BX390371	BX390371	949	108.5	9.6	282	5	BU973380	BU973380
877	117	10.4	639	4	BJ010521	BJ010521	BJ010521	950	108.5	9.6	308	1	AA296020	AA296020
878	117	10.4	669	2	AW18198	AW18198	xj93f03.x	951	108.5	9.6	1116	1	AL571513	AL571513
879	117	10.4	1320	9	CU104582	CU104582	ISB1-43F1	952	108	9.6	233	2	AW839650	AW839650
880	117	10.4	445	2	BB840170	BB840170	BB840170	953	108	9.6	508	4	B1671638	B1671638
881	116.5	10.4	558	4	BG896846	BG896846	HOA50-1-H	954	108	9.6	563	1	AL874048	AL874048
882	116.5	10.4	558	4	BG896846	BG896846	HOA50-1-H	955	108	9.6	654	4	BM697249	BM697249
883	116.5	10.4	696	2	BF529489	BF529489	602043246	956	108	9.6	659	7	CO872953	CO872953
884	116	10.3	366	5	BY324757	BY324757	BY324757	957	108	9.6	701	6	CD354133	CD354133
885	116	10.3	366	6	BY767081	BY767081	BY767081	958	108	9.6	756	7	CO738793	CO738793
886	116	10.3	366	6	BY767081	BY767081	BY767081	959	108	9.6	756	7	CO738793	SLUE04C21

959	108	9.6	775	9	AY418554	Homo sapi	1032	103	9.2	357	5	BY131735	BY131735
c 960	108	9.6	778	6	CA411964	UI-H-EZO-	1033	103	9.2	357	5	BY310928	BY310928
961	108	9.6	794	7	CK458738	9231144 MA	1034	103	9.2	738	7	CO423312	GBZHT100
962	108	9.6	839	7	CV490818	AGENCOURT	1035	103	9.2	932	6	BF346240	602018425
c 963	108	9.6	846	7	CK457667	921992 MA	1036	102.5	9.1	495	6	CA343718	673899 NC
964	108	9.6	1029	1	AL539422	AL539422	1037	102.5	9.1	578	5	BX666919	BX666919
965	108	9.6	1042	2	BF527690	602040687	1038	102.5	9.1	606	6	CA728823	wd11c.pk0
966	108	9.6	1161	4	BM467077	AGENCOURT	1039	102.5	9.1	639	4	BM489811	pgm2n.pk0
967	108	9.6	1278	3	CR597704	full-leng	1040	102.5	9.1	640	4	BM637828	170006875
968	108	9.6	1383	3	AK017865	Mus muscu	1041	102.5	9.1	672	4	BM577341	170006871
969	108	9.6	1433	3	AK016123	Mus muscu	1042	102.5	9.1	694	4	BM620184	170006874
c 970	108	9.6	1630	3	CR605965	full-leng	1043	102.5	9.1	749	8	BZ637147	OGCCJ87TC
971	107.5	9.6	686	7	CF179894	814933 MA	c1044	102.5	9.1	930	9	AL399235	T3 end of
972	107	9.5	383	6	CD471716	Leuko86.4	1045	102	9.1	356	5	BU969369	HJ11F08r
973	107	9.5	561	2	BF527166	602039844	c1046	102	9.1	424	1	AJ689562	ABJ689562
974	107	9.5	598	5	BU400752	603485038	1047	102	9.1	646	9	AG075707	Pan trogl
975	107	9.5	680	5	BU249879	603403239	c1048	102	9.1	646	9	AG075708	Pan trogl
976	107	9.5	700	4	BG910156	602805533	1049	102	9.1	707	6	CA274759	SCSBSD102
977	107	9.5	716	7	CF536406	UI-M-GVO-	1050	102	9.1	821	5	BM944051	UI-M-EHOP
978	107	9.5	745	7	CF723087	UI-M-GVO-	1051	102	9.1	882	5	BU249765	603403663
979	107	9.5	763	5	BU410360	603158087	1052	101.5	9.0	955	2	BE039709	OC02G02 O
980	107	9.5	785	4	BG911337	602807633	1053	101.5	9.0	956	2	BF345477	602019224
981	107	9.5	798	6	CD802962	UI-M-GVO-	1054	101.5	9.0	2736	9	AY402613	Pan trogl
982	107	9.5	941	5	BU409087	603158870	1055	101	9.0	308	6	CD740276	4029308 1
983	107	9.5	979	5	BU410188	602955232	1056	101	9.0	345	1	AI873583	wk29h08.x
984	107	9.5	1158	5	BU409151	603158151	1057	101	9.0	414	2	AA655801	107075 MA
c 985	106.5	9.5	457	7	CN153458	940572 MA	c1058	101	9.0	466	1	AA454641	zkx99d05.s
986	106.5	9.5	555	6	CD180838	MS1-0027T	1059	101	9.0	531	6	CA915507	PCSC16313
987	106.5	9.5	755	7	CN155571	942876 MA	1060	101	9.0	660	6	CA883427	B0103806-
988	106.5	9.5	824	5	BU369144	603596992	1061	101	9.0	684	2	BB614952	BB614952
989	106.5	9.5	850	9	CR198040	Forward s	1062	101	9.0	751	6	CD351061	UI-M-GIO-
990	106.5	9.5	888	5	BU468347	603372362	1063	101	9.0	797	4	BG819983	602782506
991	106	9.4	362	2	BY173138	BY173138	1064	101	9.0	872	5	BX336450	BX336450
992	106	9.4	378	2	AW486980	79517 MAR	1065	101	9.0	896	5	BU160160	AGENCOURT
993	106	9.4	873	5	BU427310	603232069	1066	100.5	8.9	304	1	AA285261	PMY0643 K
994	105.5	9.4	371	6	CA599565	wawic.pk0	1067	100.5	8.9	535	1	AL909801	AL909801
995	105.5	9.4	681	2	BF347167	602020964	1068	100.5	8.9	581	4	BM087557	500346 MA
996	105.5	9.4	791	6	CB998003	AGENCOURT	1069	100.5	8.9	586	7	CK494474	rswwb0.00
997	105.5	9.4	857	9	BX968872	Forward s	1070	100.5	8.9	765	2	BF345919	602017920
998	105.5	9.4	948	9	BX989560	Reverse s	1071	100.5	8.9	865	6	CD459095	FQ08 0490
999	105	9.3	372	4	BM757210	K-EST0035	1072	100.5	8.9	902	5	BU409490	603158722
1000	105	9.3	499	5	BU534446	AGENCOURT	1073	100.5	8.9	9330	3	AK090118	Mus muscu
c1001	105	9.3	756	6	CB327411	UI-R-FSO-	1074	100	8.9	359	2	AW417692	54636 MAR
c1002	104.5	9.3	444	2	BF389806	UI-R-B82-	1075	100	8.9	376	4	BM742648	K-EST0015
1003	104.5	9.3	649	6	CD312012	StrPu691.	1076	100	8.9	379	6	CB139630	K-EST0192
1004	104.5	9.3	690	6	CD294616	StrPu691.	1077	100	8.9	564	6	CA905778	PCS04511
1005	104.5	9.3	999	5	BX446538	BX446538	c1078	100	8.9	618	1	AI973128	wr47h08.x
1006	104.5	9.3	1253	5	BQ884322	AGENCOURT	1079	100	8.9	631	5	BQ246369	Tae15012F
1007	104	9.2	503	5	BU480294	603844970	c1080	100	8.9	719	6	CA412730	UI-H-EZO-
1008	104	9.2	663	7	CN368025	170005999	1081	100	8.9	935	2	BU410207	603159488
1009	104	9.2	664	1	AJ637165	AJ637165	1082	100	8.9	848	5	BF580970	602100673
1010	104	9.2	668	1	AJ637187	AJ637187	1083	99.5	8.8	563	6	CA998062	S234X H10
1011	104	9.2	707	7	CK836545	4061500 B	c1084	99.5	8.8	532	1	AL950438	wq35d10.x
c1012	104	9.2	952	3	CNS08HPM	Single re	1085	99.5	8.8	722	1	AI950438	AI950438
1013	104	9.2	962	2	BF300451	602032375	c1086	99.5	8.8	652	2	CD349219	UI-M-FY0-
1014	104	9.2	1070	5	BX359755	BX359755	c1087	99.5	8.8	727	4	BJ778009	BJ778009
1015	104	9.2	2248	3	AK081264	Mus muscu	1088	99.5	8.8	845	7	CO571803	BJ811105
1016	104	9.2	7102	9	AY418552	Pan trogl	c1089	99.5	8.8	872	3	CNS08HUS	AGENCOURT
1017	103.5	9.2	657	7	CK494148	rswwb0.00	1090	99.5	8.8	941	3	CNS08HUS	Single re
1018	103.5	9.2	672	5	BQ263492	faa23607.	1091	99.5	8.8	1040	5	BF714183	Single re
1019	103.5	9.2	680	7	CK499523	rswwb0.00	1092	99.5	8.8	1116	2	BQ527687	602040683
1020	103.5	9.2	708	2	BE193339	HVSMH008	1093	99	8.8	449	6	CB743206	AMGNNUC:N
1021	103.5	9.2	710	1	AU002237	AU002237	c1094	99	8.8	507	2	BE655314	UI-M-BHO-
1022	103.5	9.2	723	1	AU002317	AD002317	1095	99	8.8	532	1	AU265139	AU265139
1023	103.5	9.2	767	6	CD777760	TDeubs_R2	1096	99	8.8	553	4	BG367700	HVSMH001
1024	103.5	9.2	781	1	AL669025	AL669025	c1097	99	8.8	652	6	CD369984	UI-H-FT1-
1025	103.5	9.2	888	2	BF581527	602101046	1098	99	8.8	686	6	CD535240	Leukon5 1
c1026	103.5	9.2	942	1	AL538775	AL538775	c1099	99	8.8	711	6	CD193256	MS1-0078G
1027	103.5	9.2	963	2	BE196206	HVSMH009	1100	99	8.8	836	7	CO738752	S1LE04c21
1028	103	9.2	353	5	BY135479	BY135479	c1101	99	8.8	885	3	CNS08EMW	Single re
1029	103	9.2	353	5	BY337424	BY337424	1102	99	8.8	922	5	BQ949185	Single re
1030	103	9.2	354	5	BY132505	BY132505	1103	99	8.8	940	7	CF454398	AGENCOURT
1031	103	9.2	355	5	BY312652	BY312652	1104	99	8.8	1002	3	CNS08YUL	CF454398

1105	99	8.8	1018	4	BM552398	1178	96	8.5	516	6	CA915481
1106	99	8.8	1025	3	BC024540	1179	96	8.5	518	6	CA915482
1107	98.5	8.8	419	1	AA448601	c1180	96	8.5	532	6	CA915482
1108	98.5	8.8	441	7	CN282071	1181	96	8.5	538	6	CA915489
1109	98.5	8.8	548	7	CO876287	1182	96	8.5	543	6	CA915489
1110	98.5	8.8	582	2	BF695021	1183	96	8.5	584	6	CA915502
c1111	98.5	8.8	592	6	BF695021	1184	96	8.5	612	6	CA915502
c1112	98.5	8.8	597	6	BF695021	1185	96	8.5	648	6	CA915502
c1113	98.5	8.8	598	6	BF695021	1186	96	8.5	653	6	CA915502
c1114	98.5	8.8	624	2	BF695021	1187	96	8.5	655	6	CA915502
c1115	98.5	8.8	638	4	BF695021	1188	96	8.5	656	6	CA915502
c1116	98.5	8.8	654	1	BF695021	1189	96	8.5	676	6	CA915502
c1117	98.5	8.8	713	2	BF695021	1190	96	8.5	696	6	CA915502
c1118	98.5	8.8	872	7	BF695021	1191	96	8.5	807	9	CA915502
c1119	98.5	8.8	877	6	BF695021	1192	96	8.5	900	5	CA915502
c1120	98.5	8.8	922	3	BF695021	1193	96	8.5	1799	2	CA915502
c1121	98.5	8.8	954	3	BF695021	1194	95.5	8.5	280	5	CA915502
c1122	98.5	8.8	977	3	BF695021	1195	95.5	8.5	297	5	CA915502
c1123	98	8.7	487	2	BF695021	1196	95.5	8.5	529	6	CA915502
c1124	98	8.7	581	2	BF695021	1197	95.5	8.5	537	2	CA915502
c1125	98	8.7	719	4	BF695021	1198	95.5	8.5	538	6	CA915502
c1126	98	8.7	794	6	BF695021	1199	95.5	8.5	554	1	CA915502
c1127	98	8.7	801	6	BF695021	1200	95.5	8.5	566	5	CA915502
c1128	98	8.7	823	7	BF695021	1201	95.5	8.5	583	5	CA915502
c1129	98	8.7	835	5	BF695021	1202	95.5	8.5	601	4	CA915502
c1130	98	8.7	837	1	BF695021	1203	95.5	8.5	615	6	CA915502
c1131	98	8.7	886	5	BF695021	1204	95.5	8.5	651	4	CA915502
c1132	98	8.7	889	7	BF695021	1205	95.5	8.5	663	7	CA915502
c1133	98	8.7	898	4	BF695021	1206	95.5	8.5	707	8	CA915502
c1134	98	8.7	921	3	BF695021	1207	95.5	8.5	745	9	CA915502
c1135	98	8.7	1134	5	BF695021	1208	95.5	8.5	780	4	CA915502
c1136	97.5	8.7	510	5	BF695021	1209	95.5	8.5	788	8	CA915502
c1137	97.5	8.7	513	5	BF695021	1210	95.5	8.5	824	9	CA915502
c1138	97.5	8.7	558	5	BF695021	1211	95.5	8.5	830	7	CA915502
c1139	97.5	8.7	581	2	BF695021	1212	95.5	8.5	839	4	CA915502
c1140	97.5	8.7	588	1	BF695021	1213	95.5	8.5	888	5	CA915502
c1141	97.5	8.7	592	5	BF695021	1214	95.5	8.5	891	3	CA915502
c1142	97.5	8.7	698	1	BF695021	1215	95.5	8.5	926	7	CA915502
c1143	97.5	8.7	713	5	BF695021	1216	95.5	8.5	962	3	CA915502
c1144	97.5	8.7	742	5	BF695021	1217	95.5	8.5	963	3	CA915502
c1145	97.5	8.7	751	7	BF695021	1218	95	8.4	238	4	CA915502
c1146	97.5	8.7	835	1	BF695021	1219	95	8.4	418	5	CA915502
c1147	97.5	8.7	836	1	BF695021	1220	95	8.4	447	8	CA915502
c1148	97.5	8.7	893	2	BF695021	1221	95	8.4	513	6	CA915502
c1149	97.5	8.7	977	3	BF695021	1222	95	8.4	515	9	CA915502
c1150	97.5	8.7	995	2	BF695021	1223	95	8.4	541	6	CA915502
c1151	97.5	8.7	1441	3	BF695021	1224	95	8.4	552	6	CA915502
c1152	97	8.6	419	7	BF695021	1225	95	8.4	557	4	CA915502
c1153	97	8.6	538	4	BF695021	1226	95	8.4	598	4	CA915502
c1154	97	8.6	665	4	BF695021	1227	95	8.4	598	6	CA915502
c1155	97	8.6	719	9	BF695021	1228	95	8.4	606	2	CA915502
c1156	97	8.6	876	4	BF695021	1229	95	8.4	617	7	CA915502
c1157	97	8.6	1130	1	BF695021	1230	95	8.4	627	7	CA915502
c1158	97	8.6	1518	3	BF695021	1231	95	8.4	652	2	CA915502
c1159	96.5	8.6	461	6	BF695021	1232	95	8.4	675	6	CA915502
c1160	96.5	8.6	517	6	BF695021	1233	95	8.4	711	6	CA915502
c1161	96.5	8.6	522	5	BF695021	1234	95	8.4	717	5	CA915502
c1162	96.5	8.6	525	2	BF695021	1235	95	8.4	730	5	CA915502
c1163	96.5	8.6	534	9	BF695021	1236	95	8.4	758	5	CA915502
c1164	96.5	8.6	569	5	BF695021	1237	95	8.4	839	8	CA915502
c1165	96.5	8.6	593	9	BF695021	1238	95	8.4	937	5	CA915502
c1166	96.5	8.6	597	6	BF695021	1239	95	8.4	1114	4	CA915502
c1167	96.5	8.6	598	6	BF695021	1240	95	8.4	1599	3	CA915502
c1168	96.5	8.6	603	2	BF695021	1241	94.5	8.4	268	7	CA915502
c1169	96.5	8.6	633	6	BF695021	1242	94.5	8.4	399	5	CA915502
c1170	96.5	8.6	659	6	BF695021	1243	94.5	8.4	450	1	CA915502
c1171	96.5	8.6	659	6	BF695021	1244	94.5	8.4	479	6	CA915502
c1172	96.5	8.6	665	7	BF695021	1245	94.5	8.4	503	6	CA915502
c1173	96.5	8.6	743	7	BF695021	1246	94.5	8.4	520	6	CA915502
c1174	96.5	8.6	750	6	BF695021	1247	94.5	8.4	526	6	CA915502
c1175	96.5	8.6	860	4	BF695021	1248	94.5	8.4	531	6	CA915502
c1176	96.5	8.6	939	4	BF695021	1249	94.5	8.4	532	6	CA915502
c1177	96	8.5	515	6	BF695021	1250	94.5	8.4	542	6	CA915502

C1251	94.5	8.4	548	6	CD071768	CD071768 MA2-0033T	C1324	94	8.4	810	8	BZ560225	BZ560225 pacs2-164
C1252	94.5	8.4	555	6	CD180833	CD180833 MS1-0027T	1325	94	8.4	929	7	BE195896	BE195896 HVSMH009
C1253	94.5	8.4	558	4	BG637332	BG637332 SD15266.5	1326	94	8.4	979	2	CN812392	CN812392 Fq13_01b2
C1254	94.5	8.4	571	4	BG637402	BG637402 AT31301.5	1327	94	8.4	1017	5	EX382734	EX382734 BX382734
C1255	94.5	8.4	574	8	BZ711348	BZ711348 OGEAK29TC	1328	94	8.4	1137	6	CD505293	CD505293 CDA72-H08
C1256	94.5	8.4	597	4	BI947849	BI947849 HVSMEL1000	1329	94	8.4	1174	8	CD251710	CD251710 CH261-75N
C1257	94.5	8.4	597	6	CD084848	CD084848 MC1-0013T	C1330	94	8.4	1250	3	AK005742	AK005742 Mus muscu
C1258	94.5	8.4	597	6	CD084875	CD084875 MC1-0013T	1331	93.5	8.3	334	5	BU967799	BU967799 HB05G19r
C1259	94.5	8.4	597	6	CD084878	CD084878 MC1-0013T	1332	93.5	8.3	384	5	BU972101	BU972101 HB20J19r
C1260	94.5	8.4	597	6	CD084908	CD084908 MC1-0013T	1333	93.5	8.3	385	5	BU969625	BU969625 HB12B07r
C1261	94.5	8.4	598	4	BI578851	BI578851 RE72782.5	1334	93.5	8.3	386	5	BU971033	BU971033 HB16G15r
C1262	94.5	8.4	606	6	CD067866	CD067866 MA1-0051P	1335	93.5	8.3	389	5	BU971093	BU971093 HB16J11r
C1263	94.5	8.4	609	4	BI635691	BI635691 SD17118.5	1336	93.5	8.3	391	5	BU971031	BU971031 HB16G13r
C1264	94.5	8.4	610	1	AI258299	AI258299 LP01451.5	1337	93.5	8.3	395	5	BU970580	BU970580 HB15B06r
C1265	94.5	8.4	611	1	AA736027	AA736027 LM01804.5	1338	93.5	8.3	406	5	BU971066	BU971066 HB16I04r
C1266	94.5	8.4	614	6	CD084866	CD084866 MC1-0013T	1339	93.5	8.3	421	5	BU972585	BU972585 HB22B19r
C1267	94.5	8.4	614	6	CD183516	CD183516 MS1-0038U	1340	93.5	8.3	452	5	BU969621	BU969621 HB12B02r
C1268	94.5	8.4	615	6	CD084887	CD084887 MC1-0013T	1341	93.5	8.3	453	5	BU967209	BU967209 HB03J15r
C1269	94.5	8.4	615	6	CD084892	CD084892 MC1-0013T	1342	93.5	8.3	464	5	BU966976	BU966976 HB02P01r
C1270	94.5	8.4	615	7	CK662434	CK662434 LP22658.5	1343	93.5	8.3	466	5	BU971378	BU971378 HB17H02r
C1271	94.5	8.4	619	4	BI629526	BI629526 RH58408.5	1344	93.5	8.3	468	5	BU974322	BU974322 HB27J04r
C1272	94.5	8.4	621	4	BI637617	BI637617 SD19668.5	1345	93.5	8.3	482	6	CA727350	CA727350 wde1f.pk0
C1273	94.5	8.4	625	1	AI403890	AI403890 GH23431.5	1346	93.5	8.3	489	7	CF293561	CF293561 3ODGS--02
C1274	94.5	8.4	626	4	BI612186	BI612186 RH40605.5	1347	93.5	8.3	493	5	BU972925	BU972925 HB23C23r
C1275	94.5	8.4	629	1	AI259764	AI259764 LP03253.5	1348	93.5	8.3	503	5	BU972962	BU972962 HB23E22r
C1276	94.5	8.4	632	4	BI230753	BI230753 RH14785.5	1349	93.5	8.3	506	5	BU975784	BU975784 HB32E20r
C1277	94.5	8.4	633	4	BI585810	BI585810 RH25484.5	1350	93.5	8.3	524	5	BU970487	BU970487 HB14M17r
C1278	94.5	8.4	634	1	AI387752	AI387752 GH18404.5	1351	93.5	8.3	525	5	BU975382	BU975382 HB31A02r
C1279	94.5	8.4	635	4	BM350545	BM350545 MEST267-F	1352	93.5	8.3	538	5	BU971656	BU971656 HB19E09r
C1280	94.5	8.4	636	1	AI532736	AI532736 SD04336.5	1353	93.5	8.3	551	5	BU970412	BU970412 HB14J03r
C1281	94.5	8.4	637	7	CR285301	CR285301 CR285301	1354	93.5	8.3	554	5	BU971888	BU971888 HB19P15r
C1282	94.5	8.4	641	1	AI294933	AI294933 LP08424.5	1355	93.5	8.3	554	5	BU989466	BU989466 HF21N02r
C1283	94.5	8.4	641	4	BI640558	BI640558 SD23469.5	1356	93.5	8.3	555	5	BU967417	BU967417 HB04E03r
C1284	94.5	8.4	646	4	BI632782	BI632782 SD26850.5	1357	93.5	8.3	560	5	BU967176	BU967176 HB03I03r
C1285	94.5	8.4	659	4	BI484574	BI484574 R867695.5	1358	93.5	8.3	564	5	BU971409	BU971409 HB17I10r
C1286	94.5	8.4	661	4	BG636508	BG636508 SD14239.5	1359	93.5	8.3	567	5	BU974819	BU974819 HB29D10r
C1287	94.5	8.4	662	7	CK662002	CK662002 LP21896.5	C1360	93.5	8.3	575	6	CD084970	CD084970 MC1-0013U
C1288	94.5	8.4	670	7	CK659917	CK659917 LP18051.5	1361	93.5	8.3	576	5	BU987660	BU987660 HF15G10r
C1289	94.5	8.4	672	6	CD132840	CD132840 MGI-0024U	1362	93.5	8.3	578	5	BU971609	BU971609 HB19C04r
C1290	94.5	8.4	672	6	CD673033	CD673033 fgl19f07.Y	1363	93.5	8.3	578	7	CF292565	CF292565 3ODGS--01
C1291	94.5	8.4	676	4	BG640688	BG640688 SD11828.5	1364	93.5	8.3	595	5	BU970519	BU970519 HB14O06r
C1292	94.5	8.4	682	1	AA695503	AA695503 GM02930.5	1365	93.5	8.3	599	5	BU968286	BU968286 HB07A18r
C1293	94.5	8.4	682	4	BI640035	BI640035 SD22786.5	1366	93.5	8.3	599	5	BU990164	BU990164 HF24E09r
C1294	94.5	8.4	682	4	BM336252	BM336252 MEST191-E	1367	93.5	8.3	600	5	BU971236	BU971236 HB17A05r
C1295	94.5	8.4	687	4	BM625803	BM625803 170006874	1368	93.5	8.3	630	5	BM309890	BM309890 BW309890
C1296	94.5	8.4	688	4	BG641327	BG641327 SD12647.5	1369	93.5	8.3	635	5	BU970271	BU970271 HB14C12r
C1297	94.5	8.4	696	4	BI639642	BI639642 SD22278.5	1370	93.5	8.3	664	5	BU970309	BU970309 HB14E04r
C1298	94.5	8.4	701	4	BI641486	BI641486 SD24835.5	1371	93.5	8.3	667	5	BU968908	BU968908 HB08P06r
C1299	94.5	8.4	712	2	BE454779	BE454779 HVSMH009	1372	93.5	8.3	669	9	CR329616	CR329616 Medicago
C1300	94.5	8.4	717	7	CK658252	CK658252 LP15051.5	1373	93.5	8.3	682	2	BF111548	BF111548 7131b03.x
C1301	94.5	8.4	719	6	CD493958	CD493958 CDA08-A11	1374	93.5	8.3	686	5	BQ608859	BQ608859 BRY 4774
C1302	94.5	8.4	719	7	CK662192	CK662192 LP22224.5	1375	93.5	8.3	691	6	CD457109	CD457109 Fq05_0100
C1303	94.5	8.4	738	4	BM351144	BM351144 MEST2733-H	1376	93.5	8.3	700	6	CB867873	CB867873 LC02D17w
C1304	94.5	8.4	787	1	AV653736	AV653736 AV653736	1377	93.5	8.3	717	4	BM611987	BM611987 H70006871
C1305	94.5	8.4	1014	3	CNS08HPL	BK012373 Single re	1378	93.5	8.3	731	4	BI947098	BI947098 HVSMEL1000
C1306	94	8.4	357	6	BY776755	BY776755	1379	93.5	8.3	734	5	BM310209	BM310209 BW310209
C1307	94	8.4	422	4	BF962319	BF962319 CM2-NN024	1380	93.5	8.3	737	5	BU408899	BU408899 603158673
C1308	94	8.4	429	1	AV612005	AV612005 AV612005	1381	93.5	8.3	743	5	BM038390	BM038390 BW038390
C1309	94	8.4	431	1	AV613377	AV613377 AV613377	1382	93.5	8.3	758	2	BF540003	BF540003 602050633
C1310	94	8.4	440	4	BI682719	BI682719 463878 MA	1383	93.5	8.3	820	5	BE258340	BE258340 603415434
C1311	94	8.4	478	6	CD472195	CD472195 Leuk086.1	1384	93.5	8.3	821	2	BE194695	BE194695 HVSMH008
C1312	94	8.4	523	4	BJ377114	BJ377114 BJ377114	1385	93.5	8.3	883	5	BU410535	BU410535 603159084
C1313	94	8.4	558	7	CN811449	CN811449 F314_02d0	1386	93.5	8.3	895	5	BU379021	BU379021 603809204
C1314	94	8.4	559	2	BF720471	BF720471 mab54902.	1387	93.5	8.3	913	5	BX929008	BX929008 BX929008
C1315	94	8.4	576	4	BI640324	BI640324 SD23150.5	1388	93.5	8.3	933	7	CF455747	CF455747 AGENCOURT
C1316	94	8.4	579	6	CA915519	CA915519 PCSC18921	1389	93.5	8.3	954	3	CNS08NIW	CNS08NIW Single re
C1317	94	8.4	580	7	CK771636	CK771636 959996 MA	1390	93.5	8.3	986	3	AG436708	AG436708 Single re
C1318	94	8.4	648	6	BY705907	BY705907 BY705907	C1391	93.5	8.3	988	9	AC436708	AC436708 Mus muscu
C1319	94	8.4	662	6	CA915478	CA915478 PCS03761	C1392	93.5	8.3	1045	2	CNS077FZ	CNS077FZ T3 end of
C1320	94	8.4	686	5	BQ472335	BQ472335 HB09018T	1393	93.5	8.3	1438	2	BF308980	BF308980 601889651
C1321	94	8.4	725	6	CA362129	CA362129 636116 NC	C1394	93.5	8.3	2014	9	CL495734	CL495734 SAIL615
C1322	94	8.4	791	4	BG913452	BG913452 602811347	1395	93	8.3	350	5	BY333231	BY333231 BY333231
C1323	94	8.4	806	3	AY108509	AY108509 Zea mays	1396	93	8.3	350	6	CB148204	CB148204 K-E5T0204

c1397	93	8.3	400	6	CD139422	CD139422	MG1-0063P	1470	92	8.2	585	4	BM135198	BM135198	WHE04955_B
c1398	93	8.3	484	7	CR451426	CR451426		1471	92	8.2	587	1	AU060244	AU060244	AU060244
1399	93	8.3	569	4	B233925	B233925		1472	92	8.2	601	1	AU038566	AU038566	AU038566
1400	93	8.3	577	7	CO149290	EST824343		1473	92	8.2	622	1	AU039441	AU039441	AU039441
1401	93	8.3	583	5	BU061948	Fgr_1_C09		c1474	92	8.2	632	7	CK830701	CK830701	4054131_B
1402	93	8.3	599	5	BU065600	Fgr_8_A04		1475	92	8.2	637	5	BM331082	BM331082	BM331082
1403	93	8.3	602	5	BU065748	Fgr_8_G12		1476	92	8.2	641	4	B2427552	B2427552	B2427552
1404	93	8.3	611	5	BU063938	Fgr_3_M10		1477	92	8.2	641	9	CE584023	CE584023	tigr-988-
1405	93	8.3	616	5	BQ240366	Ta05018E		c1478	92	8.2	646	4	B2374149	B2374149	B2374149
c1406	93	8.3	619	7	CV062592	BNEL80g3		1479	92	8.2	649	5	BM333700	BM333700	BM333700
1407	93	8.3	628	5	BU060427	Fgr_3_C_1_C		1480	92	8.2	657	4	BI717231	BI717231	1031018F0
1408	93	8.3	629	5	BU063391	Fgr_3_A22		c1481	92	8.2	658	4	B2344640	B2344640	B2344640
1409	93	8.3	632	5	BU062861	Fgr_2_F15		c1482	92	8.2	672	5	BU289149	BU289149	603606602
1410	93	8.3	652	5	BU061832	Fgr_10_P1		1483	92	8.2	716	5	BM191082	BM191082	BM191082
1411	93	8.3	662	5	BU065057	Fgr_6_I08		1484	92	8.2	791	7	CV482121	CV482121	AGENCOURT
c1412	93	8.3	669	3	CNS08YUM	BU034586	Single re	c1485	92	8.2	799	6	CB290356	CB290356	UCRCS01_0
1413	93	8.3	673	5	BU066047	Fgr_9_D09		1486	92	8.2	803	5	BQ804754	BQ804754	WHE3558_E
1414	93	8.3	689	4	BG282894	602752945		1487	92	8.2	842	4	BJ727525	BJ727525	BJ727525
1415	93	8.3	693	2	BE585577	EST#5PSP6		1488	92	8.2	874	6	CB655800	CB655800	OSJNEC091
1416	93	8.3	698	5	BU061577	Fgr_10_E2		1489	92	8.2	962	5	BU523208	BU523208	AGENCOURT
1417	93	8.3	699	4	BM617026	170006871		1490	92	8.2	968	8	BZ782674	BZ782674	PUGDG40TD
1418	93	8.3	727	2	BF345271	602018048		c1491	92	8.2	996	9	CG128856	CG128856	PUIDR92TB
1419	93	8.3	831	9	CL959549	Osf1CC003		1492	92	8.2	1015	5	BX379260	BX379260	BX379260
1420	93	8.3	856	4	BI732810	603353915		c1493	91.5	8.1	341	2	BE171025	BE171025	QV3-HT054
1421	93	8.3	942	9	CNS02SK4	Teradon		1494	91.5	8.1	369	6	CD087457	CD087457	MC1-0037T
1422	93	8.3	967	2	BF303662	BF303662	601886309	c1495	91.5	8.1	414	1	AI991634	AI991634	wr15a02.x
1423	93	8.3	1108	5	BA446348	BA446348		c1496	91.5	8.1	465	6	CD060848	CD060848	MA1-0011G
1424	93	8.3	1120	7	CK208889	CK208889	FGA502061	c1497	91.5	8.1	471	4	BI950216	BI950216	HVSMEI001
1425	93	8.3	1139	6	CD497067	CD425-G09		1498	91.5	8.1	477	4	BG366481	BG366481	HVSMEI000
1426	93	8.3	1320	5	B0278750	AGENCOURT		1499	91.5	8.1	478	4	BG366455	BG366455	HVSMEI000
1427	93	8.3	1683	9	CI949714	Osf1SB003		1500	91.5	8.1	481	5	BQ755857	BQ755857	Ebed07_SO
1428	92.5	8.2	420	1	AJ481820	AJ481820									
1429	92.5	8.2	420	1	AJ481825	AJ481825									
1430	92.5	8.2	420	1	AJ481827	AJ481827									
c1431	92.5	8.2	469	7	CR746620	CR746620									
1432	92.5	8.2	480	1	AJ481821	AJ481821									
1433	92.5	8.2	480	1	AJ481823	AJ481823									
1434	92.5	8.2	480	1	AJ481824	AJ481824									
1435	92.5	8.2	498	2	AW207527	UI-H-B11									
1436	92.5	8.2	540	1	AJ481822	AJ481822									
1437	92.5	8.2	540	1	AJ481826	AJ481826									
1438	92.5	8.2	587	1	AJ436147	AJ436147									
1439	92.5	8.2	629	5	BU109792	BU109792	603002182								
c1440	92.5	8.2	631	6	CA111556	CA111556									
1441	92.5	8.2	641	5	BQ247185	BQ247185	TaE15028B								
c1442	92.5	8.2	659	8	BH335046	BH335046	CH230-99F								
1443	92.5	8.2	660	4	BM621556	170006874									
1444	92.5	8.2	661	7	CV041591	CV041591	4139476_B								
1445	92.5	8.2	741	2	BE194453	BE194453	HVSMEI008								
c1446	92.5	8.2	818	5	BU292688	BU292688	603607107								
1447	92.5	8.2	855	9	CC904230	CC904230	t012122ba								
c1448	92.5	8.2	946	3	CNS08NIX	CNS08NIX									
1449	92.5	8.2	964	3	CNS08EMV	CNS08EMV									
1450	92.5	8.2	1011	9	CNS06HQG	CNS06HQG									
1451	92.5	8.2	1018	4	BG913279	BG913279	602811967								
1452	92.5	8.2	1068	9	CNS06GGQ	CNS06GGQ									
1453	92.5	8.2	3219	3	AK034300	AK034300	Mus muscu								
1454	92	8.2	320	5	BQ472530	HB09E15T									
c1455	92	8.2	394	4	BJ374584	BJ374584	BJ374584								
1456	92	8.2	401	5	BX251968	BX251968									
c1457	92	8.2	414	4	BJ374319	BJ374319									
1458	92	8.2	452	1	AU034607	AU034607									
1459	92	8.2	457	4	BI230016	BI230016	RE27933.5								
1460	92	8.2	458	4	BG900403	BG900403	HOA5-1-H5								
1461	92	8.2	460	1	AU052892	AU052892									
1462	92	8.2	462	4	BI606019	BI606019	RH72092.5								
1463	92	8.2	486	4	BI578639	BI578639	RE72533.5								
1464	92	8.2	489	4	BI363185	BI363185	RE47940.5								
1465	92	8.2	506	1	AU052499	AU052499									
c1466	92	8.2	527	5	BM065908	BM065908									
1467	92	8.2	562	7	CK689591	CK689591	ZF101-P00								
c1468	92	8.2	563	4	BJ399021	BJ399021									
1469	92	8.2	566	5	BM192463	BM192463									

## ALIGNMENTS

RESULT 1	AL546217	769 bp	mrna	linear	EST 25-MAR-2004
LOCUS	AL546217	Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA			
DEFINITION	AL546217	Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA			
ACCESSION	AL546217	GI:45746685			
VERSION	AL546217.3	GI:45746685			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 769)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	On Feb 15, 2001 this sequence version replaced gi:31268051.				
	Contact: Genoscope				
	Genoscope - Centre National de Sequencage				
	2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE				
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr				
	ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime				
	end enriched, double-strand cDNA was digested with Not I and cloned				
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library				
	was normalized. Library was constructed by Life Technologies, a				
	division of Invitrogen. This sequence belongs to sequence cluster				
	5952.r				
	For more information about this cluster, see				
	http://www.genoscope.cns.fr/cdna?e=CS0D1025DH08QPl&c=5952.r.				
FEATURES	Location/Qualifiers				
source	1..769				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="CS0D1025YP16"				
	/tissue_type="PLACENTA COT 25-NORMALIZED"				
	/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"				
	/note="1st strand cDNA was primed with a NotI-oligo(dT)"				

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:  
Pred. No.: 2,41e-105 Length: 769  
Score: 1125.00 Matches: 218  
Percent Similarity: 100.00% Conservat: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-063-670-6\_COPY\_17\_234 (1-218) x AL546217 (1-769)

Qy	1	ThrArgLeuLeuValGlnGlnGlySerLeuArgAlaGluGluLeuSerlleGlnValSerCys	20
Db	113	ACGAGGCTCTGGTCCAGGCTCTTTCGTCGACAGAGCTTTCCATCCAGGTGTCTATGC	172
Qy	21	ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu	40
Db	173	AGAAATTATGGGATCACCTTGTGAGCAAAAGCGAACCCAGAGCTGAATTTCCACGAA	232
Qy	41	AlaLysGluAlaCysArgLeuLeuGlyLysSerLeuAlaGlyLysAspGlnValGluThr	60
Db	233	GCTAAGGAGGCTGTAGCTGCTGGGACTAAGTTTGGCCGCGAAGCAAGTTGAACA	292
Qy	61	AlaLeuLysAlaSerPheGluThrCysSerTyrglyTrpValGlyAspGlyPheValVal	80
Db	293	GCCTTGAAGCTAGCTTGAACCTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTC	352
Qy	81	IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp	100
Db	353	ATCTCTAGGATTAACCCAAACCCAGGTGTGGGAAAATGGGTGGGTGTCCTGATTGG	412
Qy	101	LysValProValSerArgGlnPheAlaAlaTyrcystyrAsnSerSerAspThrTrpThr	120
Db	413	AAGGTTCCAGTGAGCCACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTGGACT	472
Qy	121	AsnSerCysIleProGluIleIleThrThryLysAspProIlePheAsnThrGlnThrAla	140
Db	473	AACCTCGTCATTCAGAAATATATACCAACCAAGATCCCATATATCAACACTCAAACTGCA	532
Qy	141	ThrGlnThrThrGluPheIleValSerAspSerThrTyrsrValAlaSerProTyrsr	160
Db	533	ACACAACAACAGAAATTTATGTCAGTGACAGTACCTACTCTCGGTGGGATCCCTTACTCT	592
Qy	161	ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg	180
Db	593	ACAATACCTGCCCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCAGCGAGA	652
Qy	181	LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr	200
Db	653	AAAAAATGTATTTGTGTGCACAGAGTTTTTATGGAACCTAGCACCATGTCTACAGAACT	712
Qy	201	GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly	218
Db	713	GAACCAATTTGTTGAAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGA	766

RESULT 2  
BX459046  
LOCUS BX459046 Homo sapiens PLACENTA mRNA linear EST 05-MAY-2004  
DEFINITION S-PRIME, mRNA sequence.  
ACCESSION BX459046  
VERSION BX459046.2 GI:47051789  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1. (bases 1 to 845)  
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE  
JOURNAL  
COMMENT

Full-length cDNA libraries and normalization  
Unpublished (2001)  
On May 22, 2003 this sequence version replaced gi:31021086.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 5952.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0DE011DG10QP1&c=5952.r.

FEATURES  
source

Location/Qualifiers  
1..845  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DE011YN20"  
/tissue\_type="PLACENTA"  
/clone\_lib="Homo sapiens PLACENTA"  
/notes="Vector: pCMVSPORT\_6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."

ORIGIN

Alignment Scores:  
Pred. No.: 2,75e-105 Length: 845  
Score: 1125.00 Matches: 218  
Percent Similarity: 100.00% Conservat: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-10-063-670-6\_COPY\_17\_234 (1-218) x BX459046 (1-845)

Qy	1	ThrArgLeuLeuValGlnGlnGlySerLeuArgAlaGluGluLeuSerlleGlnValSerCys	20
Db	112	ACGAGGCTCTGGTCCAGGCTCTTTCGTCGACAGAGCTTTCCATCCAGGTGTCTATGC	171
Qy	21	ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu	40
Db	172	AGAAATTATGGGATCACCTTGTGAGCAAAAGCGAACCCAGAGCTGAATTTCCACGAA	231
Qy	41	AlaLysGluAlaCysArgLeuLeuGlyLysSerLeuAlaGlyLysAspGlnValGluThr	60
Db	232	GCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGCGAAGCAAGTTGAACA	291
Qy	61	AlaLeuLysAlaSerPheGluThrCysSerTyrglyTrpValGlyAspGlyPheValVal	80
Db	292	GCCTTGAAGCTAGCTTGAACCTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTC	351
Qy	81	IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp	100
Db	352	ATCTCTAGGATTAACCCAAACCCAGGTGTGGGAAAATGGGTGGGTGTCCTGATTGG	411
Qy	101	LysValProValSerArgGlnPheAlaAlaTyrcystyrAsnSerSerAspThrTrpThr	120
Db	412	AAGGTTCCAGTGAGCCACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTGGACT	471
Qy	121	AsnSerCysIleProGluIleIleThrThryLysAspProIlePheAsnThrGlnThrAla	140
Db	472	AACCTCGTCATTCAGAAATATATACCAACCAAGATCCCATATATCAACACTCAAACTGCA	531
Qy	141	ThrGlnThrThrGluPheIleValSerAspSerThrTyrsrValAlaSerProTyrsr	160
Db	532	ACACAACAACAGAAATTTATGTCAGTGACAGTACCTACTCTCGGTGGGATCCCTTACTCT	591
Qy	161	ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg	180



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Db      592 ACAATACCTGCCCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCAGGAGA 651
      181 LysLysLeuLeuCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
      652 AAAAAATTTGATTTGTGTACAGAGCTTTTATGGAACCTAGCACCATCTACAGAAACT 711
      201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
      712 GAACCATTTGTTGAAATTAAGACGACATTCAAGATGAAGCTGCTGGGTTTGA 765

RESULT 3
LOCUS   AL543874
DEFINITION AL543874 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1005YG13 5-PRIME, mRNA sequence.
ACCESSION AL543874
VERSION   AL543874.3 GI:45719422
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 855)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31265719.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5952.i
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1005AD07QPI&c=5952.i.
FEATURES
source
1. 855
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1005YG13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 2.8e-105 Length: 855
Score: 1125.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-063-670-6_COPY_17_234 (1-218) x AL543874 (1-855)

Qy      1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20
      147 ACGAGGCTCTGTGTCGAAGGCTCTTTGCTGCAGAAAGAGCTTTCATCCAGGTGTCATGC 206
      21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40
      207 AGAATTATGGGGATCACCTTTGTGAGCAAAAGGCGACACGACGCTGAATTTACAGAA 266
      41 AlalysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60

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Db      267 GCTAAGGAGGCTCTAGGCTCTGGGACTAAGTTTGGCCGCAAGGCAAGTTTGAACA 326
      61 AlalysLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80
      327 GCCTTGAAGAGCTAGCTTTTGAACCTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTC 386
      81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100
      387 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTCTCTGATTTGG 446
      101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120
      447 AAGTTTCAGTGCAGCCGACAGCTTTGCAGCCCTATTGTTACAACTCATCTGATCTTGGACT 506
      121 AsnSerCysIleProGluIleThrThrLysAspProIlePheAsnThrGlnThrAla 140
      507 AACTCGTGCAATCCAGAAATTTATCACCACCAAGATCCCATATTTCAACACATCAAACTGCA 566
      141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160
      567 ACACAAAACACAGAAATTTATTGTGTCAGTACACTACTCGGTGGCATCCCTTACTCT 626
      161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180
      627 ACAATACCTGCCCTACTACTACTCTCTCTCTCTCCAGCTTCCAGCTTCTATTTCACGGAGA 686
      181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
      687 AAAAAATTTGTTGTCGTCACAGAAATTTTATGGAACCTAGCACCATCTCTACAGAAACT 746
      201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
      747 GAACCATTTGTTGAAATTAAGACGACATTCAAGATGAAGCTGCTGGGTTTGA 800

RESULT 4
LOCUS   AL553858
DEFINITION AL553858 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1077YJ17 5-PRIME, mRNA sequence.
ACCESSION AL553858
VERSION   AL553858.3 GI:45858623
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 946)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31275672.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5952.i
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1077CE09QPI&c=5952.i.
FEATURES
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1. 946
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1077YJ17"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)

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primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Alignment Scores:  
 Pred. No.: 3.23e-105 Length: 946  
 Score: 1125.00 Matches: 218  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 1 Gaps: 0

US-10-063-670-6\_COPY\_17\_234 (1-218) x AL553858 (1-946)

Qy	1	ThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerlleGlnValSerCys	20
Db	142	ACGAGGCTCTGGTCCAAAGGCTCTTTCGGTGCAGAGAGCTTCCATCCAGGTGTCTATGC	201
Qy	21	ArgileMetGlylleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu	40
Db	202	AGAAATATGGGATCACCCCTTGAGCAAAAAGCGAACGAGCTGAATTTACAGAA	261
Qy	41	AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr	60
Db	262	GCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGACCAAGTTGAACA	321
Qy	61	AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal	80
Db	322	GCCTTGAAGCTAGCTTTGAACACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTC	381
Qy	81	IleSerArgileSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp	100
Db	382	ATCTTAGGATTAGCCCAACCCCAAGTGTGGNAAATGGGTGGGTGCTCTGATTGG	441
Qy	101	LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr	120
Db	442	AAGGTTCCAGTGAGCCGACAGTTTATGTCAGTACCTACTCGGTGGCATCCCTTACTCT	501
Qy	121	AsnSerCysIleProGluIlelleThrThrLysAspProillePheAsnThrGlnThrAla	140
Db	502	AACCTGTCGATTCAGAAAATTATCACCACCAAGATCCCATATTTCAACACTCAAACTGCA	561
Qy	141	ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer	160
Db	562	ACACAAACACAGAAATTTATGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCT	621
Qy	161	ThrIleProAlaProThrThrThrProAlaProAlaSerThrSerlleProArgArg	180
Db	622	ACAATACCTGCCCTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGA	681
Qy	181	LysLysLysLeulleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr	200
Db	682	AAAAAATTTGATTTGTGCACAGAGTTTATATGGAACACTAGCACCATGTCTACAGAACT	741
Qy	201	GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly	218
Db	742	GAACCATTTGTTGAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGA	795

## RESULT 5

AL552299

LOCUS

DEFINITION AL552299 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI069YN02 5-PRIME, mRNA sequence.

ACCESSION AL552299

VERSION AL552299.3

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1. (bases 1 to 965)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

## TITLE

JOURNAL

COMMENT

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31274114.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CSODI069DGO1QPL&c=5952.r.

## FEATURES

source

Location/Qualifiers

1..965

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CSODI069YN02"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

/notes="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Alignment Scores:

Pred. No.: 3.33e-105 Length: 965

Score: 1125.00 Matches: 218

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 1 Gaps: 0

US-10-063-670-6\_COPY\_17\_234 (1-218) x AL552299 (1-965)

Qy 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerlleGlnValSerCys

20

Db 142 ACGAGGCTCTGGTCCAAAGGCTCTTTCGGTGCAGAGAGCTTCCATCCAGGTGTCTATGC

201

Qy 21 ArgileMetGlylleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu

40

Db 202 AGAATTTATGGGATCACCCCTTGTGACAAAAGCGAACGAGCTGAATTTACAGAA

261

Qy 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr

60

Db 262 GCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGACCAAGTTGAACA

321

Qy 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal

80

Db 322 GCCTTGAAGCTAGCTTTGAACACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTC

381

Qy 81 IleSerArgileSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp

100

Db 382 ATCTTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATCGGGTGGGTGCTCTGATTGG

441

Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr

120

Db 442 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGACT

501

Qy 121 AsnSerCysIleProGluIlelleThrThrLysAspProillePheAsnThrGlnThrAla

140

Db 502 AACTCGTGCAATCCAGAAATTTATCACCACCAAGATCCCATATTTCAACACTCAAACTGCA

561

Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer

160

Db 562 ACACAAACACAGAAATTTATGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCT

621

Qy 161 ThrIleProAlaProThrThrThrProAlaProAlaSerThrSerlleProArgArg

180

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Db      622 ACAATACCTGCCCTACTACTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGA 681
Qy      181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
Db      682 AAAAAATGATTTGTGTGCACGAAGTTTTTATGGAAACTAGCACCATGCTACAGAAACT 741
Qy      201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
Db      742 GAACCATTTGTTGAAAAATAAGCAGCAITTCAGAAATGAAGCTGCTGGGTTTGGGA 795

RESULT 6
LOCUS   AL544430
DEFINITION AL544430 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
ACCESSION AL544430
VERSION   AL544430.3 GI:45744933
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1017)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31266274.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5952.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1018BD06Q1&c=5952.r.
FEATURES
Location/Qualifiers
source
1. 1017
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1018YG12"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 3.59e-105 Length: 1017
Score: 1125.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-063-670-6_COPY_17_234 (1-218) x AL544430 (1-1017)
Qy      1 ThrArgLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20
Db      219 ACGAGGCTCTGGTCCCAAGGCTCTTGGTGCAGAAAGCTTTCATCCAGGTGTCATGC 278
Qy      21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40
Db      279 AGAATTATGGGATCACCTTGTGAGCAAAAAGCGACACGAGCTGAATTCACAGAA 338
Qy      41 AlalysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60

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Db      339 GCTAAGGAGGCGCTGCTGGACTAGTTTGGCCGCGCAAGGACCAAGTTGAAACA 398
Qy      61 AlaleuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80
Db      399 GCCTTGAAGAGTAGCTTTTGAACCTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGTC 458
Qy      81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100
Db      459 ATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTCTCTGATTTGG 518
Qy      101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120
Db      519 AAGGTTCCAGTGACGCCACACAGTTTGCAGCCTATTGTTACAACTCATCTGATATTGGACT 578
Qy      121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140
Db      579 AACTCGTGCAATCCAGAAATTTATCACCACCAAGATCCCATATTTCAACACTCAAACTGCA 638
Qy      141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160
Db      639 ACACAAAACAACAGAAATTTATTGTGCAGTGACAGTACTACTCGTGGCATCCCTTACTCT 698
Qy      161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180
Db      699 ACAATACCTGCCCTACTACTACTCTCTCTCTCCAGTCCACTTCTATTATCCACGGAGA 758
Qy      181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
Db      759 AAAAAATGATTTGTGTGCACAGAAAGTTTTTATGAAACTAGCACCATGCTACAGAAAACT 818
Qy      201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
Db      819 GAACCATTTGTTGAAAAATAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGGA 872

RESULT 7
LOCUS   BX402505
DEFINITION BX402505 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
ACCESSION BX402505
VERSION   BX402505.2 GI:46921551
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1036)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30630733.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5952.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS1A1012ZA06Q1&c=5952.r.
FEATURES
Location/Qualifiers
source
1. 1036
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1045YA10"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was

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digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores: 3.69e-105 Length: 1036  
Pred. No.: 1125.00 Matches: 218  
Score: 1125.00  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-10-063-670-6\_COPY\_17\_234 (1-218) x BX402505 (1-1036)

Qy 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys 20  
Db 202 ACGAGGCTCTGGTCCAAAGGCTCTTTCGGTGCAGAGAGCTTCCATCCAGGTGTCAIGC 261  
Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAenPheThrGlu 40  
Db 262 AGAATTATGGGATCACCTTGTGAGCAAAAGGCAAGCAGCAGCTGAATTCACAGAA 321  
Qy 41 AlalysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60  
Db 322 GCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAACA 381  
Qy 61 AlaleuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80  
Db 382 GCCTTGAAGCTAGCTTTGAAACTTTCAGCTATGCTGGGTGGAGATGGATTCGTGGTC 441  
Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100  
Db 442 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAATGGGTGGGTGCTGCTGATTGG 501  
Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120  
Db 502 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGACTTGGACT 561  
Qy 121 AsnSerCysIleProGluIleIleThrThryLysAspProIlePheAenThrGlnThrAla 140  
Db 562 AACTCGTGATTCAGAAATATACCAACCAAGATCCCATATATCAACACTCAAACTGCA 621  
Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160  
Db 622 ACACAAACACAGAAATTAATGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCT 681  
Qy 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180  
Db 682 ACAATAGCTGCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGAGA 741  
Qy 181 LysIleLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200  
Db 742 AAAAAATTGATTGTGTCACAGAGATTTTATGGAACCTAGCACCATGCTACAGAACT 801  
Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218  
Db 802 GAACCAATTGTTGAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGA 855

RESULT 8  
AL551020 1043 bp mRNA linear EST 25-MAR-2004  
LOCUS  
DEFINITION AL551020 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CS001066YL13 5-PRIME, mRNA sequence.  
ACCESSION AL551020  
VERSION AL551020.3 GI:45751381  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1043)  
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization

JOURNAL COMMENT

Unpublished (2001)  
On Feb 15, 2001 this sequence version replaced gi:31272837.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
5952.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0D1066CF07QP1&c=5952.r.

FEATURES source

1..1043  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0D1066YL13"  
/tissue type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/notes="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores: 3.72e-105 Length: 1043  
Pred. No.: 1125.00 Matches: 218  
Score: 1125.00  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-063-670-6\_COPY\_17\_234 (1-218) x AL551020 (1-1043)

Qy 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys 20  
Db 79 ACGAGGCTCTGGTCCAAAGGCTCTTTCGGTGCAGAGAGCTTCCATCCAGGTGTCAIGC 138  
Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAenPheThrGlu 40  
Db 139 AGAATTATGGGATCACCTTGTGAGCAAAAGGCAAGCAGCAGCTGAATTCACAGAA 198  
Qy 41 AlalysGluAlaCysArgLeuLeuGlyLysSerLeuAlaGlyLysAspGlnValGluThr 60  
Db 199 GCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAACA 258  
Qy 61 AlaleuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80  
Db 259 GCCTTGAAGCTAGCTTTGAAACTTTCAGCTATGCTGGGTGGAGATGGATTCGTGGTC 318  
Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100  
Db 319 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAATGGGTGGGTGCTGCTGATTGG 378  
Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120  
Db 379 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGACTTGGACT 438  
Qy 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAenThrGlnThrAla 140  
Db 439 AACTCGTGCAATTCAGAAATATACCAACCAAGATCCCATATATCAACACTCAAACTGCA 498  
Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160  
Db 499 ACACAAACACAGAAATTAATGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCT 558  
Qy 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180  
Db 559 ACAATACCTGCCCTACTACTACTCTCTGCTCCAGCTTCCACTTCTATTCCACGAGA 618

Qy 181 LysLysLeuLeuLeuValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200  
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 Db 619 AAAAAATTGATTGTGTGCACGAAAGTTTTTATGGAACTAGCACCATCTCTACAGAACT 678  
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 Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218  
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 Db 679 GAACCATTTGTTGAAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGG 732  
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RESULT 9  
 AL547774 1056 bp mRNA linear EST 25-MAR-2004  
 LOCUS  
 DEFINITION AL547774 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
 clone CSODI033YD11 5-PRIME, mRNA sequence.

ACCESSION AL547774  
 VERSION  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Homo sapiens (human)

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 JOURNAL Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 COMMENT Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On Feb 15, 2001 this sequence version replaced gi:31269603.

CONTACT Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 5952.r

For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?s=CSODI033CB06QPl&c=5952.r.  
 Location/Qualifiers

FEATURES  
 source  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CSODI033YD11"  
 /tissue\_type="PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 3,79e-105 Length: 1056  
 Score: 1125.00 Matches: 218  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 1 Gaps: 0

US-10-063-670-6\_COPY\_17\_234 (1-218) x AL547774 (1-1056)

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 Db 244 ACGAGGCTCTGTGCTCAGAGCTCTTTGGTGCAGAGAGCTTTCCATCCAGGTGTCATGC 303  
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 Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnLeuAsnPheThrGlu 40  
 |||||  
 Db 304 AGAATTATGGGATCACCTTTGTGAGCAAAAGCGCAACAGCAGCTGAATTTACAGAA 363  
 |||||  
 Qy 41 AlalysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60  
 |||||  
 Db 364 GCTAAGGAGGCGCTGTAGGCTCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACA 423  
 |||||

Qy 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80  
 |||||  
 Db 424 GCCTTGAAGAGTAGCTTTGAAACTTGCAGCTATGCGTGGGTGGAGATGGATTCTCGTGC 483  
 |||||  
 Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100  
 |||||  
 Db 484 ATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAATGGGGTGGGTCTCTGATTTGG 543  
 |||||  
 Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120  
 |||||  
 Db 544 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACT 603  
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 Qy 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140  
 |||||  
 Db 604 AACTCGTGCATTCAGAAATTTATCACCACCAAGATCCCATATTTCAACACATCAAACTGCA 663  
 |||||  
 Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160  
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 Db 664 ACACAAACACAGAAATTTATTTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCT 723  
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 Qy 161 ThrIleProAlaProThrThrThrProAlaProAlaSerThrSerIleProArgArg 180  
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 Db 724 ACATACCTGCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCAGGAGA 783  
 |||||  
 Qy 181 LysLysLeuLeuCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200  
 |||||  
 Db 784 AAAAAATTGATTGTGTGCAGAAAGTTTTTATGGAACTAGCACCATGCTCTACAGAACT 843  
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 Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218  
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 Db 844 GAACCATTTGTTGAAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGG 897  
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RESULT 10  
 LOCUS  
 DEFINITION AL546669 1090 bp mRNA linear EST 25-MAR-2004  
 clone CSODI029YJ09 5-PRIME, mRNA sequence.

ACCESSION AL546669  
 VERSION  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Homo sapiens (human)

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 JOURNAL Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 COMMENT Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On Feb 15, 2001 this sequence version replaced gi:31268502.  
 CONTACT Genoscope

Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 5952.r

For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?s=CSODI029CE05QPl&c=5952.r.

FEATURES  
 source  
 1..1090  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CSODI029YJ09"  
 /tissue\_type="PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Alignment Scores:  
Pred. No.: 3.96e-105 Length: 1090  
Score: 1125.00 Matches: 218  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-063-670-6\_COPY\_17\_234 (1-218) x AL546669 (1-1090)

Qy 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys 20  
|||  
Db 112 ACGAGGCTCTGGTCCAGGCTCTTTGGGTGCAGAGAGCTTCCATCCAGGTGTATGC 171  
  
Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40  
|||  
Db 172 AGAATTATGGGATCACCCCTTGTGAGCAAAAAGCGAACACAGCAGCTGAATTTACAGAA 231  
  
Qy 41 AlalysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60  
|||  
Db 232 GCTAAGGAGGCTGTAGGCTGCTGGACTAAGTTTGGCCGCAAGCAAGTTGAACA 291  
  
Qy 61 AlaleuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80  
|||  
Db 292 GCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGTC 351  
  
Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100  
|||  
Db 352 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAAATGGGTGGGTCTCTGATTGG 411  
  
Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120  
|||  
Db 412 AAGTTTCCAGTGACCCGACAGTTTGCAGCCCTATTGTTACAACTCATCTGATCTGGACT 471  
  
Qy 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140  
|||  
Db 472 AACTCGTGATTCAGAAATATACCCACCAAGATCCCATATTCACACTCAAACTGCA 531  
  
Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160  
|||  
Db 532 ACACAAACACAGAAATTTATTTGTCAGTGACAGTACCTACTCTCGGTGGCATCCCTTACTCT 591  
  
Qy 161 ThrIleProAlaProThrThrProAlaProAlaSerThrSerIleProAlaArg 180  
|||  
Db 592 ACAATACCTGCCCTACTACTCTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGA 651  
  
Qy 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200  
|||  
Db 652 AAAAAATGATTGTGTACAGAGATTTTATGAAACTAGCACCATGTCTACAGAACT 711  
  
Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218  
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Db 712 GAACCAATTTGTTGAAATTAAGCAGCATTCAGAAATGAAGCTGTGGGTTTGA 765

## RESULT 11

AL550279 1091 bp mRNA linear EST 25-MAR-2004  
LOCUS  
DEFINITION AL550279 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CS001039YJ06 5-PRIME, mRNA sequence.

ACCESSION AL550279

VERSION AL550279.3 GI:45750655

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1091)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

## REFERENCE

AUTHORS

TITLE

JOURNAL

## COMMENT

On Feb 15, 2001 this sequence version replaced gi:31272096.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
S952.r

For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0DI039DE030P1&c=S952.r.

## FEATURES

## source

Location/Qualifiers

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/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DI039YJ06"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Alignment Scores:  
Pred. No.: 3.97e-105 Length: 1091  
Score: 1125.00 Matches: 218  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-10-063-670-6\_COPY\_17\_234 (1-218) x AL550279 (1-1091)

Qy 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys 20  
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Db 107 ACGAGGCTCTGGTCCAGGCTCTTTGGGTGCAGAGAGCTTCCATCCAGGTGTATGC 166  
  
Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40  
|||  
Db 167 AGAATTATGGGATCACCCCTTGTGAGCAAAAAGCGAACACAGCAGCTGAATTTACAGAA 226  
  
Qy 41 AlalysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60  
|||  
Db 227 GCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAACA 286  
  
Qy 61 AlaleuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80  
|||  
Db 287 GCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGTC 346  
  
Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100  
|||  
Db 347 ATCTTAGGATTAGCCCAACCCCAAGTGTGGGAAAAAATGGGTGGGTGTCTGATTGG 406  
  
Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120  
|||  
Db 407 AAGGTTCCAGTGAGCGCAGAGTTTGCAGCCCTATTGTTACAACTCATCTGATCTGGACT 466  
  
Qy 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140  
|||  
Db 467 AACTCGTGATTCAGAAATATATACCCACCAAGATCCCATATTCACACTCAAACTGCA 526  
  
Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160  
|||  
Db 527 ACACAAACACAGAAATTTATTTGTCAGTGACAGTACCTACTCTCGGTGGCATCCCTTACTCT 586  
  
Qy 161 ThrIleProAlaProThrThrThrProAlaProAlaSerThrSerIleProAlaArg 180  
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Db 587 ACAATACCTGCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGA 646

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Qy 181 LysLysLeuLeuValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
Db 647 AAAAAATTTGATTTGTGTACAGAACTTTTATGGAAACTAGCACCATCTACAGAAACT 706

Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
Db 707 GAACCATTTGTTGAAAAATAAGCAGCAATTCAGAAATGAAGCTGTGGGTTTGGGA 760

RESULT 12
CR598862 1781 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0D1039YJ06 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR598862.1 GI:50479669
VERSION Full-length cDNA libraries and normalization
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1781)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
REFERENCE 2 (bases 1 to 1781)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
Location/Qualifiers
1..1781
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1039YJ06"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores: 7.99e-105 Length: 1781
Pred. No.: 1125.00 Matches: 218
Score: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-063-670-6_COPY_17_234 (1-218) x CR598862 (1-1781)

Qy 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20
Db 107 ACGAGGCTCTGGTCCAGAGGCTCTTTGGTCGACAGAGAGCTTTCATCCAGGTGCATGC 166

Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40
Db 167 AGAATTATGGGATCACCTTGTGAGCAAAAAGGCAACGAGCAGCTGAATTTACAGAA 226

Qy 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerIleAlaGlyLysAspGlnValGluThr 60
Db 227 GCTAAGGAGGCTGTAGGCTGCTGGGACTAAAGTTTGGCGCGCAAGCAAGTTGAACA 286

Qy 61 AlaLeuLysAlaSerPheGluThrCysSerThrGlyTrpValGlyAspGlyPheValVal 80
Db 287 GCCTTGAAGAGCTAGCTTTTGAACCTTGCAGCTATGCTGGCTGGGTGGAGATGGATTCGTGTC 346

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Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuLeuTrp 100
Db 347 ATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGTCTCTGATTTGG 406

Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120
Db 407 AAGGTTTCAGTGAGCCGACAGCTTTTGACGCCCTATTGTTACAACTCATCTGATCATTTGACT 466

Qy 121 AsnSerCysIleProGluIleThrThrLysAspProIlePheAsnThrGlnThrAla 140
Db 467 AACTCGTGCAATTCAGAAAAATTTATCACCACCAAAAGATCCCATATTTCAACACATCAAACTGCA 526

Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160
Db 527 ACACAAAACACAGAAATTTATTGTGTCAGTAGTACTACTCGGTGGCATCCCTTACTCT 586

Qy 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180
Db 587 ACAATACTGCGCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGA 646

Qy 181 LysLysLeuLeuCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
Db 647 AAAAAATTTGATTTGTGTACAGAAAGTTTATGGAAACTAGCACCATCTACAGAAACT 706

Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
Db 707 GAACCATTTGTTGAAAAATAAGCAGCAATTCAGAAATGAAGCTGTGGGTTTGGGA 760

RESULT 13
CR614245 1786 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0D1029YJ09 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR614245
VERSION CR614245.1 GI:50495052
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1786)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
REFERENCE 2 (bases 1 to 1786)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
Location/Qualifiers
1..1786
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1029YJ09"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores: 8.02e-105 Length: 1786
Pred. No.: 1125.00 Matches: 218
Score: 100.00% Conservat: 0
Percent Similarity: 100.00%

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-063-670-6_COPY_17_234 (1-218) x CR614245 (1-1786)
Qy 1 ThrArgLeuValGlnGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20
Db 112 ACAGAGCTCTGTCCTCAAGGCTCTTTCGGTGCAGAGAGCTTCCATCCAGGTGTCTATGC 171
Qy 21 ArgIleMetGlyIleThrLeuValSerIlylsAlaSerGlnGlnLeuAsnPheThrGlu 40
Db 172 AGAATTATGGGGATCACCCCTTGTGAGCAAAAGCGAACACAGCAGCTGAATTTTCACAGAA 231
Qy 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60
Db 232 GCTAAGGAGGCTGTAGCTGCTGGGACTAGTTTGGCCGCAAGGACCAAGTTTGAACA 291
Qy 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValVal 80
Db 292 GCCTTGAAGAGCTAGCTTTGAAACTTTCAGCTATGCTGGTGGGTGGAGATGGATTCGTGGTC 351
Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyr 100
Db 352 ATCTCTAGGATTTAGCCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCCTGATTGG 411
Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThr 120
Db 412 AAGTTTCAGTGAGCCGACAGCTTTGACGCCCTATTGTTACAACTCATCTGATCTTGGACT 471
Qy 121 AsnSerCysIleProGluIleThrThrLysAspProIlePheAsnThrGlnThrAla 140
Db 472 AACTCGTGCACTTCAGAAAAATTATCACCAACAAAGATCCCATATTTCAACACTCAAACTGCA 531
Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160
Db 532 ACACAAAACAAGAAATTTATTGTGAGTGACAGTACCTACTCGGGTGGATCCCTTACTCT 591
Qy 161 ThrIleProAlaProThrThrThrProAlaProAlaSerThrSerIleProArgArg 180
Db 592 ACAATACCTGCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTTCACGGAGA 651
Qy 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
Db 652 AAAAAATTTGTTGTGCACAGAAAGTTTTTATGGAAGTCAAGCAATGAAGCTGCTGGGTTTGA 711
Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
Db 712 GAACCATTTGTTGAAAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGA 765

RESULT 14
CR604450 1797 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSOD1065YD17 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR604450
VERSION CR604450.1 GI:50485257
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1797)
AUTHORS Li W.B., Gruber C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope. 2 (bases 1 to 1797)
Direct Submission
AUTHORS Genoscope.
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL CR612000

```

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

FEATURES  
Location/Qualifiers  
source  
1..1797  
/organism="Homo sapiens"  
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/plasmid="pCMVSPORT\_6"

ORIGIN

Alignment Scores:  
Pred. No.: 8.09e-105 Length: 1797  
Score: 1125.00 Matches: 218  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-10-063-670-6\_COPY\_17\_234 (1-218) x CR604450 (1-1797)

Qy 1 ThrArgLeuValGlnGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20  
Db 142 ACAGAGCTCTGTCCTCAAGGCTCTTTCGGTGCAGAGAGCTTCCATCCAGGTGTCTATGC 201  
Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40  
Db 202 AGAATTATGGGATCACCCCTTGTGACAAAAAGCGAACACAGCAGCTGAATTTTCACAGAA 261  
Qy 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60  
Db 262 GCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAAGTTTGGCCGCAAGGACCAAGTTGAACA 321  
Qy 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTyrValGlyValGlyPheValVal 80  
Db 322 GCCTTGAAGAGCTAGCTTTGAAACTTTCAGCTATGAGCTGGGTGGAGATGGATTCGTGGTC 381  
Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyr 100  
Db 382 ATCTTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTGATTGG 441  
Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThr 120  
Db 442 AAGTTTCCAGTGAGCGGACAGTTTGCAGCCCTATTGTTTACAACTCATCTGATCTTGGACT 501  
Qy 121 AsnSerCysIleProGluIleThrThrLysAspProIlePheAsnThrGlnThrAla 140  
Db 502 AACTCGTGCACTTCAGAAAAATTATCACCAACAAAGATCCCATATTTCAACACTCAAACTGCA 561  
Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160  
Db 562 ACACAAAACAAGAAATTTATTGTGTCAGTACAGTACCTACTCGGTGGCATCCCTTACTCT 621  
Qy 161 ThrIleProAlaProThrThrThrProAlaProAlaSerThrSerIleProArgArg 180  
Db 622 ACAATACCTGCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTTATTTCCACGGAGA 681  
Qy 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200  
Db 682 AAAAAATTTGATTGTTGTGCAGAAAGTTTTTATGGAAGTCAAGCAATGAAGCTGCTGGGTTTGA 741  
Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218  
Db 742 GAACCATTTGTTGAAAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGA 795

RESULT 15  
CR612000



LOCUS CR612000 1820 bp mRNA linear HTC 21-JUL-2004  
DEFINITION full-length cDNA clone CSODI069YN02 of Placenta Cot 25-normalized  
of Homo sapiens (human).  
ACCESSION CR612000  
VERSION CR612000.1 GI:50492807  
KEYWORDS HTC; CNSLT cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1820)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ InVivoGen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1820)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
Location/Qualifiers  
source 1..1820  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSODI069YN02"  
/tissue\_type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"  
ORIGIN  
Alignment Scores:  
Pred. No.: 8.24e-105 Length: 1820  
Score: 1125.00 Matches: 218  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
US-10-063-670-6\_COPY\_17\_234 (1-218) x CR612000 (1-1820)  
Qy 1 ThrArgLeuValGlnGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20  
Db 146 ACAGGGCTCCTGGTCCCAAGGCTCTTTGGTGCAGAAAGAGCTTCCATCCAGGTGCATGC 205  
Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40  
Db 206 AGAATTATGGGGATCACCTTGTGGGCAAAAAGCGAACCCAGCAGCTGAATTCACAGAA 265  
Qy 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60  
Db 266 GCTAAGGAGGCGCTGTAGGCTCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACA 325  
Qy 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80  
Db 326 GCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGCGCTGGGTTGGAGATGGATTCGTGGTC 385  
Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100  
Db 386 ATCTTAGGATTAGCCCAACCCCAAGTGTGGGAAAATATGGGGTGGGTGTCCTGATTGG 445  
Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120  
Db 446 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGACT 505  
Qy 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140

Db 506 AACTCGTGCATTCCAGAAATTTATCACCACCAAGATCCCATATTTCAACACTCAAACTGCA 565  
Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160  
Db 566 ACACAAACACAGAAATTTATTGTCACTGACAGTACCTACTCGGTGGCATCCCTTACTCT 625  
Qy 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180  
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Search completed: October 8, 2005, 22:45:17  
Job time : 2833.6 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 8, 2005, 22:45:22 ; Search time 582.544 Seconds  
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Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

# SUMMARIES

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2	1125	100.0	2029	22	US-10-820-474A-198	Sequence 198, App
3	1125	100.0	2324	18	US-10-276-774-999	Sequence 999, App
6	1125	100.0	2372	9	US-09-905-291A-200	Sequence 200, App
95	1125	100.0	2372	15	US-10-223-085-31	Sequence 31, Appl
96	1125	100.0	2372	15	US-10-223-084-31	Sequence 31, Appl
97	1125	100.0	2372	15	US-10-223-088-31	Sequence 31, Appl
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236	1125	100.0	2372	17	US-10-425-447-200	Sequence 200, App
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255	645	57.3	411	10	US-09-918-995-8107	Sequence 8107, Ap
256	508.5	45.2	531	21	US-10-696-639-2768	Sequence 2768, Ap
257	281.5	25.0	457	9	US-09-864-761-15431	Sequence 15431, A
258	277	24.6	492	15	US-10-291-634-12	Sequence 12, Appl
259	221.5	19.7	559	15	US-10-079-111-3	Sequence 3, Appli
260	213.5	19.0	2747	9	US-09-917-800A-1588	Sequence 1588, Ap
261	213.5	19.0	2747	22	US-10-024-607-7	Sequence 7, Appli
262	209.5	18.6	1177	22	US-10-024-607-24	Sequence 24, Appl
263	209.5	18.6	5452	19	US-10-741-601-57	Sequence 57, Appl
264	209.5	18.6	5452	21	US-10-741-600-219	Sequence 219, App
265	207	18.4	1089	22	US-10-024-607-25	Sequence 25, Appl
266	203	18.0	3091	22	US-10-741-600-226	Sequence 226, App
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270	203	18.0	5468	19	US-10-741-601-60	Sequence 60, Appl
271	203	18.0	5468	21	US-10-741-600-225	Sequence 225, App
272	203	18.0	5674	19	US-10-741-601-54	Sequence 54, Appl
273	203	18.0	5674	21	US-10-741-600-218	Sequence 218, App
274	203	18.0	5739	19	US-10-741-601-55	Sequence 55, Appl
275	203	18.0	5739	21	US-10-741-600-221	Sequence 221, App
276	202	18.0	3083	21	US-10-690-880-18	Sequence 18, Appl
277	199.5	17.7	2316	11	US-09-836-544-33	Sequence 33, Appl
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284	198.5	17.6	4674	15	US-10-084-817-181	Sequence 181, Appl	357	135.5	12.0	3153	10	US-10-189-123-73	Sequence 73, Appl
285	198.5	17.6	4675	22	US-10-765-700-97	Sequence 97, Appl	358	135.5	12.0	3153	16	US-10-188-495-73	Sequence 73, Appl
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287	197.5	17.6	5053	21	US-10-741-600-216	Sequence 216, Appl	360	131.5	11.7	2652	14	US-10-195-970-4	Sequence 4, Appl
288	197	17.5	1354	11	US-09-836-544-31	Sequence 31, Appl	361	131.5	11.7	2652	7	US-10-453-420-4	Sequence 1, Appl
289	197	17.5	1794	15	US-10-007-926A-376	Sequence 376, Appl	362	131.5	11.7	4706	9	US-09-842-930A-1	Sequence 1, Appl
290	197	17.5	1794	21	US-10-482-029-254	Sequence 254, Appl	363	131.5	11.7	4706	15	US-10-133-172-1	Sequence 1, Appl
291	197	17.5	1794	21	US-10-852-335A-36	Sequence 36, Appl	364	131.5	11.7	4706	21	US-10-990-844-1	Sequence 1, Appl
292	197	17.5	1794	21	US-10-956-157-443	Sequence 443, Appl	365	130.5	11.6	7137	21	US-10-956-157-562	Sequence 562, Appl
293	197	17.5	4335	19	US-10-741-601-56	Sequence 56, Appl	366	130.5	11.6	7137	22	US-10-287-436A-235	Sequence 235, Appl
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295	197	17.5	4633	19	US-10-741-601-61	Sequence 61, Appl	368	127.5	11.3	1365	13	US-10-098-841-328	Sequence 328, App
296	197	17.5	4633	21	US-10-741-600-224	Sequence 224, Appl	369	127.5	11.3	1925	20	US-10-723-860-6530	Sequence 6530, Ap
297	197	17.5	4723	19	US-10-741-601-53	Sequence 53, Appl	372	127.5	11.3	1985	9	US-09-905-291A-212	Sequence 212, App
298	197	17.5	4723	21	US-10-741-600-217	Sequence 217, Appl	902	127.5	11.3	1985	16	US-10-174-587-27	Sequence 27, Appl
299	197	17.5	4874	19	US-10-741-601-59	Sequence 59, Appl	937	127.5	11.3	1985	16	US-10-299-976-212	Sequence 212, App
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322	188	16.7	336	21	US-10-487-620-7	Sequence 7, Appl	984	127.5	11.3	2652	14	US-10-195-970-5	Sequence 5, Appl
323	186	16.5	336	21	US-10-487-620-9	Sequence 9, Appl	986	127.5	11.3	2730	10	US-09-759-1308-329	Sequence 329, App
324	184	16.4	336	21	US-10-487-620-11	Sequence 11, Appl	987	127.5	11.3	2730	14	US-10-189-123-59	Sequence 59, Appl
325	182	16.2	336	21	US-10-487-620-3	Sequence 3, Appl	988	127.5	11.3	2730	16	US-10-188-495-59	Sequence 59, Appl
326	175.5	15.6	2764	22	US-10-450-763-17058	Sequence 17058, A	989	127.5	11.3	2730	17	US-10-741-790-329	Sequence 329, App
327	170.5	15.2	2273	22	US-10-450-763-17062	Sequence 17062, A	990	127.5	11.3	2878	17	US-10-453-420-7	Sequence 7, Appl
328	170	15.1	106	9	US-09-864-761-31946	Sequence 31946, A	991	127.5	11.3	2878	17	US-10-295-027-259	Sequence 259, App
329	166.5	14.8	399	10	US-09-918-995-36412	Sequence 36412, A	992	127.5	11.3	3438	18	US-10-312-352-60	Sequence 60, Appl
330	164.5	14.6	444	21	US-10-696-639-1827	Sequence 1827, Ap	1001	127.5	11.3	3476	14	US-10-237-535-51	Sequence 51, Appl
331	158	14.0	549	15	US-10-101-510-85	Sequence 85, Appl	1010	127.5	11.3	3476	14	US-10-239-196-51	Sequence 51, Appl
332	158	14.0	549	21	US-10-505-680-476	Sequence 476, Appl	1101	127.5	11.3	3476	21	US-10-936-626-11	Sequence 11, Appl
333	153.5	13.6	270	20	US-09-927-463-7	Sequence 7, Appl	1102	127.5	11.3	3476	21	US-10-938-061-11	Sequence 11, Appl
334	153.5	13.6	270	20	US-10-837-671-7	Sequence 7, Appl	1103	127.5	11.3	2465	9	US-09-917-800A-500	Sequence 500, App
335	150	13.3	2863	17	US-10-104-047-610	Sequence 610, Appl	1104	126	11.2	201	21	US-10-741-600-7000	Sequence 7000, Ap
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1126	125	11.1	1414	11	US-09-968-007A-208	Sequence 208, App	1199	108	9.6	1640	14	US-10-091-438-33	Sequence 33, Appl
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1147	118.5	10.5	12319	16	US-10-240-965-240	Sequence 240, App	1220	107	9.5	2011	22	US-10-667-723-3	Sequence 3, Appli
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1169	113	10.0	12644	14	US-10-161-803-45	Sequence 45, Appl	1242	105.5	9.4	1308	20	US-10-613-076-14	Sequence 14, Appl
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1175	112.5	10.0	4642	15	US-10-133-172-3	Sequence 3, Appli	1248	104	9.2	4767	11	US-09-973-278-731	Sequence 731, App
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1188	109	9.7	6310	9	US-09-795-651-45	Sequence 45, Appl	1261	100.5	8.9	1825	19	US-10-437-963-93701	Sequence 93701, A
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1311	93.5	8.3	9416	19	US-10-755-889-614	Sequence 614, App	1384	89	7.9	1251	14	US-10-125-635A-383	Sequence 383, App
1312	93.5	8.3	9416	21	US-10-489-740-114	Sequence 114, App	1385	89	7.9	1251	16	US-10-195-833-383	Sequence 383, App
1313	93.5	8.3	11917	22	US-10-765-700-32	Sequence 32, Appli	1386	89	7.9	1251	17	US-10-286-333-383	Sequence 383, App
1314	93.5	8.3	11950	16	US-10-252-157-218	Sequence 218, App	1387	89	7.9	1251	17	US-10-244-830-383	Sequence 383, App
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1316	93	8.3	1909	18	US-10-425-114-7404	Sequence 7404, Ap	1389	89	7.9	1251	19	US-10-648-780-383	Sequence 383, App
1317	93	8.3	2111	18	US-10-424-599-105989	Sequence 105989, A	1390	89	7.9	1251	19	US-10-648-780-383	Sequence 383, App
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150	86	7.6	25375	4	US-09-949-016-12849	Sequence 12849, A	223	84.5	7.5	5697	3	US-08-812-829-11	Sequence 11, Appl
151	85.5	7.6	1320	3	US-09-221-654-1	Sequence 1, Appl	224	84.5	7.5	51723	4	US-09-949-016-12152	Sequence 12152, A
152	85.5	7.6	1320	3	US-08-989-358A-1	Sequence 1, Appl	225	84.5	7.5	51723	4	US-09-949-016-16991	Sequence 16991, A
153	85.5	7.6	1323	4	US-09-475-515-35	Sequence 35, Appl	226	84.5	7.5	276237	4	US-09-949-016-17504	Sequence 17504, A
154	85.5	7.6	1387	4	US-09-475-515-34	Sequence 34, Appl	C 227	84	7.5	564	4	US-09-583-110-2585	Sequence 2585, Ap
155	85.5	7.6	1453	4	US-09-475-515-33	Sequence 33, Appl	228	84	7.5	795	4	US-09-248-796A-7800	Sequence 7800, Ap
156	85.5	7.6	1593	3	US-08-933-359-23	Sequence 23, Appl	229	84	7.5	1125	2	US-08-997-080-153	Sequence 153, App
157	85.5	7.6	1593	4	US-09-482-558A-23	Sequence 23, Appl	230	84	7.5	1125	3	US-08-997-362-153	Sequence 153, App
158	85.5	7.6	1638	4	US-09-799-451-412	Sequence 412, App	231	84	7.5	1125	3	US-09-095-855-153	Sequence 153, App
159	85.5	7.6	1836	4	US-09-475-515-41	Sequence 41, Appl	232	84	7.5	1125	3	US-09-324-542-153	Sequence 153, App
160	85.5	7.6	1836	4	US-09-475-515-44	Sequence 44, Appl	233	84	7.5	1125	3	US-09-205-426-153	Sequence 153, App
161	85.5	7.6	1836	4	US-09-475-515-47	Sequence 47, Appl	234	84	7.5	1176	2	US-08-387-942C-17	Sequence 17, Appl
162	85.5	7.6	1896	3	US-09-620-412C-324	Sequence 324, App	235	84	7.5	5163	3	US-08-387-942C-17	Sequence 17, Appl
163	85.5	7.6	1896	4	US-09-598-419-324	Sequence 324, App	236	84	7.5	5163	3	US-08-928-361B-4	Sequence 4, Appl
164	85.5	7.6	1944	4	US-09-475-515-37	Sequence 37, Appl	237	84	7.5	5163	4	US-08-928-361B-4	Sequence 4, Appl
165	85.5	7.6	1944	4	US-09-475-515-38	Sequence 38, Appl	238	84	7.5	5318	3	US-08-700-651-1	Sequence 2, Appl
166	85.5	7.6	1944	4	US-09-475-515-40	Sequence 40, Appl	239	84	7.5	5318	3	US-08-928-361B-3	Sequence 3, Appl
167	85.5	7.6	1944	4	US-09-475-515-43	Sequence 43, Appl	240	84	7.5	5318	4	US-09-588-995A-1	Sequence 3, Appl
168	85.5	7.6	1944	4	US-09-475-515-46	Sequence 46, Appl	241	84	7.5	5511	3	US-08-928-361B-2	Sequence 2, Appl
169	85.5	7.6	2025	4	US-09-475-515-36	Sequence 36, Appl	242	84	7.5	5511	3	US-09-588-995A-2	Sequence 2, Appl
170	85.5	7.6	2025	4	US-09-475-515-39	Sequence 39, Appl	243	84	7.5	5679	3	US-08-814-052-9	Sequence 9, Appl
171	85.5	7.6	2025	4	US-09-475-515-42	Sequence 42, Appl	244	84	7.5	5679	3	US-08-812-829-9	Sequence 9, Appl
172	85.5	7.6	2025	4	US-09-475-515-45	Sequence 45, Appl	245	84	7.5	7334	3	US-08-928-361B-1	Sequence 1, Appl
173	85.5	7.6	2028	4	US-09-107-532A-1973	Sequence 1973, Ap	246	84	7.5	7334	3	US-09-588-995A-1	Sequence 1, Appl
174	85.5	7.6	2298	4	US-09-476-242-22	Sequence 22, Appl	247	84	7.5	12598	2	US-08-387-942C-1	Sequence 1, Appl
175	85.5	7.6	2298	4	US-09-476-242-23	Sequence 23, Appl	248	84	7.5	99960	4	US-09-762-311-2	Sequence 2, Appl
176	85.5	7.6	2298	4	US-09-476-242-24	Sequence 24, Appl	249	83.5	7.4	1107	2	US-08-991-300-1	Sequence 1, Appl
177	85.5	7.6	2310	4	US-09-476-242-3	Sequence 3, Appl	250	83.5	7.4	1459	3	US-09-377-557-13	Sequence 13, Appl

251	83.5	7.4	2353	4	US-09-369-247-12	Sequence 12, Appl	324	80	7.1	597	4	US-09-902-540-8148	Sequence 8148, Ap
252	83.5	7.4	2455	3	US-09-103-429A-1	Sequence 1, Appl	c 325	80	7.1	744	4	US-09-252-991A-15538	Sequence 15538, A
253	83.5	7.4	2455	4	US-09-294-663-1	Sequence 1, Appl	c 326	80	7.1	807	4	US-09-252-991A-15537	Sequence 15427, A
254	83.5	7.4	2821	3	US-09-103-429A-2	Sequence 2, Appl	327	80	7.1	975	3	US-09-365-150-4	Sequence 4, Appl
255	83.5	7.4	2821	4	US-09-294-663-2	Sequence 2, Appl	328	80	7.1	1275	4	US-09-252-991A-15254	Sequence 15254, A
256	83.5	7.4	65848	4	US-09-949-016-13285	Sequence 13285, A	329	80	7.1	1359	4	US-09-252-991A-15302	Sequence 15302, A
257	83	7.4	630	4	US-09-270-767-1924	Sequence 1924, Ap	c 330	80	7.1	2538	4	US-09-248-796A-3859	Sequence 3859, Ap
258	83	7.4	630	4	US-09-270-767-17206	Sequence 17206, A	331	80	7.1	6269	4	US-09-902-540-836	Sequence 836, App
259	83	7.4	966	4	US-09-252-991A-11896	Sequence 11896, A	332	80	7.1	6301	4	US-09-902-540-842	Sequence 842, App
260	83	7.4	2905	4	US-09-949-016-410	Sequence 410, App	333	80	7.1	9960	3	US-08-822-586-46	Sequence 46, Appl
261	83	7.4	2906	4	US-09-949-016-5249	Sequence 5249, Ap	c 334	80	7.1	16265	4	US-09-902-540-1126	Sequence 1126, Ap
262	83	7.4	4063	4	US-09-902-540-595	Sequence 595, App	c 335	80	7.1	40408	4	US-09-949-016-16331	Sequence 16331, A
263	83	7.4	4545	3	US-09-221-017B-1011	Sequence 1011, Ap	c 336	80	7.1	247781	4	US-09-949-016-14133	Sequence 14133, A
264	83	7.4	72704	4	US-09-902-540-1273	Sequence 1273, Ap	337	80	7.1	254405	4	US-09-949-016-14381	Sequence 14381, A
265	83	7.4	1230230	4	US-09-438-185A-1	Sequence 1, Appl	c 338	80	7.1	536165	4	US-09-214-808-1	Sequence 1, Appl
266	82.5	7.3	1842	4	US-09-016-434-1236	Sequence 1336, Ap	c 339	79.5	7.1	601	4	US-09-949-016-22247	Sequence 2247, A
267	82.5	7.3	2298	4	US-09-252-991A-13540	Sequence 13540, A	c 340	79.5	7.1	601	4	US-09-949-016-51354	Sequence 51354, A
268	82.5	7.3	2412	4	US-09-252-991A-13908	Sequence 13908, A	341	79.5	7.1	612	4	US-09-270-767-3415	Sequence 3415, Ap
269	82.5	7.3	6022	4	US-08-956-171E-92	Sequence 92, Appl	342	79.5	7.1	612	4	US-09-270-767-18657	Sequence 18697, A
270	82.5	7.3	6022	4	US-08-781-986A-92	Sequence 92, Appl	343	79.5	7.1	768	4	US-09-248-796A-7148	Sequence 7148, A
271	82.5	7.3	23847	4	US-09-902-540-1177	Sequence 1177, Ap	344	79.5	7.1	909	4	US-09-252-991A-2103	Sequence 2103, Ap
272	82.5	7.3	194937	4	US-09-949-016-17032	Sequence 17032, A	345	79.5	7.1	959	4	US-09-902-540-102	Sequence 102, App
273	82.5	7.3	194937	4	US-09-949-016-17033	Sequence 17033, A	346	79.5	7.1	975	4	US-09-489-039A-1422	Sequence 1422, Ap
274	82	7.3	423	1	US-08-470-179-160	Sequence 160, App	347	79.5	7.1	1002	4	US-09-252-991A-2014	Sequence 2014, Ap
275	82	7.3	466	2	US-08-892-880-13	Sequence 13, Appl	348	79.5	7.1	1270	4	US-09-270-767-12871	Sequence 12871, A
c 276	82	7.3	855	4	US-09-252-991A-10673	Sequence 10673, A	349	79.5	7.1	1371	4	US-09-252-991A-9440	Sequence 9440, Ap
277	82	7.3	875	4	US-09-443-067-27	Sequence 27, Appl	350	79.5	7.1	1965	2	US-08-809-763-5	Sequence 5, Appl
278	82	7.3	933	4	US-09-252-991A-10494	Sequence 10494, A	351	79.5	7.1	1965	3	US-08-956-253-5	Sequence 5, Appl
c 279	82	7.3	1383	4	US-09-489-039A-3928	Sequence 3928, Ap	352	79.5	7.1	3048	1	US-08-188-228-47	Sequence 47, Appl
280	82	7.3	1662	1	US-08-651-572-1	Sequence 1, Appl	353	79.5	7.1	3048	1	US-08-332-643-41	Sequence 41, Appl
281	82	7.3	1662	3	US-09-066-544-1	Sequence 1, Appl	354	79.5	7.1	3048	1	US-08-332-638-47	Sequence 47, Appl
282	82	7.3	1662	3	US-08-951-086-1	Sequence 1, Appl	355	79.5	7.1	4359	4	US-08-943-144-3	Sequence 3, Appl
283	82	7.3	1662	3	US-09-430-669-1	Sequence 1, Appl	356	79.5	7.1	5491	4	US-09-262-537-5	Sequence 5, Appl
c 284	82	7.3	4808	4	US-09-774-528-19	Sequence 19, Appl	357	79.5	7.1	5597	4	US-09-262-537-1	Sequence 1, Appl
285	82	7.3	13926	3	US-08-961-527-5	Sequence 5, Appl	358	79.5	7.1	5598	4	US-09-262-537-33	Sequence 33, Appl
286	82	7.3	40585	4	US-09-949-016-16965	Sequence 16965, A	359	79.5	7.1	5617	4	US-09-262-537-3	Sequence 3, Appl
c 287	81.5	7.2	879	5	PCT-US96-03916-16	Sequence 16, Appl	360	79.5	7.1	6474	4	US-09-854-856-51	Sequence 51, Appl
288	81.5	7.2	2309	3	US-09-091-725-9	Sequence 9, Appl	361	79.5	7.1	6558	4	US-09-854-856-35	Sequence 35, Appl
289	81.5	7.2	2406	2	US-08-687-702-2	Sequence 2, Appl	362	79.5	7.1	6654	4	US-09-854-856-19	Sequence 19, Appl
290	81.5	7.2	12687	1	US-08-676-169-1	Sequence 1, Appl	363	79.5	7.1	6738	4	US-09-854-856-3	Sequence 3, Appl
291	81.5	7.2	12687	3	US-08-981-459-1	Sequence 1, Appl	364	79.5	7.1	6885	4	US-09-854-856-49	Sequence 49, Appl
292	81.5	7.2	12687	3	US-08-063-431A-1	Sequence 1, Appl	365	79.5	7.1	6969	4	US-09-854-856-33	Sequence 33, Appl
293	81.5	7.2	13473	5	PCT-US96-03916-1	Sequence 1, Appl	366	79.5	7.1	7065	4	US-09-854-856-17	Sequence 17, Appl
294	81.5	7.2	18912	5	PCT-US96-03916-59	Sequence 59, Appl	367	79.5	7.1	7149	4	US-09-854-856-1	Sequence 1, Appl
295	81.5	7.2	20250	4	US-09-902-540-1213	Sequence 1213, Ap	368	79.5	7.1	20870	4	US-09-949-016-16017	Sequence 16017, A
c 296	81.5	7.2	421491	4	US-09-949-016-12805	Sequence 12805, A	369	79.5	7.1	121427	4	US-09-949-016-11950	Sequence 11950, A
c 297	81.5	7.2	421494	4	US-09-949-016-14060	Sequence 14060, A	370	79.5	7.1	121433	4	US-09-949-016-13230	Sequence 13230, A
298	81	7.2	621	1	US-08-028-463-7	Sequence 7, Appl	c 371	79.5	7.1	157866	4	US-09-949-016-12982	Sequence 12982, A
299	81	7.2	621	1	US-08-461-836-7	Sequence 7, Appl	c 372	79.5	7.1	157866	4	US-09-949-016-12983	Sequence 12983, A
300	81	7.2	1389	4	US-09-602-787A-77	Sequence 77, Appl	c 373	79.5	7.1	157866	4	US-09-949-016-12984	Sequence 12984, A
301	81	7.2	1850	4	US-09-848-726-1	Sequence 1, Appl	374	79.5	7.1	1664976	4	US-08-916-421B-1	Sequence 1, Appl
302	81	7.2	2465	5	PCT-US92-08090-1	Sequence 1, Appl	375	79.5	7.1	1664976	4	US-09-692-570-1	Sequence 1, Appl
c 303	81	7.2	2911	4	US-09-799-451-888	Sequence 888, App	385	79	7.0	465	4	US-09-377-502-58	Sequence 58, Appl
c 304	81	7.2	3498	4	US-09-520-781-3	Sequence 3, Appl	386	79	7.0	714	4	US-09-252-991A-8966	Sequence 8966, Ap
c 305	81	7.2	23673	3	US-09-773-816-1	Sequence 1, Appl	387	79	7.0	767	4	US-09-270-767-2226	Sequence 2226, Ap
306	80.5	7.2	771	4	US-09-902-540-5814	Sequence 5814, Ap	388	79	7.0	767	4	US-09-270-767-17508	Sequence 17508, A
307	80.5	7.2	1099	4	US-09-949-016-1829	Sequence 1829, Ap	c 389	79	7.0	837	4	US-09-252-991A-9123	Sequence 9123, Ap
308	80.5	7.2	1227	3	US-09-074-912-3	Sequence 3, Appl	c 390	79	7.0	975	4	US-09-498-520A-1	Sequence 1, Appl
309	80.5	7.2	1227	3	US-09-290-136-3	Sequence 3, Appl	c 391	79	7.0	975	4	US-09-583-110-1252	Sequence 1252, Ap
c 310	80.5	7.2	2458	3	US-09-071-101-5	Sequence 5, Appl	c 392	79	7.0	975	4	US-09-968-129-1	Sequence 1, Appl
c 311	80.5	7.2	2458	3	US-09-369-618-6	Sequence 6, Appl	c 393	79	7.0	996	4	US-09-107-433-2480	Sequence 2480, Ap
c 312	80.5	7.2	2458	3	US-09-369-617-6	Sequence 6, Appl	c 394	79	7.0	1470	3	US-09-292-225-40	Sequence 40, Appl
c 313	80.5	7.2	5220	4	US-09-677-046A-1	Sequence 1, Appl	c 395	79	7.0	1470	3	US-09-292-225-42	Sequence 42, Appl
c 314	80.5	7.2	7948	4	US-09-949-016-14929	Sequence 14929, A	c 396	79	7.0	1527	3	US-09-292-225-37	Sequence 37, Appl
c 315	80.5	7.2	7960	4	US-09-949-016-14930	Sequence 14930, A	c 397	79	7.0	1527	3	US-09-292-225-39	Sequence 39, Appl
c 316	80.5	7.2	9542	3	US-08-968-685A-9	Sequence 9, Appl	c 398	79	7.0	1621	3	US-09-292-225-34	Sequence 34, Appl
c 317	80.5	7.2	12180	4	US-09-949-016-12527	Sequence 12527, A	c 399	79	7.0	1621	3	US-09-292-225-36	Sequence 36, Appl
c 318	80.5	7.2	12180	4	US-09-949-016-14323	Sequence 14323, A	400	79	7.0	1686	4	US-09-252-991A-7673	Sequence 7673, Ap
319	80.5	7.2	16924	4	US-09-949-016-13720	Sequence 13720, A	401	79	7.0	1867	4	US-09-949-016-4889	Sequence 4889, Ap
320	80.5	7.2	16924	4	US-09-949-016-13297	Sequence 13297, A	402	79	7.0	1867	4	US-09-949-016-4890	Sequence 4890, Ap
321	80	7.1	156	1	US-08-225-477B-7	Sequence 7, Appl	403	79	7.0	2032	3	US-09-241-581B-5	Sequence 5, Appl
322	80	7.1	156	5	PCT-US95-04353-7	Sequence 7, Appl	404	79	7.0	2032	3	US-08-265-428-5	Sequence 5, Appl
323	80	7.1	288	4	US-09-252-991A-11933	Sequence 11933, A	405	79	7.0	2032	5	PCT-US95-07721-5	Sequence 5, Appl

406	79	7.0	2313	3	US-08-738-168B-14	Sequence 14, Appl	479	78	6.9	2804	1	US-08-446-794A-3	Sequence 3, Appl
c 407	79	7.0	2379	4	US-09-252-991A-9205	Sequence 9205, Ap	480	78	6.9	3793	4	US-09-902-540-587	Sequence 587, App
c 408	79	7.0	2553	4	US-09-949-016-488	Sequence 488, App	481	78	6.9	4152	3	US-08-826-134-5	Sequence 107, App
c 409	79	7.0	3767	4	US-09-823-038A-44	Sequence 44, Appl	482	78	6.9	4792	3	US-09-221-017B-107	Sequence 107, App
c 410	79	7.0	3813	4	US-09-902-540-7085	Sequence 7085, Ap	483	78	6.9	5280	4	US-09-949-016-5586	Sequence 5586, Ap
c 411	79	7.0	3815	4	US-09-902-540-634	Sequence 634, App	484	78	6.9	5293	4	US-09-949-016-524	Sequence 524, App
c 412	79	7.0	3919	1	US-08-301-722A-1	Sequence 1, Appl	485	78	6.9	5294	3	US-08-826-134-1	Sequence 1, Appl
c 413	79	7.0	3926	4	US-09-949-016-1224	Sequence 1224, App	486	78	6.9	5541	1	US-08-920-812-20	Sequence 20, Appl
c 414	79	7.0	3946	4	US-09-949-016-146	Sequence 146, App	487	78	6.9	5541	1	US-08-920-827-20	Sequence 20, Appl
c 415	79	7.0	3960	4	US-09-902-540-8918	Sequence 8918, App	488	78	6.9	5541	1	US-08-921-177-20	Sequence 20, Appl
c 416	79	7.0	4014	4	US-09-949-016-4648	Sequence 4648, Ap	489	78	6.9	5541	1	US-08-362-577C-20	Sequence 20, Appl
c 417	79	7.0	4014	4	US-09-949-016-4648	Sequence 4648, Ap	490	78	6.9	5541	2	US-08-920-828-20	Sequence 20, Appl
c 418	79	7.0	4200	1	US-07-841-654B-1	Sequence 1, Appl	491	78	6.9	6008	4	US-09-949-016-5058	Sequence 5058, Ap
c 419	79	7.0	4200	1	US-07-946-234A-1	Sequence 1, Appl	492	78	6.9	6312	1	US-08-531-601-3	Sequence 3, Appl
c 420	79	7.0	4200	1	US-08-123-161A-1	Sequence 1, Appl	493	78	6.9	6312	2	US-08-859-032-3	Sequence 3, Appl
c 421	79	7.0	4200	1	US-08-483-278-1	Sequence 1, Appl	494	78	6.9	10085	4	US-09-302-540-964	Sequence 964, App
c 422	79	7.0	4200	5	PCT-US93-01560-0-1	Sequence 1, Appl	495	78	6.9	84875	4	US-09-949-016-17334	Sequence 17334, A
c 423	79	7.0	5183	1	US-08-459-568-3	Sequence 3, Appl	496	78	6.9	84875	4	US-09-949-016-17335	Sequence 17335, A
c 424	79	7.0	5183	2	US-08-399-411-3	Sequence 3, Appl	497	78	6.9	84875	4	Sequence 17336, A	Sequence 17336, A
c 425	79	7.0	5868	3	US-08-516-859A-3	Sequence 3, Appl	498	78	6.9	84875	4	US-09-949-016-17337	Sequence 17337, A
c 426	79	7.0	5868	3	US-09-586-472-3	Sequence 3, Appl	499	78	6.9	85152	4	Sequence 12665, A	Sequence 12665, A
c 427	79	7.0	5868	3	US-09-528-706-3	Sequence 3, Appl	500	78	6.9	85152	4	US-09-949-016-12666	Sequence 12666, A
c 428	79	7.0	6173	4	US-09-949-016-5511	Sequence 5511, Ap	501	78	6.9	85152	4	US-09-949-016-12667	Sequence 12667, A
c 429	79	7.0	6173	4	US-09-949-016-5512	Sequence 5512, Ap	502	78	6.9	85152	4	US-09-949-016-12668	Sequence 12668, A
c 430	79	7.0	9367	4	US-09-902-540-951	Sequence 951, App	503	78	6.9	152481	4	US-09-949-016-12521	Sequence 12521, A
c 431	79	7.0	19702	3	US-08-961-527-7	Sequence 7, Appl	504	78	6.9	152798	4	US-09-949-016-12775	Sequence 12775, A
c 432	79	7.0	42672	4	US-09-949-016-17253	Sequence 17253, A	505	78	6.9	152822	4	US-09-949-016-17518	Sequence 17518, A
c 433	79	7.0	42672	4	US-09-949-016-17254	Sequence 17254, A	506	78	6.9	152822	4	US-09-949-016-17519	Sequence 17519, A
c 434	79	7.0	44019	4	US-09-949-016-14902	Sequence 14902, A	507	78	6.9	536165	4	US-09-214-808-1	Sequence 1, Appl
c 435	79	7.0	154746	4	US-09-827-688-8	Sequence 8, Appl	508	77.5	6.9	522	4	US-09-621-976-2854	Sequence 2854, Ap
c 436	78.5	7.0	532	4	US-09-270-767-1305	Sequence 1305, Ap	509	77.5	6.9	601	4	US-09-949-016-45651	Sequence 45651, A
c 437	78.5	7.0	532	4	US-09-270-767-16587	Sequence 16587, Ap	510	77.5	6.9	1119	4	US-09-252-991A-9448	Sequence 9448, Ap
c 438	78.5	7.0	966	4	US-09-248-796A-9577	Sequence 9577, Ap	511	77.5	6.9	1239	4	US-09-252-991A-9383	Sequence 9383, Ap
c 439	78.5	7.0	1023	4	US-09-492-709A-102	Sequence 102, App	512	77.5	6.9	1425	4	US-09-578-063-2	Sequence 2, Appl
c 440	78.5	7.0	1291	2	US-08-887-365-35	Sequence 35, Appl	513	77.5	6.9	1482	4	US-09-252-991A-9689	Sequence 9689, Ap
c 441	78.5	7.0	1315	4	US-09-902-540-215	Sequence 215, App	514	77.5	6.9	1505	1	US-07-915-246-1	Sequence 1, Appl
c 442	78.5	7.0	1401	4	US-09-252-991A-10908	Sequence 10908, A	515	77.5	6.9	1614	4	US-09-252-991A-9607	Sequence 9607, Ap
c 443	78.5	7.0	1440	4	US-09-252-991A-11041	Sequence 11041, A	516	77.5	6.9	1623	4	US-09-252-991A-9650	Sequence 9650, Ap
c 444	78.5	7.0	1722	4	US-09-902-540-9668	Sequence 9668, Ap	517	77.5	6.9	1656	4	US-09-578-063-1	Sequence 1, Appl
c 445	78.5	7.0	1764	4	US-09-857-669-5	Sequence 5, Appl	518	77.5	6.9	1857	3	US-09-377-557-9	Sequence 9, Appl
c 446	78.5	7.0	1770	4	US-09-902-540-7164	Sequence 7164, Ap	519	77.5	6.9	1874	4	US-09-270-767-11069	Sequence 11069, A
c 447	78.5	7.0	1779	4	US-09-302-626B-5	Sequence 5, Appl	520	77.5	6.9	2325	2	US-08-714-677-3	Sequence 3, Appl
c 448	78.5	7.0	1870	3	US-09-071-709-6	Sequence 6, Appl	521	77.5	6.9	2325	2	US-08-393-540-3	Sequence 3, Appl
c 449	78.5	7.0	2055	4	US-09-248-796A-6094	Sequence 6094, Ap	522	77.5	6.9	2325	2	US-08-714-537-3	Sequence 3, Appl
c 450	78.5	7.0	2158	4	US-09-949-016-3018	Sequence 3018, Ap	523	77.5	6.9	3073	2	US-08-714-677-11	Sequence 11, Appl
c 451	78.5	7.0	2158	4	US-09-949-016-3026	Sequence 3026, Ap	524	77.5	6.9	3073	2	US-08-393-540-11	Sequence 11, Appl
c 452	78.5	7.0	2341	4	US-09-520-781-9	Sequence 9, Appl	525	77.5	6.9	3073	2	US-08-714-537-11	Sequence 11, Appl
c 453	78.5	7.0	2467	4	US-09-799-451-628	Sequence 628, App	526	77.5	6.9	8132	3	US-08-766-528-3	Sequence 3, Appl
c 454	78.5	7.0	2482	4	US-09-742-201-1	Sequence 11, Appl	527	77.5	6.9	8132	4	US-09-661-858-3	Sequence 3, Appl
c 455	78.5	7.0	2607	4	US-09-520-781-11	Sequence 11, Appl	528	77.5	6.9	9171	2	US-08-629-001A-2	Sequence 2, Appl
c 456	78.5	7.0	3352	4	US-10-101-464A-868	Sequence 868, App	529	77.5	6.9	9171	3	US-08-642-274D-2	Sequence 2, Appl
c 457	78.5	7.0	3424	3	US-09-336-643A-9	Sequence 9, Appl	530	77.5	6.9	9171	3	US-08-952-127-2	Sequence 2, Appl
c 458	78.5	7.0	3941	4	US-09-902-540-660	Sequence 660, App	531	77.5	6.9	9171	3	US-08-952-014C-2	Sequence 2, Appl
c 459	78.5	7.0	14555	4	US-09-902-540-1096	Sequence 1096, Ap	532	77.5	6.9	9385	2	US-08-984-090-1	Sequence 1, Appl
c 460	78.5	7.0	16011	4	US-09-600-319-3	Sequence 3, Appl	533	77.5	6.9	9385	2	US-08-874-266-1	Sequence 1, Appl
c 461	78.5	7.0	1230025	4	US-09-198-452A-1	Sequence 1, Appl	534	77.5	6.9	9385	3	US-09-360-416-1	Sequence 1, Appl
c 462	78	6.9	510	4	US-09-252-991A-9469	Sequence 9469, Ap	535	77.5	6.9	9389	4	US-09-949-016-4409	Sequence 4409, Ap
c 463	78	6.9	786	4	US-09-248-796A-176	Sequence 176, App	536	77.5	6.9	9870	1	US-08-508-836A-9	Sequence 9, Appl
c 464	78	6.9	1245	4	US-09-489-039A-5399	Sequence 5399, Ap	537	77.5	6.9	11706	4	US-09-302-540-1038	Sequence 1038, Ap
c 465	78	6.9	1510	1	US-08-361-920-26	Sequence 26, Appl	538	77.5	6.9	13987	2	US-08-804-227C-13	Sequence 13, Appl
c 466	78	6.9	1510	1	US-08-479-939-26	Sequence 26, Appl	539	77.5	6.9	28804	2	US-08-592-874-1	Sequence 1, Appl
c 467	78	6.9	1510	1	US-08-483-432-26	Sequence 26, Appl	540	77.5	6.9	28804	3	US-09-096-942-2	Sequence 2, Appl
c 468	78	6.9	1596	1	US-08-531-601-2	Sequence 2, Appl	541	77.5	6.9	28804	3	US-09-096-867-2	Sequence 2, Appl
c 469	78	6.9	1596	2	US-08-859-032-2	Sequence 2, Appl	542	77.5	6.9	30922	4	US-09-949-016-16700	Sequence 16700, A
c 470	78	6.9	1758	4	US-09-902-540-9019	Sequence 9019, Ap	543	77.5	6.9	43280	2	US-08-804-227C-1	Sequence 1, Appl
c 471	78	6.9	2007	3	US-09-052-089A-7	Sequence 7, Appl	544	77.5	6.9	110243	4	US-09-949-016-13698	Sequence 13698, A
c 472	78	6.9	2007	4	US-09-949-016-793	Sequence 793, App	545	77.5	6.9	137949	4	US-09-949-016-12196	Sequence 12196, A
c 473	78	6.9	2016	4	US-09-949-016-5734	Sequence 5734, Ap	546	77.5	6.9	137956	4	US-09-949-016-17260	Sequence 17260, A
c 474	78	6.9	2065	2	US-08-968-751-1	Sequence 1, Appl	547	77.5	6.9	150394	4	US-09-949-016-13042	Sequence 13042, A
c 475	78	6.9	2071	4	US-09-949-016-1517	Sequence 1517, Ap	548	77	6.8	346	4	US-09-377-502-53	Sequence 53, Appl
c 476	78	6.9	2157	4	US-09-252-991A-15294	Sequence 15294, A	549	77	6.8	542	4	US-09-167-206-23	Sequence 23, Appl
c 477	78	6.9	2361	4	US-09-252-991A-15546	Sequence 15546, A	550	77	6.8	543	4	US-09-489-039A-5453	Sequence 5453, Ap
c 478	78	6.9	2454	4	US-09-614-221A-393	Sequence 393, App	551	77	6.8	939	4	US-09-252-991A-9154	Sequence 9154, Ap

C 552	77	6.8	1092	4	US-09-252-991A-14341	Sequence 14341, A	625	76.5	6.8	2496	2	US-08-757-653-2	Sequence 2, Appli
C 553	77	6.8	1167	4	US-09-252-991A-14278	Sequence 14278, A	626	76.5	6.8	2496	2	US-08-599-491-2	Sequence 2, Appli
C 554	77	6.8	1206	4	US-09-252-991A-13220	Sequence 13220, A	627	76.5	6.8	2496	2	US-08-756-386-2	Sequence 2, Appli
555	77	6.8	1632	1	US-08-324-243-34	Sequence 34, Appl	628	76.5	6.8	2496	3	US-08-823-516-2	Sequence 2, Appli
556	77	6.8	1632	1	US-08-532-390-34	Sequence 34, Appl	629	76.5	6.8	2496	3	US-08-682-853A-2	Sequence 2, Appli
557	77	6.8	1632	3	US-08-717-294-34	Sequence 34, Appl	630	76.5	6.8	2496	3	US-08-759-038-2	Sequence 2, Appli
558	77	6.8	1632	5	PCT-US95-11511-34	Sequence 34, Appl	631	76.5	6.8	2496	3	US-08-758-314-2	Sequence 2, Appli
559	77	6.8	1719	4	US-09-252-991A-12741	Sequence 12741, A	632	76.5	6.8	2496	3	US-09-350-309-2	Sequence 2, Appli
C 560	77	6.8	1745	4	US-09-489-039A-4884	Sequence 4884, Ap	633	76.5	6.8	2496	3	US-08-520-946-2	Sequence 2, Appli
C 561	77	6.8	1879	4	US-09-252-991A-8812	Sequence 8812, Ap	634	76.5	6.8	2496	4	US-08-684-938-2	Sequence 2, Appli
C 562	77	6.8	1998	4	US-09-949-016-444	Sequence 44, App	635	76.5	6.8	2496	4	US-09-308-825A-2	Sequence 2, Appli
C 563	77	6.8	2040	3	US-08-604-789B-1	Sequence 1, Appli	636	76.5	6.8	2496	4	US-09-758-282B-2	Sequence 2, Appli
C 564	77	6.8	2040	3	US-08-604-789B-12	Sequence 12, Appl	637	76.5	6.8	2496	4	US-09-655-378A-2	Sequence 2, Appli
C 565	77	6.8	2040	3	US-09-312-721A-1	Sequence 1, Appli	638	76.5	6.8	2496	4	US-09-940-244-2	Sequence 2, Appli
C 566	77	6.8	2040	3	US-09-312-721A-12	Sequence 12, Appl	639	76.5	6.8	2496	4	US-09-333-145-2	Sequence 2, Appli
C 567	77	6.8	2040	4	US-09-733-300-1	Sequence 1, Appli	640	76.5	6.8	2496	4	US-09-577-304A-2	Sequence 2, Appli
C 568	77	6.8	2040	4	US-09-733-300-12	Sequence 12, Appl	641	76.5	6.8	2586	4	US-10-101-464A-883	Sequence 883, App
569	77	6.8	2430	4	US-09-252-991A-12709	Sequence 12709, A	642	76.5	6.8	2850	2	US-08-224-482-7	Sequence 7, Appli
570	77	6.8	2463	4	US-08-252-991A-8582	Sequence 8582, Ap	643	76.5	6.8	3818	4	US-09-949-016-5445	Sequence 5445, Ap
571	77	6.8	2481	1	US-08-324-243-35	Sequence 35, Appl	644	76.5	6.8	3889	3	US-09-484-970B-39	Sequence 39, Appl
572	77	6.8	2481	1	US-08-532-390-35	Sequence 35, Appl	645	76.5	6.8	4289	4	US-09-949-016-627	Sequence 627, App
573	77	6.8	2481	3	US-08-717-294-35	Sequence 35, Appl	646	76.5	6.8	4403	2	US-08-284-941-1	Sequence 1, Appli
574	77	6.8	2481	5	PCT-US95-11511-35	Sequence 35, Appl	647	76.5	6.8	4403	2	US-08-447-642-1	Sequence 1, Appli
575	77	6.8	2517	4	US-09-252-991A-9238	Sequence 9238, Ap	648	76.5	6.8	4403	3	US-08-236-503-1	Sequence 1, Appli
576	77	6.8	2571	4	US-08-552-950-4	Sequence 4, Appli	649	76.5	6.8	4403	3	US-09-949-016-369	Sequence 369, App
C 577	77	6.8	2571	4	US-09-936-572-4	Sequence 4, Appli	650	76.5	6.8	4403	5	PCT-US93-02147A-1	Sequence 1, Appli
C 578	77	6.8	2607	4	US-09-252-991A-13249	Sequence 13249, A	651	76.5	6.8	4851	4	US-09-902-540-647	Sequence 647, App
579	77	6.8	2744	3	US-09-071-101-1	Sequence 1, Appli	652	76.5	6.8	10106	4	US-09-949-016-17187	Sequence 17187, A
580	77	6.8	2744	3	US-09-369-618-1	Sequence 1, Appli	653	76.5	6.8	10318	4	US-09-902-540-973	Sequence 973, App
C 581	77	6.8	2744	3	US-09-369-617-1	Sequence 1, Appli	654	76.5	6.8	27933	4	US-09-949-016-12369	Sequence 12369, A
C 582	77	6.8	2748	4	US-09-252-991A-8662	Sequence 8662, Ap	655	76.5	6.8	30350	4	US-10-118-328-3	Sequence 3, Appli
583	77	6.8	3464	4	US-09-949-016-1167	Sequence 1167, Ap	656	76.5	6.8	32379	4	US-09-949-016-15217	Sequence 15217, A
C 584	77	6.8	3924	1	US-08-395-246C-1	Sequence 1, Appli	657	76.5	6.8	32379	4	US-09-949-016-15218	Sequence 15218, A
585	77	6.8	4108	3	US-08-981-729-8	Sequence 8, Appli	658	76.5	6.8	32379	4	US-09-949-016-15219	Sequence 15219, A
586	77	6.8	4108	3	US-08-981-446B-1	Sequence 1, Appli	659	76.5	6.8	32379	4	US-09-949-016-15220	Sequence 15220, A
587	77	6.8	4108	4	US-08-613-811-8	Sequence 8, Appli	660	76.5	6.8	32379	4	US-09-949-016-15221	Sequence 15221, A
588	77	6.8	6359	4	US-09-475-252-1	Sequence 1, Appli	661	76.5	6.8	32379	4	US-09-949-016-15222	Sequence 15222, A
589	77	6.8	7559	2	US-08-250-848-2	Sequence 2, Appli	662	76.5	6.8	32379	4	US-09-949-016-15223	Sequence 15223, A
C 590	77	6.8	16225	4	US-09-949-016-15152	Sequence 15152, A	663	76.5	6.8	32379	4	US-09-949-016-15224	Sequence 15224, A
C 591	77	6.8	16225	4	US-09-949-016-15160	Sequence 15160, A	664	76.5	6.8	32379	4	US-09-949-016-15225	Sequence 15225, A
C 592	77	6.8	16225	4	US-09-949-016-15196	Sequence 15196, A	665	76.5	6.8	32379	4	US-09-949-016-15226	Sequence 15226, A
C 593	77	6.8	36519	3	US-08-923-137-2	Sequence 2, Appli	666	76.5	6.8	40897	4	US-09-949-016-13910	Sequence 13910, A
C 594	77	6.8	38909	4	US-09-596-002-30	Sequence 30, Appl	667	76.5	6.8	40897	4	US-09-949-016-13911	Sequence 13911, A
C 595	77	6.8	134987	4	US-09-949-016-15348	Sequence 15348, A	668	76.5	6.8	40897	4	US-09-949-016-13912	Sequence 13912, A
C 596	77	6.8	134987	4	US-09-949-016-15349	Sequence 15349, A	669	76.5	6.8	40897	4	US-09-949-016-13913	Sequence 13913, A
C 597	77	6.8	134987	4	US-09-949-016-15350	Sequence 15350, A	670	76.5	6.8	40897	4	US-09-949-016-14409	Sequence 14409, A
C 598	77	6.8	134987	4	US-09-949-016-15507	Sequence 15507, A	671	76.5	6.8	40897	4	US-09-949-016-14410	Sequence 14410, A
C 599	77	6.8	134987	4	US-09-949-016-15508	Sequence 15508, A	672	76.5	6.8	40897	4	US-09-949-016-14411	Sequence 14411, A
C 600	77	6.8	134987	4	US-09-949-016-15509	Sequence 15509, A	673	76.5	6.8	40897	4	US-09-949-016-14412	Sequence 14412, A
601	76.5	6.8	405	4	US-09-248-796A-13214	Sequence 13214, A	674	76.5	6.8	64377	4	US-09-949-016-15212	Sequence 15212, A
C 602	76.5	6.8	801	4	US-09-489-039A-1028	Sequence 1028, Ap	675	76.5	6.8	64377	4	US-09-949-016-15213	Sequence 15213, A
C 603	76.5	6.8	909	4	US-09-248-796A-166	Sequence 166, App	676	76.5	6.8	64377	4	US-09-949-016-15214	Sequence 15214, A
C 604	76.5	6.8	957	4	US-09-902-540-358A	Sequence 358A, Ap	677	76.5	6.8	64377	4	US-09-949-016-15215	Sequence 15215, A
C 605	76.5	6.8	975	4	US-09-252-991A-7594	Sequence 7594, Ap	678	76.5	6.8	64377	4	US-09-949-016-15216	Sequence 15216, A
606	76.5	6.8	1122	4	US-09-902-540-7103	Sequence 7103, Ap	679	76.5	6.8	100463	4	US-09-949-016-12511	Sequence 12511, A
607	76.5	6.8	1141	4	US-09-270-767-12501	Sequence 12501, A	680	76.5	6.8	100463	4	US-09-949-016-13725	Sequence 13725, A
608	76.5	6.8	1356	4	US-09-248-796A-2116	Sequence 2116, Ap	681	76	6.8	966	4	US-09-489-039A-6043	Sequence 6043, Ap
609	76.5	6.8	1417	4	US-09-949-016-4521	Sequence 4521, Ap	682	76	6.8	1074	4	US-09-902-540-4288	Sequence 4288, Ap
610	76.5	6.8	1476	4	US-09-976-594-147	Sequence 147, App	683	76	6.8	1122	4	US-09-902-540-4288	Sequence 4288, Ap
611	76.5	6.8	1620	3	US-08-844-052-12	Sequence 12, Appl	684	76	6.8	1143	3	US-09-134-001C-1721	Sequence 1721, Ap
612	76.5	6.8	1620	3	US-08-814-052-13	Sequence 13, Appl	685	76	6.8	1173	4	US-09-902-540-2437	Sequence 2437, Ap
C 613	76.5	6.8	1770	3	US-09-377-155-18	Sequence 18, Appl	686	76	6.8	1185	4	US-09-252-991A-11261	Sequence 11261, A
C 614	76.5	6.8	1770	3	US-09-669-974-18	Sequence 18, Appl	687	76	6.8	1211	2	US-08-997-080-40	Sequence 40, Appl
C 615	76.5	6.8	1770	4	US-09-797-862-18	Sequence 18, Appl	688	76	6.8	1211	2	US-08-997-362-40	Sequence 40, Appl
616	76.5	6.8	2001	4	US-09-248-796A-4560	Sequence 4560, Ap	689	76	6.8	1211	3	US-08-873-370-40	Sequence 40, Appl
617	76.5	6.8	2001	3	US-08-510-646B-17	Sequence 17, Appl	690	76	6.8	1211	3	US-09-095-855-40	Sequence 40, Appl
C 618	76.5	6.8	2439	4	US-09-023-655-1455	Sequence 1455, Ap	691	76	6.8	1211	3	US-08-705-347A-40	Sequence 40, Appl
619	76.5	6.8	2496	1	US-08-073-384C-2	Sequence 2, Appli	692	76	6.8	1211	3	US-09-324-542-40	Sequence 40, Appl
620	76.5	6.8	2496	1	US-08-254-359A-2	Sequence 2, Appli	693	76	6.8	1211	3	US-09-205-426-40	Sequence 40, Appl
621	76.5	6.8	2496	1	US-08-483-043-2	Sequence 2, Appli	694	76	6.8	1211	3	US-09-200-643-40	Sequence 40, Appl
622	76.5	6.8	2496	1	US-08-481-238-2	Sequence 2, Appli	695	76	6.8	1308	4	US-09-801-861-4	Sequence 4, Appli
623	76.5	6.8	2496	2	US-08-471-066B-2	Sequence 2, Appli	696	76	6.8	1308	4	US-10-224-562-4	Sequence 4, Appli
624	76.5	6.8	2496	2	US-08-484-956-2	Sequence 2, Appli	697	76	6.8	1347	4	US-09-252-991A-10926	Sequence 10926, A

698	76	6.8	1395	4	US-09-252-991A-10988	Sequence 10988, A	780	75.5	6.7	31063	4	US-09-596-002-20	Sequence 20, Appl
C 699	76	6.8	1440	4	US-09-270-767-12289	Sequence 12289, A	C 781	75.5	6.7	35081	2	US-08-752-760A-1	Sequence 1, Appl
C 700	76	6.8	1647	4	US-09-540-236-469	Sequence 469, App	C 782	75.5	6.7	38239	4	US-09-949-016-12348	Sequence 12348, A
701	76	6.8	1659	4	US-08-252-991A-6121	Sequence 6121, Ap	C 783	75.5	6.7	38252	4	US-09-949-016-13570	Sequence 13570, A
702	76	6.8	1795	4	US-09-197-970B-6	Sequence 6, Appl	C 784	75.5	6.7	51552	4	US-09-733-294A-30	Sequence 30, Appl
C 703	76	6.8	1878	4	US-09-252-991A-6434	Sequence 6434, Ap	C 785	75.5	6.7	139936	4	US-09-949-016-11782	Sequence 11782, A
704	76	6.8	2203	4	US-09-801-861-1	Sequence 1, Appl	C 786	75.5	6.7	139952	4	US-09-949-016-13280	Sequence 13280, A
705	76	6.8	2203	4	US-10-324-562-1	Sequence 1, Appl	C 787	75.5	6.7	767677	4	US-09-949-016-12147	Sequence 12147, A
706	76	6.8	2452	1	US-08-524-051-1	Sequence 1, Appl	C 788	75.5	6.7	767677	4	US-09-949-016-12147	Sequence 12147, A
716	76	6.8	3468	1	US-07-951-715A-2	Sequence 2, Appl	C 789	75.5	6.7	767677	4	US-09-949-016-17361	Sequence 17361, A
717	76	6.8	3468	1	US-07-951-715A-4	Sequence 4, Appl	C 790	75.5	6.7	767677	4	US-09-949-016-17361	Sequence 17361, A
718	76	6.8	3468	2	US-08-459-448A-2	Sequence 2, Appl	C 791	75	6.7	656	3	US-08-998-416-5974	Sequence 974, App
719	76	6.8	3468	2	US-08-459-448A-4	Sequence 4, Appl	C 792	75	6.7	1086	4	US-09-540-236-244	Sequence 244, App
720	76	6.8	3468	3	US-08-459-595A-2	Sequence 2, Appl	C 793	75	6.7	1123	3	US-09-894-698-9	Sequence 9, Appl
721	76	6.8	3468	3	US-08-459-595A-4	Sequence 4, Appl	C 794	75	6.7	1123	3	US-09-894-698-11	Sequence 11, Appl
722	76	6.8	3468	3	US-08-459-504B-2	Sequence 2, Appl	C 795	75	6.7	1143	2	US-08-387-942C-19	Sequence 19, Appl
723	76	6.8	3468	3	US-08-459-504B-4	Sequence 4, Appl	C 796	75	6.7	1239	4	US-09-949-016-3238	Sequence 3238, Ap
724	76	6.8	3468	3	US-08-459-444-2	Sequence 2, Appl	C 797	75	6.7	1350	4	US-09-252-991A-11976	Sequence 11976, A
725	76	6.8	3468	3	US-08-459-444-4	Sequence 4, Appl	C 798	75	6.7	1374	4	US-09-252-991A-8560	Sequence 8560, Ap
726	76	6.8	3468	3	US-09-053-549-3	Sequence 3, Appl	C 799	75	6.7	1374	3	US-09-894-698-6	Sequence 6, Appl
727	76	6.8	3468	3	US-09-053-549-5	Sequence 5, Appl	C 800	75	6.7	1383	3	US-09-894-698-8	Sequence 8, Appl
728	76	6.8	3468	3	US-09-547-422-2	Sequence 2, Appl	C 801	75	6.7	1398	4	US-09-902-540-3237	Sequence 3237, Ap
729	76	6.8	3468	3	US-09-547-422-4	Sequence 4, Appl	C 802	75	6.7	1425	4	US-09-252-991A-2830	Sequence 2830, Ap
730	76	6.8	3468	4	US-09-988-462-2	Sequence 2, Appl	C 803	75	6.7	1449	3	US-09-894-698-4	Sequence 4, Appl
731	76	6.8	3468	4	US-09-988-462-4	Sequence 4, Appl	C 804	75	6.7	1449	3	US-09-894-698-5	Sequence 5, Appl
C 732	76	6.8	3604	4	US-09-016-434-1180	Sequence 1180, Ap	C 805	75	6.7	1491	4	US-09-902-540-3335	Sequence 3335, Ap
C 733	76	6.8	4032	4	US-09-949-016-5588	Sequence 5588, Ap	C 806	75	6.7	1494	4	US-09-252-991A-14961	Sequence 14961, A
734	76	6.8	8442	3	US-09-272-032-6	Sequence 6, Appl	C 807	75	6.7	1509	4	US-09-252-991A-14669	Sequence 14669, A
735	76	6.8	11707	3	US-09-136-574A-1	Sequence 1, Appl	C 808	75	6.7	1522	3	US-08-993-359-25	Sequence 25, Appl
C 736	76	6.8	14899	4	US-09-902-540-1107	Sequence 1107, Ap	C 809	75	6.7	1522	4	US-09-482-558A-25	Sequence 25, Appl
C 737	76	6.8	16738	4	US-09-949-016-12168	Sequence 12168, A	C 810	75	6.7	1530	3	US-09-504-358-21	Sequence 21, Appl
C 738	76	6.8	16738	4	US-09-949-016-14678	Sequence 14678, A	C 811	75	6.7	1590	3	US-09-954-314-21	Sequence 21, Appl
739	76	6.8	19269	4	US-09-902-540-1175	Sequence 1175, Ap	C 812	75	6.7	1590	4	US-10-230-562-21	Sequence 21, Appl
740	76	6.8	30922	4	US-09-949-016-16700	Sequence 16700, A	C 813	75	6.7	1668	4	US-09-252-991A-15085	Sequence 15085, A
C 741	76	6.8	43550	4	US-09-949-016-12400	Sequence 12400, A	C 814	75	6.7	1697	4	US-09-248-796A-4647	Sequence 4647, Ap
C 742	76	6.8	43555	4	US-09-949-016-13993	Sequence 13993, A	C 815	75	6.7	1956	3	US-09-489-039A-3520	Sequence 3520, Ap
C 743	76	6.8	43986	4	US-09-949-016-17155	Sequence 17155, A	C 816	75	6.7	2035	3	US-09-894-698-1	Sequence 1, Appl
744	76	6.8	49235	4	US-09-902-540-1269	Sequence 1269, Ap	C 817	75	6.7	2035	3	US-09-894-698-3	Sequence 3, Appl
745	76	6.8	62909	4	US-09-596-002-32	Sequence 32, Appl	C 818	75	6.7	2114	4	US-09-270-767-14640	Sequence 14640, A
C 746	76	6.8	68702	4	US-09-949-016-16328	Sequence 16328, A	C 819	75	6.7	2125	4	US-09-485-529-14	Sequence 14, Appl
747	76	6.8	71100	4	US-09-949-016-16418	Sequence 16418, A	C 820	75	6.7	2134	4	US-09-902-540-2930	Sequence 2930, Ap
C 748	76	6.8	100848	4	US-09-596-002-39	Sequence 39, Appl	C 821	75	6.7	2225	4	US-09-949-016-5647	Sequence 5647, Ap
749	76	6.8	197496	4	US-09-877-177A-10	Sequence 10, Appl	C 822	75	6.7	2472	4	US-09-603-208A-271	Sequence 271, App
750	75.5	6.7	601	4	US-09-949-016-175056	Sequence 175056, A	C 823	75	6.7	2539	3	US-09-000-016-3	Sequence 3, Appl
C 751	75.5	6.7	693	4	US-09-252-991A-697	Sequence 697, App	C 824	75	6.7	2539	3	US-09-514-340-3	Sequence 3, Appl
C 752	75.5	6.7	921	4	US-09-252-991A-16185	Sequence 16185, A	C 825	75	6.7	2662	4	US-09-774-528-94	Sequence 94, Appl
C 753	75.5	6.7	1011	4	US-09-252-991A-16405	Sequence 16405, A	C 826	75	6.7	2748	4	US-09-270-767-14866	Sequence 14866, A
C 754	75.5	6.7	1065	4	US-09-340-798A-31	Sequence 31, Appl	C 827	75	6.7	2809	3	US-09-000-016-1	Sequence 1, Appl
C 755	75.5	6.7	1185	4	US-09-902-540-4942	Sequence 4942, Ap	C 828	75	6.7	2809	3	US-09-514-340-1	Sequence 1, Appl
756	75.5	6.7	1212	4	US-09-602-777A-93	Sequence 93, Appl	C 829	75	6.7	2893	4	US-09-902-540-9663	Sequence 9663, Ap
757	75.5	6.7	1308	3	US-09-500-569-13	Sequence 13, Appl	C 830	75	6.7	3159	4	US-09-134-000C-3215	Sequence 3215, Ap
758	75.5	6.7	1308	4	US-09-971-823B-13	Sequence 13, Appl	C 831	75	6.7	3243	3	US-09-543-681A-1875	Sequence 1875, Ap
759	75.5	6.7	1329	4	US-09-252-991A-15277	Sequence 15277, A	C 832	75	6.7	3283	3	US-09-651-656-16	Sequence 16, Appl
760	75.5	6.7	1530	4	US-09-902-540-4172	Sequence 4172, Ap	C 833	75	6.7	3283	3	US-09-850-855-16	Sequence 16, Appl
761	75.5	6.7	1551	4	US-09-252-991A-15327	Sequence 15327, A	C 834	75	6.7	3283	3	US-09-799-451-287	Sequence 287, App
762	75.5	6.7	1615	4	US-09-949-016-4275	Sequence 4275, Ap	C 835	75	6.7	5239	4	US-09-949-016-14980	Sequence 14980, A
763	75.5	6.7	1641	4	US-09-235-153-4	Sequence 4, Appl	C 836	75	6.7	5516	4	US-09-949-016-13954	Sequence 13954, A
764	75.5	6.7	1875	3	US-09-039-609-1	Sequence 1, Appl	C 837	75	6.7	7390	4	US-09-566-921-95	Sequence 95, Appl
765	75.5	6.7	2192	1	US-08-035-392-1	Sequence 1, Appl	C 838	75	6.7	9461	3	US-09-221-017B-513	Sequence 513, App
766	75.5	6.7	2192	1	US-08-504-511A-1	Sequence 1, Appl	C 839	75	6.7	10480	4	US-09-732-615-13	Sequence 13, Appl
C 767	75.5	6.7	2203	4	US-09-902-540-4252	Sequence 4252, Ap	C 840	75	6.7	10480	4	US-10-273-051-13	Sequence 13, Appl
C 768	75.5	6.7	2205	1	US-08-035-392-3	Sequence 3, Appl	C 841	75	6.7	11471	3	US-09-504-358-16	Sequence 16, Appl
769	75.5	6.7	2205	1	US-08-504-511A-3	Sequence 3, Appl	C 842	75	6.7	11471	3	US-09-954-314-16	Sequence 16, Appl
770	75.5	6.7	4451	3	US-08-717-294-42	Sequence 42, Appl	C 843	75	6.7	11471	4	US-10-230-562-16	Sequence 16, Appl
771	75.5	6.7	4881	4	US-09-252-991A-7234	Sequence 7234, Ap	C 844	75	6.7	11672	3	US-09-441-340-2	Sequence 2, Appl
772	75.5	6.7	5492	4	US-09-949-016-5817	Sequence 5817, Ap	C 845	75	6.7	14555	4	US-09-902-540-1096	Sequence 1096, Ap
C 773	75.5	6.7	8060	3	US-08-766-528-1	Sequence 1, Appl	C 846	75	6.7	16387	4	US-09-902-540-1156	Sequence 1156, Ap
C 774	75.5	6.7	8060	4	US-09-661-858-1	Sequence 1, Appl	C 847	75	6.7	17726	4	US-09-902-540-1148	Sequence 1148, Ap
775	75.5	6.7	8916	3	US-05-579-181-11	Sequence 11, Appl	C 848	75	6.7	23417	4	US-09-902-540-1207	Sequence 1207, Ap
776	75.5	6.7	9354	3	US-09-579-181-10	Sequence 10, Appl	C 849	75	6.7	23718	4	US-09-902-540-1203	Sequence 1203, Ap
777	75.5	6.7	22301	4	US-09-902-540-1208	Sequence 1208, Ap	C 850	75	6.7	31300	4	US-09-949-016-16967	Sequence 16967, A
C 778	75.5	6.7	24791	4	US-09-902-540-1211	Sequence 1211, Ap	C 851	75	6.7	44821	4	US-09-949-016-13764	Sequence 13764, A
C 779	75.5	6.7	30780	4	US-09-902-540-1243	Sequence 1243, Ap	C 852	75	6.7	152132	4	US-09-949-016-13845	Sequence 13845, A

C 853	75	6.7	152145	4	US-09-949-016-12371	Sequence 12371, A	926	74	6.6	447	2	US-08-387-942C-33	Sequence 33, Appl
C 854	74.5	6.6	330	4	US-09-107-532A-1345	Sequence 1345, Ap	C 927	74	6.6	601	4	US-09-949-016-92200	Sequence 92200, A
C 855	74.5	6.6	437	4	US-09-513-999C-1334	Sequence 1334, Ap	928	74	6.6	601	4	US-09-949-016-175055	Sequence 175055, A
C 856	74.5	6.6	561	4	US-09-252-991A-3862	Sequence 3862, Ap	929	74	6.6	601	4	US-09-949-016-203314	Sequence 203314, A
C 857	74.5	6.6	590	2	US-08-809-763-1	Sequence 1, Appli	930	74	6.6	615	4	US-09-134-000C-149	Sequence 149, App
C 858	74.5	6.6	590	3	US-08-956-253-1	Sequence 1, Appli	931	74	6.6	615	4	US-08-248-796A-7881	Sequence 7881, Ap
C 859	74.5	6.6	601	4	US-09-949-016-203315	Sequence 203315, A	932	74	6.6	772	4	US-09-367-572-3	Sequence 3, Appli
C 860	74.5	6.6	601	4	US-09-949-016-203664	Sequence 203664, A	933	74	6.6	807	4	US-09-902-540-5423	Sequence 5423, Ap
C 861	74.5	6.6	813	4	US-09-602-777A-293	Sequence 293, App	934	74	6.6	966	4	US-08-248-796A-3126	Sequence 3126, Ap
C 862	74.5	6.6	884	2	US-08-901-200A-11	Sequence 11, Appl	935	74	6.6	977	4	US-09-602-777A-5	Sequence 5, Appli
C 863	74.5	6.6	884	3	US-09-219-391-11	Sequence 11, Appl	936	74	6.6	980	4	US-09-602-777A-3	Sequence 3, Appli
C 864	74.5	6.6	900	4	US-09-270-767-12771	Sequence 72771, A	937	74	6.6	987	4	US-08-489-039A-5632	Sequence 5632, Ap
C 865	74.5	6.6	915	4	US-09-107-532A-79	Sequence 79, Appl	938	74	6.6	1084	4	US-09-949-016-2175	Sequence 2175, Ap
C 866	74.5	6.6	1002	4	US-09-107-532A-2821	Sequence 2821, Ap	939	74	6.6	1084	4	US-09-949-016-2176	Sequence 2176, Ap
C 867	74.5	6.6	1057	3	US-09-452-239-5	Sequence 5, Appli	C 940	74	6.6	1112	4	US-09-270-767-5802	Sequence 5802, Ap
C 868	74.5	6.6	1350	4	US-09-475-515-55	Sequence 55, Appl	C 941	74	6.6	1112	4	US-09-270-767-21084	Sequence 21084, A
C 869	74.5	6.6	1359	4	US-09-252-991A-12056	Sequence 12056, A	C 942	74	6.6	1140	4	US-09-489-039A-4643	Sequence 4643, Ap
C 870	74.5	6.6	1392	4	US-09-071-252-5	Sequence 5, Appli	C 943	74	6.6	1296	4	US-08-248-796A-4810	Sequence 4810, Ap
C 871	74.5	6.6	1476	4	US-09-252-991A-2443	Sequence 2443, Ap	C 944	74	6.6	1340	4	US-09-513-999C-14928	Sequence 14928, A
C 872	74.5	6.6	1476	4	US-09-248-796A-2443	Sequence 2443, Ap	C 945	74	6.6	1347	2	US-08-822-830B-5	Sequence 5, Appli
C 873	74.5	6.6	1578	4	US-09-107-532A-2089	Sequence 2089, Ap	946	74	6.6	1347	2	US-09-157-452B-5	Sequence 5, Appli
C 874	74.5	6.6	1599	4	US-09-475-515-54	Sequence 54, Appl	947	74	6.6	1347	2	US-09-157-452B-5	Sequence 5, Appli
C 875	74.5	6.6	1695	4	US-09-252-991A-6969	Sequence 6969, Ap	C 948	74	6.6	1383	4	US-09-252-991A-12039	Sequence 12039, A
C 876	74.5	6.6	1818	4	US-09-475-515-59	Sequence 59, Appl	C 949	74	6.6	1547	4	US-08-270-767-12408	Sequence 12408, A
C 877	74.5	6.6	1818	4	US-09-475-515-61	Sequence 61, Appl	C 950	74	6.6	1596	4	US-09-252-991A-9478	Sequence 9478, Ap
C 878	74.5	6.6	1818	4	US-09-475-515-62	Sequence 62, Appl	C 951	74	6.6	1650	4	US-09-252-991A-9352	Sequence 9352, Ap
C 879	74.5	6.6	1863	4	US-09-475-515-63	Sequence 63, Appl	C 952	74	6.6	1650	4	US-09-489-039A-1643	Sequence 1643, Ap
C 880	74.5	6.6	1941	5	PCT-US91-07635-5	Sequence 5, Appli	C 953	74	6.6	1771	4	US-09-949-016-4307	Sequence 4307, Ap
C 881	74.5	6.6	1974	3	US-09-221-017B-726	Sequence 726, App	954	74	6.6	1776	1	US-08-522-229B-1	Sequence 1, Appli
C 882	74.5	6.6	2031	4	US-09-475-515-60	Sequence 60, Appl	955	74	6.6	1776	2	US-08-102-433-1	Sequence 1, Appli
C 883	74.5	6.6	2031	4	US-09-475-515-67	Sequence 67, Appl	956	74	6.6	1782	4	US-09-949-016-1954	Sequence 1954, Ap
C 884	74.5	6.6	2112	4	US-09-799-451-772	Sequence 772, App	C 957	74	6.6	1927	4	US-09-949-016-3372	Sequence 3372, Ap
C 885	74.5	6.6	2112	4	US-09-475-515-56	Sequence 56, Appl	958	74	6.6	2181	4	US-09-443-067-19	Sequence 19, Appl
C 886	74.5	6.6	2181	4	US-09-475-515-57	Sequence 57, Appl	959	74	6.6	2220	2	US-08-932-376A-3	Sequence 3, Appli
C 887	74.5	6.6	2275	4	US-09-475-515-58	Sequence 58, Appl	960	74	6.6	2378	3	US-09-521-780-1	Sequence 1, Appli
C 888	74.5	6.6	2275	4	US-08-850-977-1	Sequence 1, Appli	961	74	6.6	2553	4	US-08-735-101-1	Sequence 1, Appli
C 889	74.5	6.6	2340	4	US-09-898-762-1	Sequence 67, Appl	962	74	6.6	2640	4	US-09-962-357-1	Sequence 1, Appli
C 890	74.5	6.6	2340	4	US-09-475-515-67	Sequence 67, Appl	C 963	74	6.6	2680	4	US-09-489-847-47	Sequence 47, Appl
C 891	74.5	6.6	2385	4	US-09-252-991A-11998	Sequence 11998, A	964	74	6.6	3180	4	US-09-248-796A-1061	Sequence 1061, Ap
C 892	74.5	6.6	2385	4	US-09-475-515-68	Sequence 68, Appl	C 965	74	6.6	3324	4	US-09-489-039A-1719	Sequence 1719, Ap
C 893	74.5	6.6	2502	4	US-09-902-540-7704	Sequence 7704, Ap	966	74	6.6	3825	4	US-09-902-540-6744	Sequence 6744, Ap
C 894	74.5	6.6	2538	4	US-09-475-515-65	Sequence 65, Appl	967	74	6.6	3976	4	US-09-902-540-544	Sequence 544, App
C 895	74.5	6.6	2553	4	US-09-620-312D-340	Sequence 340, App	C 968	74	6.6	4518	3	US-08-669-785-3	Sequence 3, Appli
C 896	74.5	6.6	2553	4	US-09-475-515-66	Sequence 66, Appl	969	74	6.6	5114	4	US-09-949-016-11951	Sequence 11951, A
C 897	74.5	6.6	2582	4	US-09-270-767-12851	Sequence 12851, A	C 970	74	6.6	6002	4	US-09-949-016-13696	Sequence 13696, A
C 898	74.5	6.6	2634	3	US-09-475-515-64	Sequence 64, Appl	971	74	6.6	7890	4	US-09-949-016-17356	Sequence 17356, A
C 899	74.5	6.6	2760	3	US-09-221-017B-462	Sequence 462, App	972	74	6.6	7890	4	US-08-305-790B-1	Sequence 1, Appli
C 900	74.5	6.6	2793	1	US-08-209-747-1	Sequence 1, Appli	C 973	74	6.6	8598	4	US-08-227-536-1	Sequence 1, Appli
C 901	74.5	6.6	2793	1	US-08-458-238-1	Sequence 38, Appl	974	74	6.6	9046	5	PCT-US95-04682-1	Sequence 14, Appli
C 902	74.5	6.6	2839	5	PCT-US94-07297-38	Sequence 38, Appl	975	74	6.6	13011	2	US-08-791-849A-14	Sequence 14, Appli
C 903	74.5	6.6	3531	4	US-09-949-016-2301	Sequence 2301, Ap	C 976	74	6.6	16007	4	US-09-949-016-17496	Sequence 17496, A
C 904	74.5	6.6	3805	4	US-09-220-132-9	Sequence 9, Appli	C 977	74	6.6	18994	1	US-08-459-586-4	Sequence 4, Appli
C 905	74.5	6.6	3825	4	US-09-252-991A-3815	Sequence 3815, Ap	C 978	74	6.6	18994	2	US-08-282-696-4	Sequence 4, Appli
C 906	74.5	6.6	3871	4	US-09-949-016-631	Sequence 73, Appl	C 979	74	6.6	20235	3	US-07-642-734C-3	Sequence 3, Appli
C 907	74.5	6.6	4472	4	US-09-475-515-75	Sequence 75, Appl	980	74	6.6	20235	3	US-08-439-009A-3	Sequence 3, Appli
C 908	74.5	6.6	4506	4	US-09-252-991A-3695	Sequence 3695, Ap	C 981	74	6.6	22301	4	US-09-902-540-1208	Sequence 1208, Ap
C 909	74.5	6.6	4647	4	US-09-252-991A-5730	Sequence 5730, Ap	C 982	74	6.6	24459	4	US-09-902-540-5004	Sequence 5004, Ap
C 910	74.5	6.6	4766	4	US-09-475-515-73	Sequence 73, Appl	C 983	74	6.6	32241	4	US-09-902-540-1247	Sequence 1247, Ap
C 911	74.5	6.6	5971	4	US-09-902-540-761	Sequence 761, App	984	74	6.6	32241	4	US-09-902-540-1247	Sequence 1, Appli
C 912	74.5	6.6	6418	1	US-08-480-528A-11	Sequence 11, Appl	985	74	6.6	32798	4	US-09-604-694B-1	Sequence 1, Appli
C 913	74.5	6.6	6418	1	US-08-479-666-11	Sequence 11, Appl	C 986	74	6.6	34953	4	US-09-902-540-1263	Sequence 1263, Ap
C 914	74.5	6.6	6418	5	PCT-US93-10520-11	Sequence 11, Appl	987	74	6.6	68750	3	US-09-335-409-1	Sequence 1, Appli
C 915	74.5	6.6	15163	4	US-09-949-016-13246	Sequence 13246, A	C 988	74	6.6	68750	3	US-09-568-102-1	Sequence 1, Appli
C 916	74.5	6.6	19818	4	US-09-949-016-12198	Sequence 12198, A	989	74	6.6	68750	3	US-09-567-969-1	Sequence 1, Appli
C 917	74.5	6.6	19819	4	US-09-949-016-16987	Sequence 16987, A	990	74	6.6	68750	3	US-09-568-480-1	Sequence 1, Appli
C 918	74.5	6.6	21164	4	US-09-949-016-16457	Sequence 16457, A	991	74	6.6	68750	3	US-09-568-480-1	Sequence 1, Appli
C 919	74.5	6.6	24393	4	US-08-949-016-15431	Sequence 15431, A	992	74	6.6	68750	3	US-09-568-480-1	Sequence 1, Appli
C 920	74.5	6.6	30660	3	US-08-814-095-7	Sequence 7, Appli	993	74	6.6	68750	3	US-09-567-899-1	Sequence 1, Appli
C 921	74.5	6.6	46244	4	US-09-949-016-13508	Sequence 13508, A	C 994	74	6.6	134008	4	US-09-949-016-13841	Sequence 13841, A
C 922	74.5	6.6	49472	4	US-09-949-016-17478	Sequence 17478, A	995	74	6.6	187916	4	US-09-949-016-12980	Sequence 12980, A
C 923	74.5	6.6	50878	4	US-09-949-016-11787	Sequence 11787, A	C 996	74	6.6	192956	4	US-09-949-016-14382	Sequence 14382, A
C 924	74.5	6.6	75787	4	US-09-949-016-13637	Sequence 13637, A	997	74	6.6	229354	4	US-09-705-400-64	Sequence 64, Appl
C 925	74.5	6.6	1664976	4	US-08-916-4218-1	Sequence 1, Appli	C 998	74	6.6	229354	4	US-09-705-400-64	Sequence 64, Appl
C 926	74.5	6.6	1664976	4	US-09-692-570-1	Sequence 1, Appli	999	74	6.6	229354	4	US-09-705-400-64	Sequence 64, Appl



999	74	6.6	387902	4	US-09-949-016-14543	Sequence 14543, A	c1072	73.5	6.5	66219	4	US-09-949-016-12038	Sequence 12038, A
1000	74	6.6	421883	4	US-09-949-016-12557	Sequence 12557, A	c1073	73.5	6.5	66227	4	US-09-949-016-15303	Sequence 15303, A
1001	73.5	6.5	601	4	US-09-949-016-121628	Sequence 121628, A	1074	73.5	6.5	69737	4	US-09-949-016-15140	Sequence 15140, A
1002	73.5	6.5	786	4	US-09-248-796A-9113	Sequence 9113, Ap	c1075	73.5	6.5	71989	3	US-09-443-501A-2	Sequence 2, Appl
c1003	73.5	6.5	804	4	US-09-540-236-1105	Sequence 1105, Ap	1076	73.5	6.5	81819	4	US-09-949-016-16661	Sequence 16661, A
c1004	73.5	6.5	951	4	US-09-252-991A-14310	Sequence 14310, A	1077	73.5	6.5	81819	4	US-09-949-016-16662	Sequence 16662, A
1005	73.5	6.5	1063	4	US-09-949-016-5303	Sequence 5303, Ap	1078	73.5	6.5	94077	4	US-09-949-016-13635	Sequence 13635, A
c1006	73.5	6.5	1239	4	US-09-603-208A-263	Sequence 263, App	c1079	73.5	6.5	154746	4	US-09-827-688-8	Sequence 8, Appl
1007	73.5	6.5	1269	1	US-08-265-429A-4	Sequence 4, Appl	1080	73	6.5	468	4	US-09-252-991A-13953	Sequence 13953, A
1008	73.5	6.5	1269	5	PCT-US95-09069-4	Sequence 4, Appl	1081	73	6.5	601	4	US-09-252-991A-13953	Sequence 13953, A
1009	73.5	6.5	1308	4	US-09-252-991A-683	Sequence 683, App	c1082	73	6.5	774	4	US-09-949-016-66454	Sequence 66454, A
c1010	73.5	6.5	1413	4	US-09-252-991A-11269	Sequence 11269, A	1083	73	6.5	891	4	US-09-489-039A-991	Sequence 991, App
1011	73.5	6.5	1450	1	US-07-923-692C-5	Sequence 5, Appl	1084	73	6.5	903	4	US-09-417-251A-11	Sequence 11, Appl
1012	73.5	6.5	1450	2	US-08-184-237-5	Sequence 5, Appl	c1085	73	6.5	972	4	US-09-602-787A-391	Sequence 391, App
1013	73.5	6.5	1450	2	US-08-482-920-5	Sequence 5, Appl	c1086	73	6.5	1035	4	US-09-902-540-5986	Sequence 5986, Ap
1014	73.5	6.5	1450	3	US-08-484-341-5	Sequence 5, Appl	1087	73	6.5	1080	4	US-09-252-991A-13953	Sequence 13953, A
c1015	73.5	6.5	1464	4	US-09-902-540-3904	Sequence 3904, Ap	1088	73	6.5	1209	3	US-09-302-540-8824	Sequence 8824, Ap
1016	73.5	6.5	1464	3	US-09-338-671-1	Sequence 1, Appl	1089	73	6.5	1284	4	US-09-345-882-24	Sequence 24, Appl
c1017	73.5	6.5	1590	4	US-09-252-991A-14397	Sequence 14397, A	c1090	73	6.5	1314	3	US-09-489-039A-841	Sequence 841, App
c1018	73.5	6.5	1629	4	US-09-489-039A-4596	Sequence 4596, Ap	1091	73	6.5	1422	4	US-08-800-682-1	Sequence 1, Appl
1019	73.5	6.5	1677	4	US-09-252-991A-9544	Sequence 9544, Ap	c1092	73	6.5	1545	4	US-09-252-991A-10234	Sequence 10234, A
1020	73.5	6.5	1713	4	US-09-565-501A-102	Sequence 102, App	1093	73	6.5	1680	2	US-09-366-965-31	Sequence 31, Appl
1021	73.5	6.5	1713	4	US-09-639-206A-102	Sequence 102, App	c1094	73	6.5	1680	3	US-08-759-581B-3	Sequence 3, Appl
1022	73.5	6.5	1713	4	US-09-874-923-102	Sequence 102, App	c1095	73	6.5	1680	3	US-09-304-711-3	Sequence 3, Appl
1023	73.5	6.5	1749	4	US-09-821-167-13	Sequence 13, Appl	c1096	73	6.5	1785	3	US-09-173-281-3	Sequence 3, Appl
1024	73.5	6.5	1941	4	US-09-902-540-4762	Sequence 4762, Ap	c1097	73	6.5	1785	3	US-09-377-155-6	Sequence 6, Appl
1025	73.5	6.5	2067	4	US-09-252-991A-1398	Sequence 1398, Ap	c1098	73	6.5	1785	4	US-09-669-974-6	Sequence 6, Appl
1026	73.5	6.5	2093	1	US-08-287-001A-1	Sequence 1, Appl	c1099	73	6.5	1794	4	US-09-797-862-6	Sequence 6, Appl
1027	73.5	6.5	2093	5	PCT-US95-09941-1	Sequence 1, Appl	1100	73	6.5	1794	4	US-09-902-540-3791	Sequence 3791, Ap
c1028	73.5	6.5	2100	4	US-09-252-991A-1209	Sequence 1209, Ap	1101	73	6.5	1875	3	US-09-877-730-23	Sequence 23, Appl
1029	73.5	6.5	2340	4	US-09-248-796A-2599	Sequence 2599, Ap	1102	73	6.5	1917	4	US-09-877-730-21	Sequence 21, Appl
1030	73.5	6.5	2421	4	US-09-565-501A-103	Sequence 103, App	c1103	73	6.5	2319	4	US-09-252-991A-13875	Sequence 13875, A
1031	73.5	6.5	2421	4	US-09-639-206A-103	Sequence 103, App	1104	73	6.5	1977	2	US-07-797-556-1	Sequence 1, Appl
1032	73.5	6.5	2421	4	US-09-874-923-103	Sequence 103, App	1105	73	6.5	2369	1	US-08-825-558-3	Sequence 3, Appl
1033	73.5	6.5	2798	4	US-09-336-115C-1	Sequence 1, Appl	1106	73	6.5	2096	4	US-09-312-611-3	Sequence 3, Appl
1034	73.5	6.5	3025	1	US-08-444-734D-1	Sequence 1, Appl	c1107	73	6.5	2369	4	US-09-252-991A-13079	Sequence 13079, A
1035	73.5	6.5	3317	3	US-09-193-562D-1	Sequence 1, Appl	c1108	73	6.5	2369	4	US-09-799-451-592	Sequence 592, App
1036	73.5	6.5	3317	4	US-10-055-412B-1	Sequence 1, Appl	1109	73	6.5	2369	1	US-09-252-991A-13875	Sequence 13875, A
1037	73.5	6.5	3404	1	US-08-265-429A-1	Sequence 1, Appl	1110	73	6.5	2369	1	US-07-797-556-1	Sequence 1, Appl
1038	73.5	6.5	3404	5	PCT-US95-09069-1	Sequence 1, Appl	1111	73	6.5	2369	2	US-08-308-881-1	Sequence 1, Appl
1039	73.5	6.5	3503	4	US-09-373-272-2	Sequence 2, Appl	1112	73	6.5	2369	2	US-09-058-263-1	Sequence 1, Appl
1040	73.5	6.5	3597	3	US-09-199-637A-404	Sequence 404, App	1113	73	6.5	2369	3	US-09-059-099-1	Sequence 1, Appl
1041	73.5	6.5	3622	4	US-09-949-016-2172	Sequence 2172, Ap	1114	73	6.5	2369	4	US-09-058-264-1	Sequence 1, Appl
1042	73.5	6.5	3627	2	US-08-232-087A-1	Sequence 1, Appl	1115	73	6.5	2369	5	PCT-US95-06530-1	Sequence 1, Appl
1043	73.5	6.5	3630	4	US-09-023-655-1028	Sequence 1028, Ap	c1116	73	6.5	2382	3	US-09-455-962-1	Sequence 1, Appl
1044	73.5	6.5	3630	4	US-09-949-016-177	Sequence 177, App	c1117	73	6.5	2430	4	US-09-877-730-27	Sequence 27, Appl
1045	73.5	6.5	3754	4	US-09-561-709B-6	Sequence 6, Appl	1118	73	6.5	2734	2	US-09-252-991A-6324	Sequence 6324, Ap
c1046	73.5	6.5	3801	4	US-09-252-991A-14280	Sequence 14280, A	1119	73	6.5	2734	2	US-08-825-558-5	Sequence 5, Appl
1047	73.5	6.5	4125	4	US-10-237-551-76	Sequence 76, Appl	1120	73	6.5	2734	3	US-09-312-611-5	Sequence 5, Appl
1048	73.5	6.5	4125	4	US-10-237-551-149	Sequence 149, App	1121	73	6.5	2976	3	US-09-252-991A-6221	Sequence 6221, Ap
1049	73.5	6.5	4125	4	US-10-237-551-210	Sequence 210, App	1122	73	6.5	2976	3	US-09-877-730-11	Sequence 11, Appl
1050	73.5	6.5	4149	4	US-10-237-551-84	Sequence 84, Appl	1123	73	6.5	3085	3	US-08-795-473B-4	Sequence 4, Appl
1051	73.5	6.5	4192	3	US-09-122-126B-1	Sequence 1, Appl	1124	73	6.5	3085	4	US-09-439-856-4	Sequence 4, Appl
1052	73.5	6.5	4192	4	US-09-634-286A-1	Sequence 1, Appl	c1125	73	6.5	3085	4	US-09-023-655-1131	Sequence 1131, Ap
1053	73.5	6.5	4192	4	US-10-247-685-1	Sequence 1, Appl	c1126	73	6.5	3117	2	US-08-747-536-1	Sequence 1, Appl
c1054	73.5	6.5	4591	4	US-09-902-540-3369	Sequence 3369, Ap	1127	73	6.5	3219	3	US-09-877-730-1	Sequence 1, Appl
1055	73.5	6.5	4776	4	US-09-555-352-1	Sequence 1, Appl	1128	73	6.5	3453	3	US-09-877-730-7	Sequence 7, Appl
c1056	73.5	6.5	5874	4	US-09-561-709B-2	Sequence 2, Appl	1129	73	6.5	3477	4	US-09-877-730-7	Sequence 7, Appl
1057	73.5	6.5	5967	4	US-09-902-540-2012	Sequence 2012, Ap	1130	73	6.5	3507	4	US-09-313-942-23	Sequence 23, Appl
c1058	73.5	6.5	6288	4	US-09-949-016-12483	Sequence 12483, A	c1131	73	6.5	3525	4	US-09-313-942-23	Sequence 23, Appl
c1059	73.5	6.5	7198	3	US-08-994-035C-4	Sequence 4, Appl	1132	73	6.5	3759	4	US-09-252-991A-12708	Sequence 12708, A
c1060	73.5	6.5	7198	3	US-09-395-861-4	Sequence 4, Appl	1133	73	6.5	3874	3	US-09-560-385A-15	Sequence 15, Appl
c1061	73.5	6.5	7950	4	US-09-949-016-14352	Sequence 14352, A	1134	73	6.5	3905	1	US-09-877-730-31	Sequence 31, Appl
c1062	73.5	6.5	8530	4	US-09-949-016-16812	Sequence 16812, A	1135	73	6.5	3906	4	US-09-452-083-1	Sequence 1, Appl
1063	73.5	6.5	9406	4	US-09-949-016-16812	Sequence 16812, A	1136	73	6.5	3906	4	US-09-252-991A-13251	Sequence 13251, A
1064	73.5	6.5	11188	4	US-09-821-167-1	Sequence 1, Appl	c1137	73	6.5	3930	4	US-09-360-385A-13	Sequence 13, Appl
1065	73.5	6.5	12122	4	US-09-949-016-16902	Sequence 16902, A	1138	73	6.5	4188	4	US-09-252-991A-13774	Sequence 13774, A
1066	73.5	6.5	17125	4	US-09-902-540-1158	Sequence 1158, Ap	1139	73	6.5	4226	4	US-09-620-312D-480	Sequence 480, App
1067	73.5	6.5	19222	4	US-09-902-540-1192	Sequence 1192, Ap	1140	73	6.5	4658	4	US-09-949-016-1452	Sequence 1452, App
c1068	73.5	6.5	20235	1	US-07-642-734C-3	Sequence 3, Appl	1141	73	6.5	4602	3	US-09-949-016-941	Sequence 941, App
c1069	73.5	6.5	20235	3	US-08-439-009A-3	Sequence 3, Appl	1142	73	6.5	6330	4	US-09-345-882-4	Sequence 4, Appl
c1070	73.5	6.5	26492	4	US-09-902-540-1234	Sequence 1234, Ap	1143	73	6.5	6898	4	US-09-949-016-15506	Sequence 15506, A
1071	73.5	6.5	42235	3	US-09-199-637A-1	Sequence 1, Appl	1144	73	6.5	7055	4	US-09-902-540-862	Sequence 862, App
												US-09-976-594-941	Sequence 941, App



c1145	73	6.5	7066	4	US-09-919-039-362	Sequence 362, App	c1218	72.5	6.4	1896	4	US-09-252-991A-1429	Sequence 1429, Ap
c1146	73	6.5	8211	4	US-09-252-991A-13656	Sequence 13656, A	1219	72.5	6.4	1908	4	US-09-252-991A-15075	Sequence 15075, A
c1147	73	6.5	13229	4	US-09-902-540-1079	Sequence 1079, Ap	1220	72.5	6.4	1984	1	US-07-885-970A-25	Sequence 25, Appl
c1148	73	6.5	14352	4	US-09-902-540-1070	Sequence 1070, Ap	1221	72.5	6.4	1985	1	US-08-298-687A-25	Sequence 25, Appl
c1149	73	6.5	18034	4	US-09-266-965-75	Sequence 75, Appl	1222	72.5	6.4	1985	1	US-08-298-829-25	Sequence 25, Appl
c1150	73	6.5	18331	4	US-09-266-965-96	Sequence 96, Appl	c1223	72.5	6.4	2001	1	US-08-674-168-24	Sequence 24, Appl
c1151	73	6.5	18551	4	US-09-902-540-1187	Sequence 1187, Ap	c1224	72.5	6.4	2001	1	US-08-985-308-10	Sequence 20, Appl
c1152	73	6.5	22108	3	US-09-053-187A-3	Sequence 3, Appl	c1225	72.5	6.4	2001	3	US-08-852-730-23	Sequence 23, Appl
c1153	73	6.5	22108	3	US-09-085-761A-3	Sequence 3, Appl	c1226	72.5	6.4	2020	4	US-09-902-540-449	Sequence 44, App
c1154	73	6.5	53500	4	US-09-266-965-76	Sequence 76, Appl	1227	72.5	6.4	2106	4	US-09-902-540-6818	Sequence 6818, Ap
c1155	73	6.5	57280	4	US-09-949-016-11796	Sequence 11796, A	1228	72.5	6.4	2213	3	US-09-383-586-27	Sequence 27, Appl
c1156	73	6.5	57280	4	US-09-949-016-12843	Sequence 12843, A	1229	72.5	6.4	2213	3	US-09-383-586-27	Sequence 27, Appl
c1157	73	6.5	57280	4	US-09-949-016-12844	Sequence 12844, A	1230	72.5	6.4	2225	4	US-09-383-586-27	Sequence 27, Appl
c1158	73	6.5	57280	4	US-09-949-016-12846	Sequence 12846, A	1231	72.5	6.4	2249	4	US-09-383-586-27	Sequence 27, Appl
c1159	73	6.5	57280	4	US-09-949-016-12846	Sequence 12846, A	c1232	72.5	6.4	2441	4	US-09-949-016-4246	Sequence 19, Appl
c1160	73	6.5	57280	4	US-09-949-016-13543	Sequence 13543, A	1233	72.5	6.4	2550	4	US-09-949-016-4246	Sequence 19, Appl
c1161	73	6.5	57280	4	US-09-949-016-13543	Sequence 13543, A	1234	72.5	6.4	2550	4	US-09-949-016-4246	Sequence 19, Appl
c1162	73	6.5	57280	4	US-09-949-016-13545	Sequence 13545, A	1235	72.5	6.4	2694	4	US-09-949-016-4246	Sequence 19, Appl
c1163	73	6.5	57280	4	US-09-949-016-14633	Sequence 14633, A	1236	72.5	6.4	2712	3	US-09-949-016-4246	Sequence 19, Appl
c1164	73	6.5	57280	4	US-09-949-016-14633	Sequence 14633, A	1237	72.5	6.4	2754	1	US-09-949-016-4246	Sequence 19, Appl
c1165	73	6.5	57280	4	US-09-949-016-14633	Sequence 14633, A	c1238	72.5	6.4	2763	4	US-09-949-016-4246	Sequence 19, Appl
c1166	73	6.5	57280	4	US-09-949-016-14633	Sequence 14633, A	1239	72.5	6.4	2769	4	US-09-949-016-4246	Sequence 19, Appl
c1167	73	6.5	57280	4	US-09-949-016-14633	Sequence 14633, A	1240	72.5	6.4	2788	3	US-09-949-016-4246	Sequence 19, Appl
c1168	73	6.5	57280	4	US-09-949-016-14633	Sequence 14633, A	c1241	72.5	6.4	2925	4	US-09-949-016-4246	Sequence 19, Appl
c1169	73	6.5	57280	4	US-09-949-016-14633	Sequence 14633, A	1242	72.5	6.4	2948	4	US-09-949-016-4246	Sequence 19, Appl
c1170	73	6.5	57280	4	US-09-949-016-14633	Sequence 14633, A	1243	72.5	6.4	3026	3	US-09-949-016-4246	Sequence 19, Appl
c1171	73	6.5	116652	4	US-09-949-016-13413	Sequence 13413, A	1244	72.5	6.4	3062	4	US-09-949-016-4246	Sequence 19, Appl
c1172	73	6.5	162450	3	US-09-345-882-1	Sequence 1, Appl	1245	72.5	6.4	3074	4	US-09-949-016-4246	Sequence 19, Appl
c1173	72.5	6.4	399	4	US-09-270-767-7130	Sequence 7130, Ap	1246	72.5	6.4	3074	4	US-09-949-016-4246	Sequence 19, Appl
c1174	72.5	6.4	399	4	US-09-270-767-22412	Sequence 22412, A	1247	72.5	6.4	3187	5	US-09-949-016-4246	Sequence 19, Appl
c1175	72.5	6.4	558	4	US-09-248-796A-4208	Sequence 4208, Ap	1248	72.5	6.4	3192	1	US-09-949-016-4246	Sequence 19, Appl
c1176	72.5	6.4	598	4	US-09-902-540-6452	Sequence 6452, Ap	1249	72.5	6.4	3192	1	US-09-949-016-4246	Sequence 19, Appl
c1177	72.5	6.4	601	4	US-09-949-016-85721	Sequence 85721, A	1250	72.5	6.4	3833	1	US-09-949-016-4246	Sequence 19, Appl
c1178	72.5	6.4	601	4	US-09-949-016-137497	Sequence 137497, A	1251	72.5	6.4	3833	1	US-09-949-016-4246	Sequence 19, Appl
c1179	72.5	6.4	687	3	US-09-048-052-5	Sequence 5, Appl	c1252	72.5	6.4	3900	4	US-09-949-016-4246	Sequence 19, Appl
c1180	72.5	6.4	687	3	US-09-160-246-5	Sequence 5, Appl	1253	72.5	6.4	4048	4	US-09-949-016-4246	Sequence 19, Appl
c1181	72.5	6.4	687	3	US-09-333-019-5	Sequence 5, Appl	c1254	72.5	6.4	4079	4	US-09-949-016-4246	Sequence 19, Appl
c1182	72.5	6.4	786	4	US-09-894-844-51	Sequence 51, Appl	1255	72.5	6.4	4280	4	US-09-949-016-4246	Sequence 19, Appl
c1183	72.5	6.4	813	4	US-09-134-000C-148	Sequence 148, App	1256	72.5	6.4	4412	4	US-09-949-016-4246	Sequence 19, Appl
c1184	72.5	6.4	882	4	US-09-496-320-4	Sequence 4, Appl	c1257	72.5	6.4	4517	4	US-09-949-016-4246	Sequence 19, Appl
c1185	72.5	6.4	894	4	US-09-902-540-6508	Sequence 6508, Ap	1258	72.5	6.4	4519	4	US-09-949-016-4246	Sequence 19, Appl
c1186	72.5	6.4	913	1	US-08-217-327-3	Sequence 3, Appl	c1259	72.5	6.4	4519	4	US-09-949-016-4246	Sequence 19, Appl
c1187	72.5	6.4	913	1	US-08-885-970A-3	Sequence 3, Appl	c1260	72.5	6.4	4519	4	US-09-949-016-4246	Sequence 19, Appl
c1188	72.5	6.4	913	1	US-08-298-687A-3	Sequence 3, Appl	1261	72.5	6.4	5288	2	US-09-949-016-4246	Sequence 19, Appl
c1189	72.5	6.4	913	1	US-08-530-797-2	Sequence 2, Appl	1262	72.5	6.4	5288	3	US-09-949-016-4246	Sequence 19, Appl
c1190	72.5	6.4	913	1	US-08-298-629-3	Sequence 3, Appl	1263	72.5	6.4	5288	3	US-09-949-016-4246	Sequence 19, Appl
c1191	72.5	6.4	913	2	US-08-787-335-2	Sequence 2, Appl	1264	72.5	6.4	5288	3	US-09-949-016-4246	Sequence 19, Appl
c1192	72.5	6.4	913	2	US-09-252-991A-4926	Sequence 4926, Ap	1265	72.5	6.4	5288	4	US-09-949-016-4246	Sequence 19, Appl
c1193	72.5	6.4	922	3	US-09-189-060B-73	Sequence 73, Appl	1266	72.5	6.4	5288	4	US-09-949-016-4246	Sequence 19, Appl
c1194	72.5	6.4	1069	4	US-09-252-991A-4931	Sequence 4931, Ap	1267	72.5	6.4	5288	5	US-09-949-016-4246	Sequence 19, Appl
c1195	72.5	6.4	1069	4	US-09-949-016-2654	Sequence 2654, Ap	1268	72.5	6.4	5337	4	US-09-949-016-4246	Sequence 19, Appl
c1196	72.5	6.4	1069	4	US-09-949-016-2655	Sequence 2655, Ap	1269	72.5	6.4	5337	4	US-09-949-016-4246	Sequence 19, Appl
c1197	72.5	6.4	1291	4	US-09-394-142B-1	Sequence 1, Appl	1270	72.5	6.4	5931	3	US-09-949-016-4246	Sequence 19, Appl
c1198	72.5	6.4	1315	4	US-09-270-767-13795	Sequence 13795, A	1271	72.5	6.4	5931	3	US-09-949-016-4246	Sequence 19, Appl
c1199	72.5	6.4	1327	1	US-08-507-431-3	Sequence 3, Appl	c1272	72.5	6.4	6441	3	US-09-949-016-4246	Sequence 19, Appl
c1200	72.5	6.4	1327	2	US-08-700-546-1	Sequence 1, Appl	1273	72.5	6.4	6443	6	US-09-949-016-4246	Sequence 19, Appl
c1201	72.5	6.4	1327	2	US-08-902-655A-3	Sequence 3, Appl	c1274	72.5	6.4	6443	6	US-09-949-016-4246	Sequence 19, Appl
c1202	72.5	6.4	1327	2	US-09-116-622-3	Sequence 3, Appl	1275	72.5	6.4	6568	4	US-09-949-016-4246	Sequence 19, Appl
c1203	72.5	6.4	1327	3	US-09-219-277-3	Sequence 3, Appl	1276	72.5	6.4	7577	4	US-09-949-016-4246	Sequence 19, Appl
c1204	72.5	6.4	1327	3	US-09-599-661-3	Sequence 3, Appl	1277	72.5	6.4	7577	4	US-09-949-016-4246	Sequence 19, Appl
c1205	72.5	6.4	1386	4	US-09-270-767-15263	Sequence 15263, A	1278	72.5	6.4	7621	4	US-09-949-016-4246	Sequence 19, Appl
c1206	72.5	6.4	1452	4	US-09-252-991A-14679	Sequence 14679, A	1279	72.5	6.4	7621	4	US-09-949-016-4246	Sequence 19, Appl
c1207	72.5	6.4	1461	2	US-08-809-763-4	Sequence 4, Appl	1280	72.5	6.4	7930	3	US-09-949-016-4246	Sequence 19, Appl
c1208	72.5	6.4	1461	3	US-08-956-253-4	Sequence 4, Appl	c1281	72.5	6.4	10182	4	US-09-949-016-4246	Sequence 19, Appl
c1209	72.5	6.4	1515	3	US-09-292-768-5	Sequence 5, Appl	c1282	72.5	6.4	12732	3	US-09-949-016-4246	Sequence 19, Appl
c1210	72.5	6.4	1569	4	US-09-949-016-3898	Sequence 3898, Ap	c1283	72.5	6.4	12732	4	US-09-949-016-4246	Sequence 19, Appl
c1211	72.5	6.4	1725	4	US-09-943-075A-7	Sequence 7, Appl	1284	72.5	6.4	18864	4	US-09-949-016-4246	Sequence 19, Appl
c1212	72.5	6.4	1797	3	US-09-377-155-12	Sequence 12, Appl	1285	72.5	6.4	18864	4	US-09-949-016-4246	Sequence 19, Appl
c1213	72.5	6.4	1797	3	US-09-669-974-12	Sequence 12, Appl	c1286	72.5	6.4	19990	4	US-09-949-016-4246	Sequence 19, Appl
c1214	72.5	6.4	1797	4	US-09-797-862-12	Sequence 12, Appl	1287	72.5	6.4	24791	4	US-09-949-016-4246	Sequence 19, Appl
c1215	72.5	6.4	1831	1	US-09-477-135A-115	Sequence 115, App	1288	72.5	6.4	27277	4	US-09-949-016-4246	Sequence 19, Appl
c1216	72.5	6.4	1848	1	US-08-333-802-1	Sequence 1, Appl	c1289	72.5	6.4	30001	1	US-09-949-016-4246	Sequence 19, Appl
c1217	72.5	6.4	1892	3	US-09-554-225-3	Sequence 3, Appl	c1290	72.5	6.4	30001	2	US-09-949-016-4246	Sequence 19, Appl

1291	72.5	6.4	34230	4	US-09-949-016-12052	Sequence 12052, A	c1364	72	6.4	1723	3	US-08-278-730A-20	Sequence 20, Appl
1292	72.5	6.4	35100	2	US-08-770-379-19	Sequence 19, Appl	c1365	72	6.4	1723	3	US-08-889-419-5	Sequence 5, Appl
1293	72.5	6.4	35100	3	US-08-757-669A-19	Sequence 19, Appl	c1366	72	6.4	1723	3	US-08-445-467-20	Sequence 20, Appl
1294	72.5	6.4	35100	3	US-09-230-371A-19	Sequence 19, Appl	c1367	72	6.4	1723	3	US-08-480-515A-20	Sequence 20, Appl
1295	72.5	6.4	42348	4	US-09-949-016-17157	Sequence 17157, A	c1368	72	6.4	1723	3	US-09-219-391-7	Sequence 7, Appl
1296	72.5	6.4	80706	4	US-09-949-016-15347	Sequence 15347, A	c1369	72	6.4	1723	3	US-09-170-936-20	Sequence 20, Appl
1297	72.5	6.4	92581	4	US-09-949-016-12182	Sequence 12182, A	c1370	72	6.4	1723	3	US-08-402-542-5	Sequence 5, Appl
1298	72.5	6.4	92581	4	US-09-949-016-16542	Sequence 16542, A	c1371	72	6.4	1723	3	US-08-461-113-20	Sequence 20, Appl
1299	72.5	6.4	95122	4	US-09-949-016-17235	Sequence 17235, A	c1372	72	6.4	1723	4	US-08-456-033-20	Sequence 20, Appl
c1300	72.5	6.4	96739	4	US-09-949-016-15606	Sequence 15606, A	c1373	72	6.4	1723	4	US-08-643-321-19	Sequence 19, Appl
1301	72.5	6.4	128470	4	US-09-949-016-13765	Sequence 13765, A	c1374	72	6.4	1723	4	US-09-148-925C-28	Sequence 28, Appl
c1302	72.5	6.4	137226	4	US-09-949-016-13763	Sequence 13763, A	c1375	72	6.4	1723	4	US-08-957-425-28	Sequence 28, Appl
1303	72.5	6.4	197336	4	US-09-949-016-12881	Sequence 12881, A	c1376	72	6.4	1723	4	US-08-260-675-20	Sequence 20, Appl
1304	72.5	6.4	197337	4	US-09-949-016-14376	Sequence 14376, A	c1377	72	6.4	1723	5	PCT-US92-01968-20	Sequence 20, Appl
1305	72.5	6.4	234288	4	US-09-949-016-17272	Sequence 17272, A	c1378	72	6.4	1723	5	PCT-US93-05446-10	Sequence 10, Appl
1306	72	6.4	530	4	US-09-270-767-5334	Sequence 5334, Ap	c1379	72	6.4	1723	5	PCT-US93-07189-5	Sequence 5, Appl
1307	72	6.4	530	4	US-09-270-767-20616	Sequence 20616, A	c1380	72	6.4	1723	5	PCT-US93-07190-20	Sequence 20, Appl
c1308	72	6.4	601	4	US-09-949-016-45631	Sequence 45631, A	c1381	72	6.4	1723	5	PCT-US93-07231-20	Sequence 20, Appl
1309	72	6.4	601	4	US-09-949-016-112555	Sequence 112555, A	c1382	72	6.4	1723	5	PCT-US93-08742-20	Sequence 20, Appl
c1310	72	6.4	687	4	US-09-252-991A-2644	Sequence 2644, Ap	c1383	72	6.4	1723	5	PCT-US93-08808-20	Sequence 20, Appl
1311	72	6.4	702	4	US-09-107-433-124	Sequence 124, App	c1384	72	6.4	1723	5	PCT-US93-08885-20	Sequence 20, Appl
1312	72	6.4	804	4	US-09-252-991A-2187	Sequence 2187, Ap	c1385	72	6.4	1723	5	PCT-US93-10520-7	Sequence 7, Appl
1313	72	6.4	834	4	US-09-252-991A-1864	Sequence 1864, Ap	c1386	72	6.4	1749	3	US-09-545-814-4	Sequence 4, Appl
1314	72	6.4	840	4	US-09-248-796A-2756	Sequence 2756, Ap	c1387	72	6.4	1749	3	US-09-545-814-6	Sequence 6, Appl
c1315	72	6.4	906	4	US-09-252-991A-2239	Sequence 2239, Ap	c1388	72	6.4	1755	4	US-09-252-991A-7740	Sequence 7740, Ap
1316	72	6.4	907	1	US-08-821-119-1	Sequence 1, Appl	c1389	72	6.4	1818	4	US-09-148-545-87	Sequence 87, Appl
1317	72	6.4	945	4	US-09-252-991A-13854	Sequence 13854, A	c1390	72	6.4	1919	3	US-09-545-814-31	Sequence 31, Appl
c1318	72	6.4	951	4	US-09-252-991A-7855	Sequence 7855, Ap	c1391	72	6.4	1919	3	US-09-545-814-33	Sequence 33, Appl
c1319	72	6.4	1017	4	US-09-252-991A-13594	Sequence 13594, A	c1392	72	6.4	1925	4	US-09-148-545-86	Sequence 86, Appl
c1320	72	6.4	1032	3	US-08-936-165A-145	Sequence 145, App	c1393	72	6.4	1926	4	US-09-148-545-21	Sequence 21, Appl
c1321	72	6.4	1065	4	US-09-252-991A-2098	Sequence 2098, Ap	c1394	72	6.4	1958	3	US-08-665-038A-3	Sequence 3, Appl
1322	72	6.4	1083	4	US-09-489-039A-2212	Sequence 2212, Ap	c1395	72	6.4	2200	3	US-08-993-088A-1	Sequence 1, Appl
c1323	72	6.4	1161	4	US-09-902-540-5174	Sequence 5174, Ap	c1396	72	6.4	2200	3	US-08-993-424B-1	Sequence 1, Appl
1324	72	6.4	1176	3	US-09-200-090-3	Sequence 3, Appl	c1397	72	6.4	2200	4	US-09-603-680-1	Sequence 1, Appl
c1325	72	6.4	1227	4	US-09-902-540-6384	Sequence 6384, Ap	c1398	72	6.4	2220	4	US-09-373-272-9	Sequence 9, Appl
1326	72	6.4	1230	4	US-09-902-540-422	Sequence 422, App	c1399	72	6.4	2257	4	US-09-016-434-1300	Sequence 1300, Ap
1327	72	6.4	1233	4	US-09-252-991A-8880	Sequence 8880, Ap	c1400	72	6.4	2258	4	US-09-949-016-3029	Sequence 3029, Ap
c1328	72	6.4	1251	4	US-09-949-016-3106	Sequence 3106, Ap	c1401	72	6.4	2285	1	US-08-477-674-9	Sequence 9, Appl
c1329	72	6.4	1362	4	US-09-252-991A-7719	Sequence 7719, Ap	c1402	72	6.4	2285	1	US-08-473-791-9	Sequence 9, Appl
1330	72	6.4	1401	4	US-09-252-991A-1795	Sequence 1795, Ap	c1403	72	6.4	2285	2	US-08-316-714-9	Sequence 9, Appl
1331	72	6.4	1413	4	US-09-252-991A-8987	Sequence 8987, Ap	c1404	72	6.4	2285	2	US-08-473-673-9	Sequence 9, Appl
1332	72	6.4	1431	4	US-09-489-039A-1187	Sequence 1187, Ap	c1405	72	6.4	2313	4	US-09-252-991A-13752	Sequence 13752, A
1333	72	6.4	1478	3	US-09-545-814-28	Sequence 28, Appl	c1406	72	6.4	2403	1	US-08-471-033-30	Sequence 30, Appl
c1334	72	6.4	1482	3	US-09-545-814-30	Sequence 30, Appl	c1407	72	6.4	2403	2	US-08-471-044-30	Sequence 30, Appl
1335	72	6.4	1484	3	US-09-252-991A-2267	Sequence 2267, Ap	c1408	72	6.4	2403	2	US-08-463-483A-30	Sequence 30, Appl
c1336	72	6.4	1541	4	US-09-270-767-11220	Sequence 11220, Ap	c1409	72	6.4	2403	2	US-08-471-046A-30	Sequence 30, Appl
1337	72	6.4	1563	4	US-09-902-540-4269	Sequence 4269, Ap	c1410	72	6.4	2403	2	US-08-470-566B-30	Sequence 30, Appl
1338	72	6.4	1578	4	US-09-602-777A-105	Sequence 105, App	c1411	72	6.4	2403	2	US-08-838-219B-7	Sequence 7, Appl
1339	72	6.4	1674	4	US-09-248-796A-12789	Sequence 12789, A	c1412	72	6.4	2403	2	US-08-469-334-30	Sequence 30, Appl
1340	72	6.4	1677	3	US-09-545-814-13	Sequence 13, Appl	c1413	72	6.4	2403	3	US-09-300-529-30	Sequence 30, Appl
c1341	72	6.4	1677	3	US-09-545-814-15	Sequence 15, Appl	c1414	72	6.4	2403	3	US-09-233-336A-7	Sequence 7, Appl
c1342	72	6.4	1677	4	US-09-252-991A-9102	Sequence 9102, Ap	c1415	72	6.4	2403	3	US-09-233-752A-7	Sequence 7, Appl
c1343	72	6.4	1723	1	US-07-841-846-28	Sequence 28, Appl	c1416	72	6.4	2403	3	US-09-402-036-7	Sequence 7, Appl
c1344	72	6.4	1723	1	US-07-901-703-10	Sequence 10, Appl	c1417	72	6.4	2403	3	US-09-904-226-7	Sequence 7, Appl
c1345	72	6.4	1723	1	US-08-147-023-28	Sequence 28, Appl	c1418	72	6.4	2424	4	US-08-821-119-16	Sequence 16, Appl
c1346	72	6.4	1723	1	US-08-206-864-3	Sequence 3, Appl	c1419	72	6.4	2460	4	US-09-902-540-4178	Sequence 4178, Ap
c1347	72	6.4	1723	1	US-08-278-729A-20	Sequence 20, Appl	c1420	72	6.4	2610	3	US-09-545-814-1	Sequence 1, Appl
c1348	72	6.4	1723	1	US-08-480-528A-7	Sequence 7, Appl	c1421	72	6.4	2610	3	US-09-545-814-3	Sequence 3, Appl
c1349	72	6.4	1723	1	US-08-479-666-7	Sequence 7, Appl	c1422	72	6.4	2619	3	US-08-337-797A-1	Sequence 1, Appl
c1350	72	6.4	1723	1	US-08-155-343A-20	Sequence 20, Appl	c1423	72	6.4	2619	3	US-08-337-797A-3	Sequence 3, Appl
c1351	72	6.4	1723	1	US-08-406-672-20	Sequence 20, Appl	c1424	72	6.4	2619	3	US-09-258-523-1	Sequence 1, Appl
c1352	72	6.4	1723	1	US-08-643-563A-20	Sequence 20, Appl	c1425	72	6.4	2619	3	US-09-258-523-3	Sequence 3, Appl
c1353	72	6.4	1723	1	US-08-447-570-28	Sequence 28, Appl	c1426	72	6.4	2668	2	US-08-461-775-11	Sequence 11, Appl
c1354	72	6.4	1723	1	US-08-643-763A-20	Sequence 20, Appl	c1427	72	6.4	2668	3	US-09-031-606-11	Sequence 11, Appl
c1355	72	6.4	1723	1	US-08-462-623-20	Sequence 20, Appl	c1428	72	6.4	2699	3	US-09-460-145-3	Sequence 3, Appl
c1356	72	6.4	1723	1	US-08-451-953A-20	Sequence 20, Appl	c1429	72	6.4	2699	4	US-09-895-547-3	Sequence 4, Appl
c1357	72	6.4	1723	2	US-08-459-346-5	Sequence 5, Appl	c1430	72	6.4	2724	4	US-09-602-777A-103	Sequence 103, App
c1358	72	6.4	1723	2	US-08-445-468A-20	Sequence 20, Appl	c1431	72	6.4	2754	4	US-09-902-540-5587	Sequence 5587, Ap
c1359	72	6.4	1723	2	US-08-901-200A-7	Sequence 7, Appl	c1432	72	6.4	2824	3	US-07-757-022B-13	Sequence 13, Appl
c1360	72	6.4	1723	2	US-08-449-700-28	Sequence 28, Appl	c1433	72	6.4	3046	4	US-09-949-016-5700	Sequence 5700, Ap
c1361	72	6.4	1723	2	US-08-449-699A-28	Sequence 28, Appl	c1434	72	6.4	3066	3	US-07-757-022B-83	Sequence 83, Appl
c1362	72	6.4	1723	2	US-08-461-397A-20	Sequence 20, Appl	c1435	72	6.4	3085	3	US-08-827-208-2	Sequence 2, Appl
c1363	72	6.4	1723	2	US-08-912-088-20	Sequence 20, Appl	c1436	72	6.4	3085	3	US-08-827-208-4	Sequence 4, Appl

1437	72	6.4	3085	3	US-09-500-358-2	Sequence 2, Appli
1438	72	6.4	3085	3	US-09-500-358-4	Sequence 4, Appli
1439	72	6.4	3085	3	US-09-498-809-2	Sequence 4, Appli
1440	72	6.4	3085	3	US-09-498-809-4	Sequence 4, Appli
1441	72	6.4	3117	3	US-07-757-022B-73	Sequence 73, Appl
1442	72	6.4	3148	3	US-07-757-022B-57	Sequence 103, Appl
1443	72	6.4	3420	3	US-07-757-022B-103	Sequence 103, Appl
1444	72	6.4	3500	4	US-09-491-577-100	Sequence 100, Appl
1445	72	6.4	3590	1	US-08-587-889-1	Sequence 1, Appli
1446	72	6.4	3590	4	US-09-016-434-1093	Sequence 1093, Ap
1447	72	6.4	3590	5	PCT-US96-09193-1	Sequence 1, Appli
1448	72	6.4	3813	3	US-07-757-022B-43	Sequence 43, Appl
1449	72	6.4	3936	3	US-07-757-022B-41	Sequence 41, Appl
1450	72	6.4	3942	3	US-07-757-022B-141	Sequence 141, Appl
1451	72	6.4	3945	3	US-07-757-022B-49	Sequence 49, Appl
1452	72	6.4	3963	3	US-07-757-022B-45	Sequence 45, Appl
1453	72	6.4	3963	3	US-07-757-022B-59	Sequence 59, Appl
1454	72	6.4	4052	4	US-08-624-447-11	Sequence 11, Appl
1455	72	6.4	4065	3	US-07-757-022B-47	Sequence 47, Appl
1456	72	6.4	4086	3	US-07-757-022B-39	Sequence 39, Appl
1457	72	6.4	4092	3	US-07-757-022B-51	Sequence 51, Appl
1458	72	6.4	4183	3	US-09-460-145-1	Sequence 1, Appli
1459	72	6.4	4183	4	US-09-895-547-1	Sequence 1, Appli
1460	72	6.4	4215	3	US-07-757-022B-61	Sequence 61, Appl
1461	72	6.4	4291	3	US-09-351-200-1	Sequence 1, Appli
1462	72	6.4	4840	4	US-10-184-595-57	Sequence 57, Appl
1463	72	6.4	4890	4	US-09-677-046A-3	Sequence 3, Appli
1464	72	6.4	4983	4	US-09-270-767-12587	Sequence 12587, A
1465	72	6.4	5008	3	US-07-757-022B-1	Sequence 1, Appli
1466	72	6.4	5017	4	US-09-949-016-4956	Sequence 4956, Ap
1467	72	6.4	5041	4	US-09-023-655-981	Sequence 981, App
1468	72	6.4	5041	4	US-09-298-970A-2	Sequence 2, Appli
1469	72	6.4	5330	4	US-09-023-905A-1	Sequence 1, Appli
1470	72	6.4	5692	4	US-09-902-540-783	Sequence 783, App
1471	72	6.4	7112	4	US-09-949-016-14848	Sequence 14848, A
1472	72	6.4	7168	3	US-08-840-316-4	Sequence 4, Appli
1473	72	6.4	7168	3	US-08-809-523-4	Sequence 4, Appli
1474	72	6.4	7168	3	US-08-471-971-4	Sequence 4, Appli
1475	72	6.4	7168	3	US-09-402-776-4	Sequence 4, Appli
1476	72	6.4	7168	4	US-08-470-246-4	Sequence 4, Appli
1477	72	6.4	7168	4	US-08-316-765-4	Sequence 4, Appli
1478	72	6.4	7168	4	US-09-724-475-4	Sequence 4, Appli
1479	72	6.4	7168	5	PCT-US93-08849A-4	Sequence 4, Appli
1480	72	6.4	7168	5	PCT-US93-08849-4	Sequence 4, Appli
1481	72	6.4	8517	3	US-08-827-208-1	Sequence 1, Appli
1482	72	6.4	8517	3	US-09-500-358-1	Sequence 1, Appli
1483	72	6.4	8517	3	US-09-498-809-1	Sequence 1, Appli
1484	72	6.4	9408	4	US-09-418-710-14	Sequence 14, Appl
1485	72	6.4	9408	4	US-09-839-479-14	Sequence 14, Appl
1486	72	6.4	9687	3	US-09-133-944-2	Sequence 2, Appli
1487	72	6.4	9687	3	US-09-208-827-2	Sequence 2, Appli
1488	72	6.4	9687	4	US-10-043-074-2	Sequence 2, Appli
1489	72	6.4	11219	1	US-07-642-734C-1	Sequence 1, Appli
1490	72	6.4	11219	3	US-08-439-009A-1	Sequence 1, Appli
1491	72	6.4	11440	4	US-09-949-016-17442	Sequence 17442, A
1492	72	6.4	12723	4	US-09-949-016-14771	Sequence 14771, A
1493	72	6.4	19862	4	US-09-902-540-1198	Sequence 1198, Ap
1494	72	6.4	21707	4	US-09-949-016-16698	Sequence 16698, A
1495	72	6.4	26012	4	US-09-902-540-1212	Sequence 1212, Ap
1496	72	6.4	28366	4	US-09-949-016-16763	Sequence 16763, Ap
1497	72	6.4	34199	4	US-09-902-540-1255	Sequence 1255, A
1498	72	6.4	39113	4	US-09-949-016-15634	Sequence 15634, A
1499	72	6.4	41927	4	US-09-902-540-1268	Sequence 1268, Ap
1500	72	6.4	57280	4	US-09-949-016-11796	Sequence 11796, A
ALIGNMENTS						
RESULT 1						
US-09-232-160-13						
; Sequence 13, Application US/09232160						
; Patent No. 6368794						
; GENERAL INFORMATION:						
APPLICANT: Steve Daniel						
APPLICANT: James Gilmore						
APPLICANT: Susan G. Stuart						
APPLICANT: Laura Stuve						
TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL						
TITLE OF INVENTION: PROLIFERATION						
FILE REFERENCE: PA-0003 US						
CURRENT APPLICATION NUMBER: US/09/232,160						
CURRENT FILING DATE: 1999-01-15						
NUMBER OF SEQ ID NOS: 23						
SOFTWARE: PERL Program						
SEQ ID NO 13						
LENGTH: 2029						
TYPE: DNA						
ORGANISM: Homo sapiens						
FEATURE: -						
OTHER INFORMATION: 3044710						
US-09-232-160-13						
Alignment Scores:						
Pred. No.: 7.44e-122 Length: 2029						
Score: 1125.00 Matches: 218						
Percent Similarity: 100.00% Conservative: 0						
Best Local Similarity: 100.00% Mismatches: 0						
Query Match: 100.00% Indels: 0						
DB: 3 Gaps: 0						
Qy	1	ThzArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys	20			
Db	231	ACGAGGCTCTGGTCCGAGGCTCTTGGCGTGCAGAGAGCTTCCATCCAGGTGTCATGC	290			
Qy	21	ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu	40			
Db	291	AGAAATATGGGATCACCTTGTGAGCAAAAGCGAACCCAGCAGCTGAATTTCCACAGAA	350			
Qy	41	AlaIysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr	60			
Db	351	GCTAAGGAGGCGCTGTAGGCTGGGAGCTAAGTTGGCGCGGCAAGCAAGTTGAAACA	410			
Qy	61	AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValVal	80			
Db	411	GCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGATTCGTGGTC	470			
Qy	81	IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp	100			
Db	471	ATCTTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTGG	530			
Qy	101	LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr	120			
Db	531	AAGGTTCCAGTGAGCCGACAGTTTGCAGCCCTATTGTTTACAACTCATCTGATCTGGACT	590			
Qy	121	AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla	140			
Db	591	AATCTGGTCATTTCAGAAATATATACCCCAAGATATCCATATTTCAACACTCAAACTGCA	650			
Qy	141	ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer	160			
Db	651	ACACAAACACAGAAATTTATTGTCAGTGACAGTACCTACTCTCGGTGGCATCCCCCTACTCT	710			
Qy	161	ThrIleProAlaProThrThrThrProAlaProAlaSerThrSerIleProArgArg	180			
Db	711	ACAATACCTCCCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	770			
Qy	181	LysIleLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr	200			
Db	771	AAAAAATTTGATTTGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGCTCTACAGAACT	830			
Qy	201	GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly	218			
Db	831	GAACCATTTGTTGAAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTGGA	884			
RESULT 2						

US-09-949-016-1894  
; Sequence 1894, Application US/09949016  
; Patent No. 6812339

## GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1894  
; LENGTH: 2301  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-1894

## Alignment Scores:

Pred. No.:	9,09e-122	Length:	2301
Score:	1125.00	Matches:	218
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

Qy	1	ThrArgLeuLeuValGlnGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys	20
Db	140	ACGAGGCTCTGTGTCGAAGCTCTTTCGTCGACAGAGCTTTCATCCAGGTGTCATGC	199
Qy	21	ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAenPheThrGlu	40
Db	200	AGAAATATGGGGATCATCCCTTGAGCAAAAAGCGNACCAGCAGCTGAATTTACAGAA	259
Qy	41	AlaIleGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr	60
Db	260	GCTAAGGAGGCGTGTAGCTGCTGGGACTAAGTTTGGCCGGCAAGACCAAGTTGAACA	319
Qy	61	AlaIleLysAlaSerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValVal	80
Db	320	GCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTC	379
Qy	81	IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyr	100
Db	380	ATCTTAGGATTTAGCCCAACCCCAAGTGTGGGAAAATGGGTGGTGTCTGATTTGG	439
Qy	101	LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThr	120
Db	440	AAGGTTCCAGTGAGCCACAGTTTGACGCTATTGTTTACAACATCATCTGATCTTGACT	499
Qy	121	AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla	140
Db	500	AACTCGTGCAATTCAGAAAATTTATCACCAAAAATGCCATATTTCAACACTCAAACTGCA	559
Qy	141	ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer	160
Db	560	ACACAAACACAGAAATTTATGTGTCAGTCAGTACCTACTTCGGTGGCATCCCTTACTCT	619
Qy	161	ThrIleProAlaProThrThrThrProAlaProAlaSerThrSerIleProArgArg	180
Db	620	ACAATACCTGCCCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	679
Qy	181	LysIleLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr	200
Db	680	AAAAAATTTGTTGTGCAGAGAAGTTTTTATGAAACTAGCACCATCTGTCTACAGAACT	739

Qy	201	GluProPheValGluAsnLysAlaAlaPheLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly	218
Db	740	GAACCATTTGTTGAAAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGA	793

## RESULT 3

; Sequence 200, Application US/09907794A  
; Patent No. 6635468  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/907,794A  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 200  
; LENGTH: 2372  
; TYPE: DNA  
; ORGANISM: Homo sapiens

## Alignment Scores:

Pred. No.: 9.55e-122 Length: 2372  
Score: 1125.00 Matches: 218  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

Qy 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20  
Db ACAGAGCTCTGGTCCAGAGCTTTTGGTGCAGAGAGCTTTCCATCCAGGTGTCATGC 267  
Qy 21 ArgIleMetGlyIleThrLeuValSerIleValAlaGlnGlnLeuAsnPheThrGlu 40  
Db AGAATTATGGGATCACCCCTTGTGAGCAAAAGGCGAACAGCAGCTGAATTTCCAGAA 327  
Qy 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60  
Db GCTAAGGAGGCTGTAGCTGCTGGACTAAGTTTGGCGCGCAGGACCAAGTTGAACA 387  
Qy 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80  
Db GCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGCCTGGGTGGAGATGGATTCGTGTC 447  
Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100  
Db ATCTCTAGGATTATGCCCAACCCCAAGTGTGGGAAAAATGGGTGGTCTCTGATTGG 507  
Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120  
Db AAGGTTCCAGTGCACCGACAGTTTGCAGCCCTATTGTTACCACTCATCTGATCTGGACT 567  
Qy 121 AsnSerCysIleProGluIleThrThrLysAspProIlePheAsnThrGlnThrAla 140  
Db AACTCGTGCATTCAGAAATATATCACCACCAAGATCCCATATATCAACACTCAAACTGCA 627  
Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160  
Db ACACAAACACAGAAATTTATTTGTCAGTACCTACTCGGTGGCATCCCTTACTCT 687  
Qy 161 ThrIleProAlaProThrThrThrProAlaProAlaSerThrSerIleProArgArg 180  
Db ACAATACCTGCCCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 747  
Qy 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200  
Db AAAAAATTGATTTGTCGACAGAAAGTTTTTATGAAACTAGCACCATGTCTACAGAACT 807  
Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218  
Db GAACATTGTTGTAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGA 861

## RESULT 4

; Sequence 200, Application US/09905125A

; Patent No. 6664376

## GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: KJavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/905,125A  
; PRIOR FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 200  
; LENGTH: 2372  
; TYPE: DNA  
; ORGANISM: Homo sapiens

Alignment Scores:  
Pred. No.: 9.55e-122 Length: 2372  
Score: 1125.00 Matches: 218  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

Qy 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20  
Db 208 ACAGAGCTCTGGTCCAGAGCTTTTGGTGCAGAGAGCTTTCCATCCAGGTGTCATGC 267  
Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40

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Db 268 AGAATTATGGGATCATCCCTTGTGAGCAAAAGCGAACCCAGCAGCTGAATTTACAGAA 327
Qy 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60
Db 328 GCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGACCAAGTTGAACA 387
Qy 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValVal 80
Db 388 GCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTC 447
Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyr 100
Db 448 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGCAAAATGGCGTGGGTGCTGCTGATTTGG 507
Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThr 120
Db 508 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCCTATTGTTACAACTCATCTGTACTTGGACT 567
Qy 121 AsnSerCysIleProGluIleThrThrLysAspProIlePheAsnThrGlnThrAla 140
Db 568 AACTCGTGCAATTCAGAAATTATCACCCAAAGATCCCATATTTCAACTCAAACTGCA 627
Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160
Db 628 ACACAAACACAGAAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCT 687
Qy 161 ThrIleProIleProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180
Db 688 ACAATACCTCCCTCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 747
Qy 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200
Db 748 AAAAAATTGATTTGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGCTCTACAGAACT 807
Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218
Db 808 GAACCAATTTGTTGAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGA 861
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## RESULT 5

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; Sequence 200, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin D.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10

Alignment Scores:
Pred. No.: 9,55e-122 Length: 2372
Score: 1125.00 Matches: 218
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Caps: 0

Qy 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20
Db 208 ACAGAGCTCTGTGTCACAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTATGC 267
Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40
Db 268 AGAATTATGGGATCACCTTTGTGAGCAAAAGCGAACCCAGCAGCTGAATTTACAGAA 327
Qy 41 AlaLysGluAlaCysArgLeuLeuGlyLysAspGlnValGluThr 60
Db 328 GCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGACCAAGTTGAACA 387
Qy 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValVal 80
Db 388 GCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGGTC 447
Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyr 100
Db 448 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGCAAAATGGCGTGGGTGCTGCTGATTTGG 507
Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThr 120
Db 508 AAGGTTCCAGTGAGCCGACAGTTTGCAGCCCTATTGTTACAACTCATCTGTACTTGGACT 567
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Qy 121 AsnSerCysIleProGluIleThrThrLysAspProIlePheAsnThrGlnThrAla 140  
Db 568 AACTCGTGCAATTCAGAAATATCACCACCAAGATCCCATATTCACACACTCAAACTGCA 627  
Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160  
Db 628 ACACAAACACAGAAATTTATGTGAGTGACAGTACCTACCTCGGTGGCATCCCTTACTCT 687  
Qy 161 ThrIleProAlaProThrThrThrProAlaProAlaSerThrSerIleProArgArg 180  
Db 688 ACATACCTGCCCCCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 747  
Qy 181 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200  
Db 748 AAAAAATTTGATTTGTGTCACAGAAAGTTTTATGAAACTAGCACCATGTCTACAGAACT 807  
Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218  
Db 808 GAACCAATTTGTTGAAATAAAGCAGCATTCAAGAAATGAGCTGCTGGGTTTGA 861

## RESULT 6

; Sequence 200, Application US/09906700  
; Patent No. 6723535  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/906,700  
; CURRENT FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
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; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
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; PRIOR APPLICATION NUMBER: PCT/US99/30999  
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; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 200  
; LENGTH: 2372  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
Alignment Scores:  
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Score: 1125.00 Matches: 218  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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Qy 1 ThrArgLeuLeuValGlnGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys 20  
Db 208 ACAGAGCTCTGGTCCAAAGGCTCTTTCGTGCAGAGAGCTTTCCATCCAGGTGCATGC 267  
Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40  
Db 268 AGAATTTATGGGATCACCCCTTGTGAGCAAAAGCGAACCCAGCAGCTGAAATTTCCACAGAA 327  
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Db 328 GCTAAGGAGGCGCTGTAGGCTGCTGGGACTAAGTTTGGCCGCGCAAGGACCAAGTTGAAACA 387  
Qy 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValVal 80  
Db 388 GCCTTGAAGACTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGTGTC 447  
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Db 448 ATCTTAGGATTTAGCCCAACCCCAAGTGTGGGAAAAAATGGGGTGGTCTCTGATTGG 507  
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Db 628 ACACAAACACAGAAATTTATGTGAGTGACAGTACCTACCTCGGTGGCATCCCTTACTCT 687  
Qy 161 ThrIleProAlaProThrThrThrProAlaProAlaSerThrSerIleProArgArg 180  
Db 688 ACATACCTGCCCCCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 747  
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Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218  
Db 808 GAACCAATTTGTTGAAATAAAGCAGCATTCAAGAAATGAGCTGCTGGGTTTGA 861





APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/904,920A  
CURRENT FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
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PRIOR FILING DATE: 1999-11-29  
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PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
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PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 200  
LENGTH: 2372  
TYPE: DNA  
ORGANISM: Homo sapiens

Alignment Scores:  
Pred. No.: 9.55e-122 Length: 2372  
Score: 1125.00 Matches: 218  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

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21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40  
268 AGAATTATGGGATCACCTTGTGAGCAAAAGCGAACAGAGCTGAATTTACAGAA 327

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Db 448 ATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTGG 507

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Db 508 AAGGTTCCAGTGAGCCGACAGATTTCAGCCCTATTGTTTACAACCTCATCTGACTTGGACT 567

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Qy 161 ThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180  
Db 688 ACAATACCTGCCCTACTACTACTCTCTCTCCAGCTTCCACTTCTATTTCCACGGAGA 747

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Db 748 AAAAATTGATTGTGTCACAGAAAGTTTTTTATGGAAACTAGCACCATGCTCTACAGAACT 807

Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218  
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RESULT 9  
; Sequence 200, Application US/09909064  
; Patent No. 6818449  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kijavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/909,064  
; CURRENT FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048

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/ PRIOR FILING DATE: 1999-07-07
/ PRIOR APPLICATION NUMBER: US 60/145,698
/ PRIOR FILING DATE: 1999-07-26
/ PRIOR APPLICATION NUMBER: US 60/146,222
/ PRIOR FILING DATE: 1999-07-28
/ PRIOR APPLICATION NUMBER: PCT/US99/20594
/ PRIOR FILING DATE: 1999-09-08
/ PRIOR APPLICATION NUMBER: PCT/US99/20944
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: PCT/US99/21090
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/21547
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/ PRIOR APPLICATION NUMBER: PCT/US99/23089
/ PRIOR FILING DATE: 1999-10-05
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/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: PCT/US99/30911
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US99/30999
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ PRIOR FILING DATE: 2000-01-05
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 200
/ LENGTH: 2372
/ TYPE: DNA
/ ORGANISM: Homo sapiens

Alignment Scores:
Pred. No.:          9,55e-122      Length:      2372
Score:              1125.00      Matches:     218
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%   Mismatches:  0
Query Match:        100.00%      Indels:      0
DB:                 4           Gaps:        0

Qy 1 ThrArgLeuValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys 20
Db 208 ACGAGGCTCTCGTCCAAAGGCTCTTTGCGTGACAGAGAGCTTTCCATCCAGGTGTATGC 267
Qy 21 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 40
Db 268 AGAATTATGGGATATCACTCCCTTGAGCAAAAGCGAACCCAGAGCTGGAATTTTCACAGAA 327
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Db 328 GCTAAGGAGCCCTGTAGCTGCTGGGACTAAGTTTGGCCGCGAAGACCAAGTTGAAACA 387
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Db 388 GCCTTGAAGCTAGCTTGAAGCTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTC 447
Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrp 100
Db 448 ATCTTAGGATTAACCCCAACCCCAAGTGTGGGAAAATGGGGTGGGTGCTTCGATTGG 507
Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThr 120
Db 508 AAGGTTCCATGAGCCGACAGTTTGACGCCCTATTGTTACACTCACTGTACTTGGACT 567
Qy 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140
Db 568 AACTCGTGCATTCAGAAATTTATCACCACCAAGATCCCATATTTCAACACTCAAACTGCA 627

; Sequence 200, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
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; PRIOR APPLICATION NUMBER: PCT/US99/21090
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; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30

RESULT 10
; Sequence 200, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Fong, Sherman
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
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; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
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; Patent No. 6828146  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genentech, Inc.  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
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 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William, I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same

APRIL 1991; MOORE, WILLIAM, JR.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ACIDS Encoding the Same  
 FILE REFERENCE: 10466-14  
 CURRENT APPLICATION NUMBER: US/09/906,618  
 CURRENT FILING DATE: 2001-07-16  
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 PRIOR APPLICATION NUMBER: US 60/143,048  
 PRIOR FILING DATE: 1999-07-07  
 PRIOR APPLICATION NUMBER: US 60/145,698  
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 PRIOR APPLICATION NUMBER: PCT/US99/30095  
 PRIOR FILING DATE: 1999-12-16  
 PRIOR APPLICATION NUMBER: PCT/US99/30911  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: PCT/US99/30999  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: PCT/US00/00219  
 PRIOR FILING DATE: 2000-01-05  
 NUMBER OF SEQ ID NOS: 423  
 SEQ ID NO 200  
 LENGTH: 2372  
 TYPE: DNA  
 ORGANISM: Homo sapiens

RECORD 11  
; Sequence 200, Application US/099066618

Alignment Scores:



Qy 161 ThrileProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180  
Db 619 ACAATACCTGCCCTTACTACTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGA 678  
Qy 181 LysLysLeuLeuLeuValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200  
Db 679 AAAAAATTGATTGTGTACAGAGTGTATTTATGGAATAGACCATCTCTACAGAAACT 738  
Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218  
Db 739 GAACCAATTGTGTAATAAAGCAGCACTTCAAGATGAAGTGTCTGGGTGGGA 792

RESULT 13  
US-09-724-864-28  
; Sequence 28, Application US/09724864  
; Patent No. 6380362  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D  
; APPLICANT: Murison, James G  
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
; TITLE OF INVENTION: By the polynucleotides and methods for their use.  
; FILE REFERENCE: 11000.1050U1  
; CURRENT APPLICATION NUMBER: US/09/724,864  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 1896  
; TYPE: DNA  
; ORGANISM: Mouse  
US-09-724-864-28

Alignment Scores:  
Pred. No.: 2,62e-68 Length: 1896  
Score: 669.00 Matches: 133  
Percent Similarity: 73.85% Conservative: 28  
Best Local Similarity: 61.01% Mismatches: 53  
Query Match: 59.47% Indels: 4  
DB: 3 Gaps: 3

Qy 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20  
Db 110 ACTAGGCACCCAGTCCAAAGTGGCCCTTGTGGCAGAAACAAACCCACAGATGAATTTCCAGAA 166

Qy 21 ArgileMetGlyIleThrLeuValSerLysLysAlaAsnGlnLeuAsnPheThrGlu 40  
Db 167 AGAATCATGGCGGTGGCCCTTGTGGCAGAAACAAACCCACAGATGAATTTCCAGAA 226

Qy 41 AlalysGluAlaCysArgLeuLeuGlyLysSerLeuAlaGlyLysAspGlnValGluThr 60  
Db 227 GCCAACGAGGCTGTAGACTGCTGGACTGACTCTGGCCACGAGGACCAGGTAGATCA 286

Qy 61 AlaleuLysAlaSerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValVal 80  
Db 287 GCGCAGAAATCTGGCTTTGAGACTTGCAGCTATGATGGTGTGGAGAACAGTCTCTGTC 346

Qy 81 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyr 100  
Db 347 ATCCCTCGATTTTCTCAAAACCCAGGTTGGGAGAAATGCCAAGGTGTCCTGATTTGG 406

Qy 101 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThr 120  
Db 407 AATGCTCCCTCCAGCCAAAGTTCAAGCCATTATGCCACAACCTATCCGACACCTGGTT 466

Qy 121 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 140  
Db 467 AACTCCTGCATTCCAGAAATCGTTACCACATTTTATACCCCGTTGGACACTCAA----- 520

Qy 141 ThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSer 160

Db 521 ACACCCGACAGAGTTTCTGTCCAGCAGCCCTACTTGGTTCATCCCTGACTCC 580  
Qy 161 ThrileProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgArg 180  
Db 581 ACAACACCTGTTTCTGCCACACC--CGGCTCCACCTTTGACCTCCATCGCAGGAAG 637  
Qy 181 LysLysLeuLeuCysValThrGluValPheMetGluThrSerThrMetSerThrGluThr 200  
Db 638 AAAAAAAGATTTGTATCAGGAAGTTTATACAGAACCTATCACCATGGCTACAGAAACA 697  
Qy 201 GluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGly 218  
Db 698 GAAGCAITTTGTTCAGAGTGGAGCAGCAATTCAAGAACGAAGCAGCTGGGTGGGA 751

RESULT 14  
US-09-949-016-13636  
; Sequence 13636, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 13636  
; LENGTH: 14754  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-13636

Alignment Scores:  
Pred. No.: 1.14e-50 Length: 14754  
Score: 531.00 Matches: 102  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.03% Mismatches: 0  
Query Match: 47.20% Indels: 0  
DB: 4 Gaps: 0

Qy 116 SerAspThrTrpThrAsnSerCysIleProGluIleIleThrThrLysAspProIlePhe 135  
Db 9820 ACAGATACTTGGACTAAGTCTGCTGCAATTCAGAAATATATCACCACCAAGATCCCATATTC 9879

Qy 136 AsnThrGlnThrAlaThrGlnThrThrGluPheIleValSerAspSerThrTyrSerVal 155  
Db 9880 AACACTCAAACTGCACACAAACAAAGAAATTTATTGTCTAGTGACGTACTCTCGGTG 9939

Qy 156 AlaSerProTyrSerThrIleProAlaProThrThrThrProProAlaProAlaSerThr 175  
Db 9940 GCATCCCTTACTCTACAATACCTGCCCTACTACTACTCTCTCTCTCTCCAGCTTCCACT 9999

Qy 176 SerIleProArgArgLysLysLeuIleCysValThrGluValPheMetGluThrSerThr 195  
Db 10000 TCTATTCCAGGAGAAAAAATTTGATTTGTGTACAGAAAGTTTTTATGGAACATAGCACC 10059

Qy 196 MetSerThrGluThrGluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAla 215  
Db 10060 ATGTCTACAGAAACTGAACCACTTTGTTGAAAAATAAAGCAGCAATTCAGAAATGAAGCTGCT 10119

Qy 216 GlyPheGly 218  
Db 10120 GGGTTTGGGA 10128

Search completed: October 9, 2005, 01:25:42  
Job time : 189.526 secs

## RESULT 15

US-08-892-880-12  
; Sequence 12, Application US/08892880  
; Patent No. 5942417  
; GENERAL INFORMATION:  
; APPLICANT: NI, JIAN  
; APPLICANT: GENTZ, REINER L.  
; APPLICANT: DILLON, PATRICK J.  
; TITLE OF INVENTION: CD44-LIKE PROTEIN  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/892,880  
; FILING DATE: HEREWITH  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/021,762  
; FILING DATE: 15-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0490001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 492 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-892-880-12

Alignment Scores:  
Pred. No.: 3.61e-23 Length: 492  
Score: 277.00 Matches: 68  
Percent Similarity: 74.75% Conservative: 6  
Best Local Similarity: 68.69% Mismatches: 11  
Query Match: 24.62% Indels: 16  
DB: 2 Gaps: 2

Qy 1 ThrArgLeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCys 20  
Db 147 ACGAGGCTCTGTGGTCCAAAGGCTCTTTGGGTGACAGAGCTTTCCATCCAGGTGTCATGC 206  
Qy 21 ArgIleMetGlyIleThrLeuValSerIlyslsAlaAsnGlnGlnLeuAsnPheThrGlu 40  
Db 207 AGAATTATGGGGATCACCCCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTTCACAGAA 266  
Qy 41 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 60  
Db 267 GCTAAGGAGGCTCTAGTTGCTNGGACTAAGTTGGCCGCAAGGCCAGCTTG---AAC 323  
Qy 61 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGly----- 75  
Db 324 AGCTTGAAAGT-AGCTTTGAAAT-TGCAGTTTGGCTTGGTTGGGATGTTTCGNGNCATTT 381  
Qy 76 -----AspGlyPheValValIleSerArgIleSerPro 86  
Db 382 AGGTTAGCCCAACCCANTTTGGAAANTGGGTGGNNCNATTTTGNAGTCCCTTAGCCCN 438

Run on: October 8, 2005, 16:25:15 ; Search time 455.378 Seconds  
(without alignments)  
2833.919 Million cell updates/sec

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Perfect score: 1125  
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Scoring table: BLOSUM62  
Total number of hits satisfying chosen parameters: 8780412  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match Length	ID	Description
SUMMARIES				
RESULT 1				
ID	ADD04999	standard; cDNA; 1680 BP.		
DE	Human secreted/transmembrane protein cDNA, #40.			
PN	US2003104469-A1.			
PD	05-JUN-2003.			
PA	(GETH ) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 2				
ID	AAF93818	standard; cDNA; 1755 BP.		
DE	Human cDNA encoding a membrane or secretory protein clone PSEC0135.			
PN	EPI067182-A2.			
PD	10-JAN-2001.			
PA	(HELI-) HELIX RES INST.			
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 3				
ID	ADE71449	standard; cDNA; 2027 BP.		
DE	Human cDNA encoding PDEBC #2.			
PN	US2003124543-A1.			
PD	03-JUL-2003.			
PA	(STUA/) STUART S G.			
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 4				
ID	AAZ98172	standard; cDNA; 2029 BP.		
DE	Human signal peptide containing protein HSPP-64 cDNA SEQ ID NO:198.			
PN	WO20000610-A2.			
PD	06-JAN-2000.			
PA	(INCY-) INCYTE PHARM INC.			
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 5				
ID	ADE71445	standard; cDNA; 2029 BP.		
DE	Human cDNA encoding PDEBC Incyte 3044710CB1.			
PN	US2003124543-A1.			
PD	03-JUL-2003.			
PA	(STUA/) STUART S G.			
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 6				
ID	ABA09223	standard; cDNA; 2324 BP.		
DE	Human PRO263 homologue-encoding cDNA, SEQ ID NO:999.			
PN	WO200157188-A2.			
PD	09-AUG-2001.			
PA	(HYSE-) HYSEQ INC.			
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 7				
ID	ADR41319	standard; cDNA; 2369 BP.		
DE	Human CD-like molecule HEMFC27 cDNA, SEQ ID NO:118.			
PN	WO200226930-A2.			
PD	04-APR-2002.			
PA	(HUMA-) HUMAN GENOME SCI INC.			
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 8				
ID	AA522550	standard; DNA; 2372 BP.		
DE	Protein PRO263 cDNA clone DNA34431-1171.			
PN	WO9914328-A2.			
PD	25-MAR-1999.			
PA	(GETH ) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 9				
ID	ADC78520	standard; cDNA; 2372 BP.		
DE	Human PRO263 cDNA.			
PN	WO200015796-A2.			
PD	23-MAR-2000.			
PA	(GETH ) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 10				
ID	AAF72408	standard; cDNA; 2372 BP.		
DE	Human PRO263 cDNA.			
PN	WO200104311-A1.			
PD	18-JAN-2001.			
PA	(GETH ) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 11				
ID	AAF92060	standard; cDNA; 2372 BP.		
DE	Human PRO263 cDNA.			
PN	WO200116318-A2.			
PD	08-MAR-2001.			
PA	(GETH ) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 12				
ID	ABS74380	standard; cDNA; 2372 BP.		
DE	Human cDNA encoding secreted/transmembrane protein PRO263.			
PN	US2002119130-A1.			
PD	29-AUG-2002.			
PA	(GETH ) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 13				
ID	ABL88087	standard; cDNA; 2372 BP.		
DE	Human PRO263 cDNA sequence SEQ ID NO:31.			
PN	WO200200690-A2.			
PD	03-JAN-2002.			
PA	(GETH ) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 14				
ID	ABL55576	standard; cDNA; 2372 BP.		
DE	Human angio genesis related cDNA PRO263 SEQ ID NO: 31.			
PN	WO200208284-A2.			
PD	31-JAN-2002.			
PA	(GETH ) GENENTECH INC.			
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 15				
ID	BAKE71445	standard; cDNA; 2372 BP.		
DE	Human cDNA encoding PDEBC Incyte 3044710CB1.			
PN	US2003124543-A1.			
PD	03-JUL-2003.			
PA	(STUA/) STUART S G.			
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	

```
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A. J.
PA (GODO/) GODOWSKI P. J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAOW/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 15
ID ACA60164 standard; cDNA; 2372 BP.
DE Human cDNA for secreted/transmembrane protein PRO263.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 16
ID ACD07564 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 17
ID ACA91166 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 18
ID ACD81543 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 19
ID ACA60365 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 20
ID ABX71612 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 21
ID ACH06944 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO263 cDNA.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 22
ID ACH66246 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO263 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 23
ID ACA63988 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 24
ID ACA91252 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 25
ID ACD45151 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO263 cDNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 26
ID ABX96181 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #38.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 27
ID ACA05502 standard; cDNA; 2372 BP.
DE cDNA encoding human secreted protein PRO263.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 28
ID ACA93699 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 29
ID ACD20169 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO263 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 30
ID ACA67273 standard; cDNA; 2372 BP.
DE cDNA encoding human secreted polypeptide PRO263.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 31
ID ACH66246 standard; cDNA; 2372 BP.
```



DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 32  
ID ACD02300 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 33  
ID ACA89291 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 34  
ID ACA68928 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 35  
ID ACA54972 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 36  
ID ACA98450 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 37  
ID ACA63375 standard; cDNA; 2372 BP.  
DE cDNA encoding human PRO polypeptide #3.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 38  
ID ACD19807 standard; cDNA; 2372 BP.  
DE Human secreted / transmembrane polypeptide PRO263 cDNA.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 39  
ID ADB29405 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003092002-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 40  
ID ADB17062 standard; cDNA; 2372 BP.  
DE Human cDNA clone (SeqID 5) encoding the transmembrane PRO protein.

PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 41  
ID ACH03578 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane polypeptide PRO 263 cDNA.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 42  
ID ADA18261 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003039971-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 43  
ID ACD66954 standard; cDNA; 2372 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO263.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 44  
ID ADA19867 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 45  
ID ADB17250 standard; cDNA; 2372 BP.  
DE Human cDNA clone (SeqID 5) encoding the transmembrane PRO protein.  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 46  
ID ACD83115 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #36.  
PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 47  
ID ADA16236 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 48  
ID ADA20039 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 49  
ID ACD82092 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane polypeptide PRO 263 cDNA.  
PN US2003060601-A1.

PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 50  
ID ADA42381 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003054401-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 51  
ID ACD23293 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #36.  
PN US2003064367-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 52  
ID ADA00336 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane polypeptide PRO 263 cDNA.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 53  
ID ADA16660 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 54  
ID ADA13089 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003049622-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 55  
ID ADA41957 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003082540-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 56  
ID ADA17304 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003017498-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 57  
ID ADA42807 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003054351-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 58  
ID ACD23655 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #36.  
PN US2003064923-A1.  
PD 03-APR-2003.

PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 59  
ID ADB85578 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 60  
ID ADB77726 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 61  
ID ADB74862 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 62  
ID ADB68257 standard; cDNA; 2372 BP.  
DE Human PRO263 cDNA.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 63  
ID ADB68064 standard; cDNA; 2372 BP.  
DE Human PRO263 cDNA.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 64  
ID ADB90881 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 65  
ID ADC28508 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003059772-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 66  
ID ADC39708 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003059828-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 67  
ID ADC40222 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003059829-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 68
ID ADC19046 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 69
ID ADC34346 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 70
ID ADC29401 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 71
ID ADC28932 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 72
ID ADC40817 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 73
ID ADC19474 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 74
ID ADC06961 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 75
ID ADC17140 standard; cDNA; 2372 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 5).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 76
ID ADC33922 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 77
ID ADC12992 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 78
ID ADC14838 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 79
ID ADC52333 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 80
ID ADC12444 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 81
ID ADD10320 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 82
ID ADD11280 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 83
ID ADD04005 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 84
ID ADD03581 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 85
ID ADD37073 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 105  
ID ADH27546 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 106  
ID ADH37743 standard; cDNA; 2372 BP.  
DE Human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 107  
ID ADH37920 standard; cDNA; 2372 BP.  
DE Human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 108  
ID ADH57340 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 109  
ID ADH59316 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003039572-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 110  
ID ADH53482 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 111  
ID ADH53652 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 112  
ID ADH51988 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 113  
ID ADH49843 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181707-A1.

PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 114  
ID ADI25353 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 115  
ID ADH90146 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 116  
ID ADI25523 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 117  
ID ADH97697 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 118  
ID ADI38095 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 119  
ID ADI03545 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 120  
ID ADI1902 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 121  
ID ADH89976 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 122  
ID ADH98377 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181707-A1.

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PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 123
ID ADI11052 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 124
ID ADI11562 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 125
ID ADH98207 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 126
ID ADH98547 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 127
ID ADH98037 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 128
ID ACA59060 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #36.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 129
ID ACA58457 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 130
ID ADI05025 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 131
ID ADI03375 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 132
ID ADI04770 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 133
ID ADH78224 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 134
ID ADI19568 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 135
ID ADH90316 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 136
ID ADI03035 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 137
ID ADH77884 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 138
ID ADH97867 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 139
ID ADI01252 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 140
ID ADI01947 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 141  
ID AD103205 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 142  
ID AD111392 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 143  
ID AD102294 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 144  
ID AD111732 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 145  
ID AD105369 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 146  
ID ADH79441 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 147  
ID AD119398 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 148  
ID AD105199 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 149  
ID ADH79611 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
RESULT 150  
ID AD101437 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 151  
ID AD101607 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 152  
ID AD101777 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 153  
ID ADH79781 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 154  
ID AD104599 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 155  
ID AD102735 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 156  
ID ADH78054 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 157  
ID AD125693 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 158  
ID AD125863 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0

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RESULT 159
ID ADK65375 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003073821-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 160
ID ADH98717 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003191284-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 161
ID ADH79958 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003191287-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 162
ID ADJ26363 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054349-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 163
ID ADL93689 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003040013-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 164
ID ADC52143 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003130483-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 165
ID ADE79278 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003135025-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 166
ID ADE79702 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003130489-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 167
ID ADE73378 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003129592-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 168
ID ADH06575 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180852-A1.
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ID ADE41281 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003100497-A1.
PD 23-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 169
ID ADE73913 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 170
ID ADE99467 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 171
ID ADE98586 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 172
ID ADE99013 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 173
ID ADG40483 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 174
ID ADF73877 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003190312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 175
ID ADF73453 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 176
ID ADH06575 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180852-A1.
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PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 177  
ID ADH06405 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 178  
ID ADG68826 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 179  
ID ADH27716 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 180  
ID ADH25057 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 181  
ID ADH3689 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 182  
ID ADG92296 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003027145-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 183  
ID ADH02332 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 184  
ID ADH07939 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 185  
ID ADG69336 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 186  
ID ADH39157 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 187  
ID ADG92723 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003027146-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 188  
ID ADG83897 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 189  
ID ADG85441 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003168848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 190  
ID ADH06235 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 191  
ID ADH30231 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 192  
ID ADH24377 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 193  
ID ADG69506 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 194  
ID ADH07769 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 195		
ID ADG85781 standard; cDNA; 2372 BP.		
DE Novel human secreted and transmembrane protein PRO263 cDNA.		
PN US2003180861-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 196		
ID ADH39327 standard; cDNA; 2372 BP.		
DE Novel human secreted and transmembrane protein PRO263 cDNA.		
PN US2003180916-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 197		
ID ADH33519 standard; cDNA; 2372 BP.		
DE Human PRO polynucleotide #3.		
PN US2003181637-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 198		
ID ADH33859 standard; cDNA; 2372 BP.		
DE Human PRO polynucleotide #3.		
PN US2003181644-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 199		
ID ADH01069 standard; cDNA; 2372 BP.		
DE Human PRO polynucleotide #3.		
PN US2003180838-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 200		
ID ADG69676 standard; cDNA; 2372 BP.		
DE Novel human secreted and transmembrane protein PRO263 cDNA.		
PN US2003180843-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 201		
ID ADH02162 standard; cDNA; 2372 BP.		
DE Human PRO polynucleotide #3.		
PN US2003180841-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 202		
ID ADG69166 standard; cDNA; 2372 BP.		
DE Novel human secreted and transmembrane protein PRO263 cDNA.		
PN US2003180847-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 203		
ID ADG65951 standard; cDNA; 2372 BP.		
DE Novel human secreted and transmembrane protein PRO263 cDNA.		
PN US2003180862-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 204		
ID ADH24887 standard; cDNA; 2372 BP.		
DE Novel human secreted and transmembrane protein PRO263 cDNA.		
PN US2003180909-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 205		
ID ADH39504 standard; cDNA; 2372 BP.		
DE Novel human secreted and transmembrane protein PRO263 cDNA.		
PN US2003180915-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 206		
ID ADH02502 standard; cDNA; 2372 BP.		
DE Human PRO polynucleotide #3.		
PN US2003180840-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 207		
ID ADG68996 standard; cDNA; 2372 BP.		
DE Novel human secreted and transmembrane protein PRO263 cDNA.		
PN US2003180849-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 208		
ID ADH07599 standard; cDNA; 2372 BP.		
DE Novel human secreted and transmembrane protein PRO263 cDNA.		
PN US2003180850-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 209		
ID ADG86121 standard; cDNA; 2372 BP.		
DE Novel human secreted and transmembrane protein PRO263 cDNA.		
PN US2003180863-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 210		
ID ADH24717 standard; cDNA; 2372 BP.		
DE Novel human secreted and transmembrane protein PRO263 cDNA.		
PN US2003180908-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 211		
ID ADH25765 standard; cDNA; 2372 BP.		
DE Novel human secreted and transmembrane protein PRO263 cDNA.		
PN US2003180911-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
RESULT 212		
ID ADH38331 standard; cDNA; 2372 BP.		
DE Novel human secreted and transmembrane protein PRO263 cDNA.		
PN US2003180922-A1.		
PD 25-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		
Best Local Similarity: 100.00%	Mismatches: 0	Indels: 0
Query Match: 100.00%		

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RESULT 213
ID ADH20512 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004005553-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 214
ID ADH5170 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181642-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 215
ID ADH4364 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #16.
PN US2003224984-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 216
ID ADH07367 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004006211-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 217
ID ADH52158 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180921-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 218
ID ADH5912 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003215904-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 219
ID ADH4924 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180957-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 220
ID ADH06940 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004005655-A1.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 221
ID ADH90486 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181700-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 222
ID ADI11222 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181683-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 223
ID ADI18682 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003152999-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 224
ID ADH98887 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003190698-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 225
ID ADI02117 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003190699-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 226
ID ADH90656 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181701-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 227
ID ADI37665 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003096340-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 228
ID ADH97461 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003190610-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 229
ID ADI65829 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003148371-A1.
PA (GETH ) GENENTECH INC.
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 230
ID ADH60572 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 231
ID ADJ9629 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 232
ID ADL08822 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 233
ID ADJ98531 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 234
ID ADJ98701 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 235
ID ADH78860 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 236
ID ADJ9094 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 237
ID ADJ9264 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 238
ID ADR11087 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 239
ID ADH79030 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 240
ID ADK00890 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 241
ID ADK14411 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 242
ID ADM25163 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 243
ID ADM29913 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 244
ID ADK82809 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #16.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 245
ID ADM80860 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 246
ID ADO06235 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #38.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 247
ID ADR11087 standard; cDNA; 2372 BP.
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DE Human secreted/transmembrane protein cDNA, #40.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 248
ID ADRI17996 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATH J.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 249
ID ADT03672 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 250
ID ADS74635 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane cDNA #40.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATH J.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 251
ID ADO25003 standard; DNA; 2667 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7823.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 252
ID AAC59803 standard; DNA; 2967 BP.
DE Human secreted protein encoding DNA clone vb28 1.
PN WO200055375-A1.
PD 21-SEP-2000.
PA (ALPH-) ALPHAGENE INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 253
ID AAV22687 standard; DNA; 2313 BP.
DE DNA encoding a CD44-like protein.
PN WO9806839-A1.
PD 19-FEB-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 99.54% Mismatches: 1
Query Match: 99.47% Indels: 0
RESULT 254
ID ABL90698 standard; cDNA; 2369 BP.
DE Human polynucleotide SEQ ID NO 1260.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 99.54% Mismatches: 1
Query Match: 99.47% Indels: 0
RESULT 255
ID ADF65684 standard; DNA; 2313 BP.
DE Human extracellular link domain containing 1 (XLKD1) DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Best Local Similarity: 98.62% Mismatches: 2
Query Match: 98.31% Indels: 0
RESULT 256
ID ADM67137 standard; DNA; 2313 BP.
DE Human homologue of murine adipocyte specific DNA SeqID 273.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGENE INC.
Best Local Similarity: 98.62% Mismatches: 2
Query Match: 98.31% Indels: 0
RESULT 257
ID ADN05865 standard; cDNA; 2313 BP.
DE Antipsoriatic cDNA sequence #1164.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 98.62% Mismatches: 2
Query Match: 98.31% Indels: 0
RESULT 258
ID ADQ21088 standard; DNA; 2313 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3908.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 98.62% Mismatches: 2
Query Match: 98.31% Indels: 0
RESULT 259
ID ACA10111 standard; cDNA; 1127 BP.
DE Human NOVX polynucleotide #1.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
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Best Local Similarity: 88.53% Mismatches: 0
Query Match: 87.07% Indels: 25
RESULT 260
ID A008254 standard; cDNA; 1127 BP.
DE Human NOVX polynucleotide #1.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Best Local Similarity: 88.53% Mismatches: 0
Query Match: 87.07% Indels: 25
RESULT 261
ID ABT09892 standard; cDNA; 596 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 26.
PN WO200259271-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 97.88% Mismatches: 4
Query Match: 80.09% Indels: 3
RESULT 262
ID AAF94017 standard; DNA; 716 BP.
DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 451.
PN EPI067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Best Local Similarity: 94.23% Mismatches: 6
Query Match: 64.09% Indels: 3
RESULT 263
ID ADM67136 standard; DNA; 1516 BP.
DE Murine adipocyte specific DNA SeqID 272.
PN WO200401618-A2.
PD 05-FEB-2004.
PA (HMGE-) HMGNE INC.
Best Local Similarity: 61.01% Mismatches: 53
Query Match: 59.47% Indels: 4
RESULT 264
ID AAD10132 standard; cDNA; 1896 BP.
DE Mouse lymphatic endothelium-specific hyaluronan receptor LYVE-1 cDNA.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Best Local Similarity: 61.01% Mismatches: 53
Query Match: 59.47% Indels: 4
RESULT 265
ID ABLJ5066 standard; cDNA; 1896 BP.
DE Murine cDNA isolated from skin cells SEQ ID NO: 595.

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PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Best Local Similarity: 61.01% Mismatches: 53
Query Match: 59.47% Indels: 4
RESULT 266
ID ACH20895 standard; cDNA; 411 BP.
DE Human adult liver cDNA #507.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.33% Indels: 0
RESULT 267
ID AAX41156 standard; cDNA; 451 BP.
DE Human secreted protein 5' EST SEQ ID NO:100.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST/) GENSET.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.33% Indels: 0
RESULT 268
ID AAI33382 standard; DNA; 457 BP.
DE Probe #2068 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 84.51% Mismatches: 3
Query Match: 25.02% Indels: 7
RESULT 269
ID ABS01959 standard; DNA; 457 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 1950.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 84.51% Mismatches: 3
Query Match: 25.02% Indels: 7
RESULT 270
ID ADE71446 standard; cDNA; 559 BP.
DE Rat cDNA encoding PDEBC variant Incyte 702127782H1.
PN US2003124543-A1.
PD 03-JUL-2003.
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
Best Local Similarity: 54.17% Mismatches: 29
Query Match: 19.69% Indels: 7
RESULT 271
ID ABN86507 standard; cDNA; 2747 BP.
DE Rat glycoprotein CD44 polypeptide encoding cDNA.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGMH) BRIGHAM & WOMENS HOSPITAL INC.
Best Local Similarity: 32.08% Mismatches: 76
Query Match: 18.98% Indels: 7
RESULT 272
ID ABK63681 standard; cDNA; 2747 BP.
DE Rat sequence differentially expressed in response to a hepatotoxin #1588.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 32.08% Mismatches: 76
Query Match: 18.98% Indels: 7
RESULT 273
ID AAQ14263 standard; cDNA; 3207 BP.
DE p-meta-1 metastasis-specific variant of CD44 glycoprotein.
PN DE4014510-A.
PD 14-NOV-1991.
PA (GESL) KERNFORSCHUNGSZENT KARLSRUHE.
PA (UYKA-) UNIV KARLSRUHE.

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PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.  
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.  
Best Local Similarity: 32.08% Mismatches: 76  
Query Match: 18.98% Indels: 7  
RESULT 274  
ID ABN86522 standard; cDNA; 1177 BP.  
DE Nucleotide sequence of mouse CD44 cDNA.  
PN WO200238794-A2.  
PD 16-MAY-2002.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
Best Local Similarity: 32.70% Mismatches: 75  
Query Match: 18.62% Indels: 7  
RESULT 275  
ID ADQ38556 standard; DNA; 5452 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 219.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 29.29% Mismatches: 96  
Query Match: 18.62% Indels: 17  
RESULT 276  
ID ABN86523 standard; cDNA; 1089 BP.  
DE Nucleotide sequence of hamster CD44 cDNA.  
PN WO200238794-A2.  
PD 16-MAY-2002.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
Best Local Similarity: 32.76% Mismatches: 82  
Query Match: 18.40% Indels: 12  
RESULT 277  
ID AQO62316 standard; DNA; 1537 BP.  
DE B7 adhesion receptor cDNA clone.  
PN WO9011365-A.  
PD 04-OCT-1990.  
PA (HUTC-) HUTCHINSON F CANCER.  
Best Local Similarity: 27.34% Mismatches: 92  
Query Match: 18.09% Indels: 67  
RESULT 278  
ID AAX41003 standard; cDNA; 363 BP.  
DE Human secreted protein 5' EST SEQ ID NO: 215.  
PN WO9906554-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Best Local Similarity: 88.68% Mismatches: 5  
Query Match: 18.04% Indels: 1  
RESULT 279  
ID ADP65670 standard; DNA; 3091 BP.  
DE Human mRNA for transmembrane glycoprotein (CD44 gene) DNA.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Best Local Similarity: 25.96% Mismatches: 84  
Query Match: 18.04% Indels: 60  
RESULT 280  
ID ADP65097 standard; DNA; 3091 BP.  
DE Human CD44 antigen (homing function and Indian blood group DNA sequence.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Best Local Similarity: 25.96% Mismatches: 84  
Query Match: 18.04% Indels: 60  
RESULT 281  
ID ADQ38563 standard; DNA; 3091 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 226.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 25.96% Mismatches: 84  
Query Match: 18.04% Indels: 60  
RESULT 282  
ID ADR67138 standard; DNA; 3091 BP.  
DE Human bladder cancer associated nucleotide sequence.  
PN WO2004076613-A2.  
PD 10-SEP-2004.

PA (HERR/) HERR A.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (STAU/) STAUB E.  
PA (PILA/) PILARSKY C.  
PA (SPEC/) SPECHT T.  
Best Local Similarity: 25.96% Mismatches: 84  
Query Match: 18.04% Indels: 60  
RESULT 283  
ID ADQ38562 standard; DNA; 5468 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 225.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 25.96% Mismatches: 84  
Query Match: 18.04% Indels: 60  
RESULT 284  
ID ADQ38555 standard; DNA; 5674 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 218.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 25.96% Mismatches: 84  
Query Match: 18.04% Indels: 60  
RESULT 285  
ID ADQ38558 standard; DNA; 5739 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 221.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 25.96% Mismatches: 84  
Query Match: 18.04% Indels: 60  
RESULT 286  
ID ACN39193 standard; cDNA; 3083 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA325446, SEQ ID NO:3187.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 25.96% Mismatches: 84  
Query Match: 17.96% Indels: 60  
RESULT 287  
ID AAS03192 standard; cDNA; 2307 BP.  
DE Human epithelial antigen CD44 cDNA sequence.  
PN US6218525-B1.  
PD 17-APR-2001.  
PA (GEHO) GEN HOSPITAL CORP.  
Best Local Similarity: 23.57% Mismatches: 100  
Query Match: 17.73% Indels: 75  
RESULT 288  
ID AAQ21186 standard; DNA; 2308 BP.  
DE Clone CD44 coding for epithelial CD44 Antigen.  
PN WO9201049-A.  
PD 23-JAN-1992.  
PA (GEHO) GEN HOSPITAL CORP.  
Best Local Similarity: 23.57% Mismatches: 100  
Query Match: 17.73% Indels: 75  
RESULT 289  
ID AAT14725 standard; cDNA; 2308 BP.  
DE Human epithelial CD44 cDNA.  
PN US5506126-A.  
PD 09-APR-1996.  
PA (GEHO) GEN HOSPITAL CORP.  
Best Local Similarity: 23.57% Mismatches: 100  
Query Match: 17.73% Indels: 75  
RESULT 290  
ID AAV63462 standard; cDNA; 2308 BP.  
DE Human CD44 antigen cDNA.  
PN US5830731-A.  
PD 03-NOV-1998.  
PA (GEHO) GEN HOSPITAL CORP.  
Best Local Similarity: 23.57% Mismatches: 100  
Query Match: 17.73% Indels: 75  
RESULT 291

ID AAV81219 standard; cDNA; 2308 BP.  
 DE Human CD44 antigen cDNA.  
 PN US5849898-A.  
 PD 15-DEC-1998.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Best Local Similarity: 23.57% Mismatches: 100  
 Query Match: 17.73% Indels: 75  
 RESULT 292  
 ID AAA50598 standard; cDNA; 2308 BP.  
 DE Human epithelial CD44 cDNA.  
 PN US611093-A.  
 PD 29-AUG-2000.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Best Local Similarity: 23.57% Mismatches: 100  
 Query Match: 17.73% Indels: 75  
 RESULT 293  
 ID ADO49374 standard; cDNA; 2308 BP.  
 DE Human CD44 cDNA #2.  
 PN US2004072283-A1.  
 PD 15-APR-2004.  
 PA (SEED/) SEED B.  
 PA (ALLE/) ALLEN J.  
 PA (ARUF/) ARUFFO A.  
 PA (CAME/) CAMERINI D.  
 PA (LAUF/) LAUFFER L.  
 PA (COUE/) OQUENDO C.  
 PA (SIMM/) SIMMONS D.  
 PA (STAM/) STAMENKOVIC I.  
 PA (STEN/) STENGELIN S.  
 PA (AMIO/) AMIOT M.  
 Best Local Similarity: 23.57% Mismatches: 100  
 Query Match: 17.73% Indels: 75  
 RESULT 294  
 ID AEN86520 standard; cDNA; 1737 BP.  
 DE Nucleotide sequence of human CD44R cDNA.  
 PN WO200238794-A2.  
 PD 16-MAY-2002.  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
 Best Local Similarity: 23.57% Mismatches: 100  
 Query Match: 17.64% Indels: 75  
 RESULT 295  
 ID ADK61304 standard; DNA; 1737 BP.  
 DE Ovarian cancer-related DNA #459 with altered ovarian cancer expression.  
 PN WO2003068054-A2.  
 PD 21-AUG-2003.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
 Best Local Similarity: 23.57% Mismatches: 100  
 Query Match: 17.64% Indels: 75  
 RESULT 296  
 ID ABX77520 standard; cDNA; 4674 BP.  
 DE Differentially expressed breast cancer associated cDNA #15.  
 PN US2002156263-A1.  
 PD 24-OCT-2002.  
 PA (CHEN/) CHEN H.  
 Best Local Similarity: 23.57% Mismatches: 100  
 Query Match: 17.64% Indels: 75  
 RESULT 297  
 ID ADJ56375 standard; cDNA; 4674 BP.  
 DE Human cDNA differentially expressed in MYCN activated cells SeqID 181.  
 PN US2003119009-A1.  
 PD 26-JUN-2003.  
 PA (STUA/) STUART S G.  
 PA (NUCH/) NUCHTERN J G.  
 PA (PLOW/) PLOW S E.  
 PA (SHOH/) SHOHET J M.  
 Best Local Similarity: 23.57% Mismatches: 100  
 Query Match: 17.64% Indels: 75  
 RESULT 298  
 ID ADM86790 standard; cDNA; 4674 BP.  
 DE Human cDNA #51 differentially expressed in lung cancer.  
 PN US2003175704-A1.  
 PD 18-SEP-2003.

PA (LASE/) LASEK A K W.  
 PA (SHYG/) SHYJAN A W.  
 PA (TURN/) TURNER C M.  
 Best Local Similarity: 23.57% Mismatches: 100  
 Query Match: 17.64% Indels: 75  
 RESULT 299  
 ID ADI61729 standard; cDNA; 4675 BP.  
 DE Human cDNA upregulated in Alzheimer's disease, INCYTE 234630.26.  
 PN US6682888-B1.  
 PD 27-JAN-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 23.57% Mismatches: 100  
 Query Match: 17.64% Indels: 75  
 RESULT 300  
 ID ADQ38553 standard; DNA; 5053 BP.  
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 216.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Best Local Similarity: 25.42% Mismatches: 93  
 Query Match: 17.56% Indels: 49  
 RESULT 301  
 ID AAQ21185 standard; DNA; 1354 BP.  
 DE Clone CD44.5 coding for haematopoietic CD44 Antigen.  
 PN WO9201049-A.  
 PD 23-JAN-1992.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Best Local Similarity: 30.86% Mismatches: 84  
 Query Match: 17.51% Indels: 14  
 RESULT 302  
 ID AAT14724 standard; cDNA; 1354 BP.  
 DE Human haematopoietic CD44 cDNA clone CD44.5.  
 PN US5506126-A.  
 PD 09-APR-1996.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Best Local Similarity: 30.86% Mismatches: 84  
 Query Match: 17.51% Indels: 14  
 RESULT 303  
 ID AAV63461 standard; cDNA; 1354 BP.  
 DE Human CD44 antigen cDNA.  
 PN US5830731-A.  
 PD 03-NOV-1998.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Best Local Similarity: 30.86% Mismatches: 84  
 Query Match: 17.51% Indels: 14  
 RESULT 304  
 ID AAV81218 standard; cDNA; 1354 BP.  
 DE Human CD44 antigen cDNA.  
 PN US5849898-A.  
 PD 15-DEC-1998.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Best Local Similarity: 30.86% Mismatches: 84  
 Query Match: 17.51% Indels: 14  
 RESULT 305  
 ID AAA50597 standard; cDNA; 1354 BP.  
 DE Human haematopoietic CD44.5 cDNA.  
 PN US611093-A.  
 PD 29-AUG-2000.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Best Local Similarity: 30.86% Mismatches: 84  
 Query Match: 17.51% Indels: 14  
 RESULT 306  
 ID AAS03191 standard; cDNA; 1354 BP.  
 DE Human haematopoietic antigen CD44 cDNA sequence.  
 PN US6218525-B1.  
 PD 17-APR-2001.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Best Local Similarity: 30.86% Mismatches: 84  
 Query Match: 17.51% Indels: 14  
 RESULT 307  
 ID ADO49372 standard; cDNA; 1354 BP.  
 DE Human CD44 cDNA #1.  
 PN US2004072283-A1.



PD 15-APR-2004.  
PA (SEED//) SEED B.  
PA (ALLE//) ALLEN J.  
PA (ARUF//) ARUFFO A.  
PA (CAME//) CAMERINI D.  
PA (LAUF//) LAUFFER L.  
PA (OQUE//) OQUENDO C.  
PA (SIMW//) SIMMONS D.  
PA (STAM//) STAMENKOVIC I.  
PA (STEN//) STENGELIN S.  
PA (AMIO//) AMIOT M.  
Best Local Similarity: 30.86% Mismatches: 84  
Query Match: 17.51% Indels: 14  
RESULT 308  
ID AAA91129 standard; DNA; 1468 BP.  
DE CD44HextraFasTm/cyto coding sequence.  
PN WO200100854-A2.  
PD 04-JAN-2001.  
PA (ANGI-) ANGIOGENE PHARM LTD.  
Best Local Similarity: 30.86% Mismatches: 84  
Query Match: 17.51% Indels: 14  
RESULT 309  
ID AAA91130 standard; DNA; 1483 BP.  
DE CD44Hextra/cmfascyto coding sequence.  
PN WO200100854-A2.  
PD 04-JAN-2001.  
PA (ANGI-) ANGIOGENE PHARM LTD.  
Best Local Similarity: 30.86% Mismatches: 84  
Query Match: 17.51% Indels: 14  
RESULT 310  
ID AA52811 standard; cDNA; 1794 BP.  
DE Human CD44 cDNA.  
PN WO200039335-A1.  
PD 22-JUN-2000.  
PA (ISIS-) ISIS PHARM INC.  
Best Local Similarity: 30.86% Mismatches: 84  
Query Match: 17.51% Indels: 14  
RESULT 311  
ID ABV94385 standard; cDNA; 1794 BP.  
DE Breast carcinoma related nucleotide sequence SEQ ID NO:376.  
PN WO200246467-A2.  
PD 13-JUN-2002.  
PA (IPSO-) IPSOGEN.  
Best Local Similarity: 30.86% Mismatches: 84  
Query Match: 17.51% Indels: 14  
RESULT 312  
ID ABK84043 standard; cDNA; 1794 BP.  
DE Human cDNA differentially expressed in granulocytic cells #614.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 30.86% Mismatches: 84  
Query Match: 17.51% Indels: 14  
RESULT 313  
ID ADH18929 standard; cDNA; 1874 BP.  
DE Human cell adhesion and extracellular matrix CADECM-25 cDNA - SEQ 56.  
PN WO2003094843-A2.  
PD 20-NOV-2003.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 27.43% Mismatches: 92  
Query Match: 17.51% Indels: 43  
RESULT 314  
ID ADQ38557 standard; DNA; 4335 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 220.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 30.86% Mismatches: 84  
Query Match: 17.51% Indels: 14  
RESULT 315  
ID ADQ38561 standard; DNA; 4633 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 224.  
PN WO2004058052-A2.

PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 30.86% Mismatches: 84  
Query Match: 17.51% Indels: 14  
RESULT 316  
ID ADQ38554 standard; DNA; 4723 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 217.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 30.86% Mismatches: 84  
Query Match: 17.51% Indels: 14  
RESULT 317  
ID ADQ38560 standard; DNA; 4874 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 223.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 30.86% Mismatches: 84  
Query Match: 17.51% Indels: 14  
RESULT 318  
ID ABZ70446 standard; cDNA; 1824 BP.  
DE Human CD44 variant CD44vRA associated with rheumatoid arthritis.  
PN WO2003014160-A2.  
PD 20-FEB-2003.  
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Best Local Similarity: 25.42% Mismatches: 93  
Query Match: 17.47% Indels: 49  
RESULT 319  
ID AD90595 standard; cDNA; 2097 BP.  
DE Human CD44v glycoprotein encoding cDNA SEQ ID NO:5.  
PN WO2003072606-A2.  
PD 04-SEP-2003.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Best Local Similarity: 25.42% Mismatches: 93  
Query Match: 17.47% Indels: 49  
RESULT 320  
ID AAA91011 standard; DNA; 2100 BP.  
DE Human CD44 splice variant (RA-CD44) coding sequence.  
PN WO200075312-A1.  
PD 14-DEC-2000.  
PA (YISS ) YISSUM RES & DEV CO.  
Best Local Similarity: 25.42% Mismatches: 93  
Query Match: 17.47% Indels: 49  
RESULT 321  
ID AD90593 standard; cDNA; 2100 BP.  
DE Human CD44v glycoprotein encoding cDNA SEQ ID NO:3.  
PN WO2003072606-A2.  
PD 04-SEP-2003.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Best Local Similarity: 25.42% Mismatches: 93  
Query Match: 17.47% Indels: 49  
RESULT 322  
ID ACN42246 standard; cDNA; 2342 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1121.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 25.42% Mismatches: 93  
Query Match: 17.47% Indels: 49  
RESULT 323  
ID ABX76192 standard; DNA; 2387 BP.  
DE Lung cancer-associated polynucleotide #63.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (BOSB-) BOS BIOTECHNOLOGY INC.  
Best Local Similarity: 25.42% Mismatches: 93  
Query Match: 17.47% Indels: 49  
RESULT 324  
ID ADU61117 standard; DNA; 2387 BP.  
DE Human protein tyrosine kinase biomarker CD44 antigen DNA.

PN WO2004020583-A2.  
 PD 11-MAR-2004.  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 Best Local Similarity: 25.42% Mismatches: 93  
 Indels: 49  
 Query Match:  
 RESULT 325  
 ID ABX63495 standard; cDNA; 2905 BP.  
 DE Human cDNA #495 differentially expressed in activated vascular tissue.  
 PN US2002137081-A1.  
 PD 26-SEP-2002.  
 PA (BAND//) BANDMAN O.  
 Best Local Similarity: 25.42% Mismatches: 93  
 Indels: 49  
 Query Match:  
 RESULT 326  
 ID ADA10891 standard; cDNA; 3474 BP.  
 DE Human cDNA differentially expressed in colon cancer #7.  
 PN US2002160382-A1.  
 PD 31-OCT-2002.  
 PA (LASE//) LASEK A W.  
 Best Local Similarity: 25.42% Mismatches: 93  
 Indels: 49  
 Query Match:  
 RESULT 327  
 ID ADD90591 standard; cDNA; 1083 BP.  
 DE Human CD44std glycoprotein encoding cDNA SEQ ID NO:1.  
 PN WO2003072606-A2.  
 PD 04-SEP-2003.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 Best Local Similarity: 30.86% Mismatches: 84  
 Indels: 14  
 Query Match:  
 RESULT 328  
 ID ADI60527 standard; DNA; 1190 BP.  
 DE Secreted polypeptide encoding gene #66.  
 PN WO2003025142-A2.  
 PD 27-MAR-2003.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 30.86% Mismatches: 84  
 Indels: 14  
 Query Match:  
 RESULT 329  
 ID AAD48131 standard; DNA; 1807 BP.  
 DE Human CD44 antigen encoding DNA.  
 PN WO200276510-A1.  
 PD 03-OCT-2002.  
 PA (AGYT-) AGY THERAPEUTICS INC.  
 Best Local Similarity: 30.86% Mismatches: 84  
 Indels: 14  
 Query Match:  
 RESULT 330  
 ID ADJ56374 standard; cDNA; 1981 BP.  
 DE Human cDNA differentially expressed in MYCN activated cells SeqID 180.  
 PN US2003119009-A1.  
 PD 26-JUN-2003.  
 PA (STUA//) STUART S G.  
 PA (NUCH//) NUCHTERN J G.  
 PA (PLON//) PLON S E.  
 PA (SHOH//) SHOHEIT J M.  
 Best Local Similarity: 30.86% Mismatches: 84  
 Indels: 14  
 Query Match:  
 RESULT 331  
 ID ABE23525 standard; cDNA; 1992 BP.  
 DE Human gene expression profile polynucleotide SEQ ID NO 436.  
 PN WO200274979-A2.  
 PD 26-SEP-2002.  
 PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
 Best Local Similarity: 30.86% Mismatches: 84  
 Indels: 14  
 Query Match:  
 RESULT 332  
 ID ADE25668 standard; cDNA; 4365 BP.  
 DE Human cDNA differentially expressed in foam cells #72.  
 PN US2003194721-A1.  
 PD 16-OCT-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 30.86% Mismatches: 84

Query Match:  
 RESULT 333  
 ID ADP10572 standard; DNA; 4633 BP.  
 DE Reference mRNA sequences for marker probe #249.  
 PN WO2004042346-A2.  
 PD 21-MAY-2004.  
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
 Best Local Similarity: 30.86% Mismatches: 84  
 Indels: 14  
 Query Match:  
 RESULT 334  
 ID ADL61887 standard; DNA; 5165 BP.  
 DE Human ovarian cancer DNA marker #20099.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Best Local Similarity: 30.86% Mismatches: 84  
 Indels: 14  
 Query Match:  
 RESULT 335  
 ID AAX51631 standard; cDNA; 373 BP.  
 DE Human secreted protein 5' EST SEQ ID NO:210.  
 PN WO9906549-A2.  
 PD 11-FEB-1999.  
 PA (GEST ) GENSET.  
 Best Local Similarity: 97.62% Mismatches: 1  
 Indels: 0  
 Query Match:  
 RESULT 336  
 ID ABN86521 standard; cDNA; 1297 BP.  
 DE Nucleotide sequence of human CD44 cDNA.  
 PN WO200238794-A2.  
 PD 16-MAY-2002.  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
 Best Local Similarity: 30.86% Mismatches: 84  
 Indels: 14  
 Query Match:  
 RESULT 337  
 ID ADI31550 standard; cDNA; 1297 BP.  
 DE Human CDNA #876.  
 PN US6607879-B1.  
 PD 19-AUG-2003.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 30.86% Mismatches: 84  
 Indels: 14  
 Query Match:  
 RESULT 338  
 ID ACC43051 standard; DNA; 339 BP.  
 DE Nucleotide sequence of a chicken CD44-hyaluronic acid binding domain.  
 PN WO2003018044-A1.  
 PD 06-MAR-2003.  
 PA (STRO//) STROEBLAD S.  
 PA (KOGE//) KOGERMAN P.  
 PA (PAEL//) PAELL T.  
 Best Local Similarity: 36.28% Mismatches: 53  
 Indels: 1  
 Query Match:  
 RESULT 339  
 ID ACC43049 standard; DNA; 336 BP.  
 DE Nucleotide sequence of a human CD44-hyaluronic acid binding domain.  
 PN WO2003018044-A1.  
 PD 06-MAR-2003.  
 PA (STRO//) STROEBLAD S.  
 PA (KOGE//) KOGERMAN P.  
 PA (PAEL//) PAELL T.  
 Best Local Similarity: 36.04% Mismatches: 51  
 Indels: 2  
 Query Match:  
 RESULT 340  
 ID ACC43052 standard; DNA; 336 BP.  
 DE Nucleotide sequence of a CD44-hyaluronic acid binding domain.  
 PN WO2003018044-A1.  
 PD 06-MAR-2003.  
 PA (STRO//) STROEBLAD S.  
 PA (KOGE//) KOGERMAN P.  
 PA (PAEL//) PAELL T.  
 Best Local Similarity: 36.04% Mismatches: 51  
 Indels: 2  
 Query Match:  
 RESULT 341  
 ID ACC43053 standard; DNA; 336 BP.

DE Nucleotide sequence of a CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEBLAD S.  
PA (KOGE/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Best Local Similarity: 36.04% Mismatches: 51  
Query Match: 16.53% Indels: 2  
RESULT 342  
ID ACC43054 standard; DNA; 336 BP.  
DE Nucleotide sequence of a CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEBLAD S.  
PA (KOGE/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Best Local Similarity: 36.04% Mismatches: 51  
Query Match: 16.36% Indels: 2  
RESULT 343  
ID ACC43050 standard; DNA; 336 BP.  
DE Nucleotide sequence of a dog CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEBLAD S.  
PA (KOGE/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Best Local Similarity: 34.23% Mismatches: 51  
Query Match: 16.18% Indels: 2  
RESULT 344  
ID AAS81254 standard; CDNA; 2764 BP.  
DE DNA encoding novel human diagnostic protein #17058.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 25.89% Mismatches: 87  
Query Match: 15.60% Indels: 49  
RESULT 345  
ID AAS81258 standard; CDNA; 2273 BP.  
DE DNA encoding novel human diagnostic protein #17062.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 25.21% Mismatches: 93  
Query Match: 15.16% Indels: 51  
RESULT 346  
ID AAI46523 standard; DNA; 106 BP.  
DE Probe #15209 used to measure gene expression in human placenta sample.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 15.11% Indels: 0  
RESULT 347  
ID ABS14478 standard; DNA; 106 BP.  
DE Human genome-derived single exon probe ORF from lung SEQ ID NO 14469.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 15.11% Indels: 0  
RESULT 348  
ID ACH49200 standard; CDNA; 399 BP.  
DE Human leukocyte CDNA #794.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Best Local Similarity: 37.36% Mismatches: 41  
Query Match: 14.80% Indels: 1  
RESULT 349

ID ABZ34973 standard; CDNA; 549 BP.  
DE Human gene expression profile polynucleotide SEQ ID NO 85.  
PN WO200274979-A2.  
PD 26-SEP-2002.  
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
Best Local Similarity: 34.92% Mismatches: 61  
Query Match: 14.04% Indels: 8  
RESULT 350  
ID ABZ31738 standard; DNA; 549 BP.  
DE Human nucleic acid sequence.  
PN WO200285308-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Best Local Similarity: 34.92% Mismatches: 61  
Query Match: 14.04% Indels: 8  
RESULT 351  
ID ADK61306 standard; DNA; 549 BP.  
DE Ovarian cancer-related DNA #461 with altered ovarian cancer expression.  
PN WO2003068054-A2.  
PD 21-AUG-2003.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
PA (SLOK) SLOAN KETTERING INST CANCER RES.  
Best Local Similarity: 34.92% Mismatches: 61  
Query Match: 14.04% Indels: 8  
RESULT 352  
ID ABD27968 standard; DNA; 549 BP.  
DE AA282906 DNA fragment.  
PN WO200285309-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Best Local Similarity: 34.92% Mismatches: 61  
Query Match: 14.04% Indels: 8  
RESULT 353  
ID ADB62456 standard; CDNA; 2863 BP.  
DE Human CDNA encoding clone FEBRA20038970.  
PN EPI308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 23.56% Mismatches: 85  
Query Match: 13.33% Indels: 56  
RESULT 354  
ID ACH48521 standard; CDNA; 425 BP.  
DE Human leukocyte CDNA #115.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Best Local Similarity: 36.59% Mismatches: 36  
Query Match: 13.20% Indels: 1  
RESULT 355  
ID ABX74436 standard; CDNA; 781 BP.  
DE Human CDNA sequence #8 up-regulated in CC-RCC patients.  
PN WO200279411-A2.  
PD 10-OCT-2002.  
PA (VAND-) VAN ANDEL INST.  
Best Local Similarity: 30.22% Mismatches: 62  
Query Match: 12.93% Indels: 13  
RESULT 356  
ID ADL13961 standard; DNA; 834 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #493.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 30.22% Mismatches: 62  
Query Match: 12.93% Indels: 13  
RESULT 357  
ID ABX63446 standard; CDNA; 1144 BP.  
DE Human CDNA #446 differentially expressed in activated vascular tissue.  
PN US2002137081-A1.

PD 26-SEP-2002.  
 PA (BAND/) BANDMAN O.  
 Best Local Similarity: 30.22% Mismatches: 62  
 Query Match: 12.93% Indels: 13  
 RESULT 358  
 ID ADE25720 standard; cDNA; 1144 BP.  
 DE Human cDNA differentially expressed in foam cells #124.  
 PN US2003194721-A1.  
 PD 16-OCT-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 30.22% Mismatches: 62  
 Query Match: 12.93% Indels: 13  
 RESULT 359  
 ID ADL13963 standard; DNA; 1414 BP.  
 DE Osteoarthritis-associated polymorphic nucleotide #495.  
 PN WO2003054166-A2.  
 PD 03-JUL-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 30.22% Mismatches: 62  
 Query Match: 12.93% Indels: 13  
 RESULT 360  
 ID ABX76382 standard; DNA; 1422 BP.  
 DE Lung cancer-associated polynucleotide #246.  
 PN WO200286443-A2.  
 PD 31-OCT-2002.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Best Local Similarity: 30.22% Mismatches: 62  
 Query Match: 12.93% Indels: 13  
 RESULT 361  
 ID ACC72678 standard; cDNA; 1422 BP.  
 DE Human cancer related protein encoding cDNA SEQ ID NO:17.  
 PN WO2003025138-A2.  
 PD 27-MAR-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Best Local Similarity: 30.22% Mismatches: 62  
 Query Match: 12.93% Indels: 13  
 RESULT 362  
 ID ADN38973 standard; cDNA; 1422 BP.  
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:291.  
 PN WO2003042661-A2.  
 PD 22-MAY-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Best Local Similarity: 30.22% Mismatches: 62  
 Query Match: 12.93% Indels: 13  
 RESULT 363  
 ID AN39702 standard; cDNA; 1430 BP.  
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C74.  
 PN WO2003042661-A2.  
 PD 22-MAY-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Best Local Similarity: 30.22% Mismatches: 62  
 Query Match: 12.93% Indels: 13  
 RESULT 364  
 ID AQ21505 standard; DNA; 1440 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4325.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Best Local Similarity: 30.22% Mismatches: 62  
 Query Match: 12.93% Indels: 13  
 RESULT 365  
 ID AQ25341 standard; DNA; 1461 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8161.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Best Local Similarity: 30.22% Mismatches: 62  
 Query Match: 12.93% Indels: 13  
 RESULT 366  
 ID ASX63445 standard; cDNA; 1728 BP.  
 DE Human cDNA #445 differentially expressed in activated vascular tissue.  
 PN US2002137081-A1.  
 PD 26-SEP-2002.

PA (BAND/) BANDMAN O.  
 Best Local Similarity: 30.22% Mismatches: 62  
 Query Match: 12.93% Indels: 13  
 RESULT 367  
 ID ADK67833 standard; cDNA; 7840 BP.  
 DE Human BRCC300 gene coding sequence.  
 PN WO2004012755-A1.  
 PD 12-FEB-2004.  
 PA (WIST-) WISTAR INST.  
 Best Local Similarity: 30.22% Mismatches: 62  
 Query Match: 12.93% Indels: 13  
 RESULT 368  
 ID ABV95472 standard; cDNA; 351 BP.  
 DE Human pancreatic cancer expressed cDNA SEQ ID NO 880.  
 PN WO200260317-A2.  
 PD 08-AUG-2002.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 32.95% Mismatches: 41  
 Query Match: 12.89% Indels: 2  
 RESULT 369  
 ID ADM80849 standard; cDNA; 813 BP.  
 DE Human CADECM-36 encoding cDNA SEQ ID NO:78.  
 PN WO2004015396-A2.  
 PD 19-FEB-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 32.95% Mismatches: 41  
 Query Match: 12.89% Indels: 2  
 RESULT 370  
 ID AAQ27190 standard; cDNA; 1414 BP.  
 DE Tumour necrosis factor-induced glycoprotein TSG-6 gene.  
 PN WO9212175-A1.  
 PD 23-JUL-1992.  
 PA (UYNV) UNIV NEW YORK STATE.  
 Best Local Similarity: 32.95% Mismatches: 41  
 Query Match: 12.89% Indels: 2  
 RESULT 371  
 ID AAV71778 standard; cDNA; 1414 BP.  
 DE Tumour necrosis factor stimulated gene 6 (TSG-6) protein encoding cDNA.  
 PN US5846763-A.  
 PD 08-DEC-1998.  
 PA (UYNV) UNIV NEW YORK STATE.  
 Best Local Similarity: 32.95% Mismatches: 41  
 Query Match: 12.89% Indels: 2  
 RESULT 372  
 ID AAD06019 standard; cDNA; 1414 BP.  
 DE Human tumour necrosis factor (TNF) stimulated gene-6 (TSG-6) cDNA.  
 PN US6210905-B1.  
 PD 03-APR-2001.  
 PA (UYNV) UNIV NEW YORK STATE.  
 Best Local Similarity: 32.95% Mismatches: 41  
 Query Match: 12.89% Indels: 2  
 RESULT 373  
 ID ABS54635 standard; cDNA; 1414 BP.  
 DE Human cDNA encoding tumour necrosis factor stimulated gene 6, TSG-6.  
 PN US2002090708-A1.  
 PD 11-JUL-2002.  
 PA (UYNV) UNIV NEW YORK STATE.  
 Best Local Similarity: 32.95% Mismatches: 41  
 Query Match: 12.89% Indels: 2  
 RESULT 374  
 ID ADS85080 standard; DNA; 1605 BP.  
 DE Mouse atopic dermatitis-related gene sequence SeqID82.  
 PN WO2004031386-A1.  
 PD 15-APR-2004.  
 PA (GENO-) GENOX RES INC.  
 Best Local Similarity: 32.95% Mismatches: 41  
 Query Match: 12.80% Indels: 2  
 RESULT 375  
 ID ACH30555 standard; cDNA; 396 BP.  
 DE Human testis cDNA #941.  
 PN US2003073623-A1.  
 PD 17-APR-2003.

PA (DRMA/) DRMANAC R T.  
 PA (LABA/) LABAT I.  
 PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.  
 Best Local Similarity: 31.58% Mismatches: 58  
 Query Match: 12.76% Indels: 13  
 RESULT 376  
 ID AAH23114 standard; DNA; 1411 BP.  
 DE Osteoarthritis tissue-derived nucleic acid sequence #44.  
 PN WO200153531-A2.  
 PD 26-JUL-2001.  
 PA (PHAA) PHARMACIA CORP.  
 Best Local Similarity: 31.62% Mismatches: 62  
 Query Match: 12.31% Indels: 13  
 RESULT 377  
 ID AAF29464 standard; cDNA; 3153 BP.  
 DE Murine brevidin cDNA.  
 PN WO200100638-A2.  
 PD 04-JAN-2001.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Best Local Similarity: 24.88% Mismatches: 97  
 Query Match: 12.04% Indels: 30  
 RESULT 378  
 ID ACD66770 standard; cDNA; 3153 BP.  
 DE Secreted polypeptide-related cDNA #76.  
 PN US200302279-A1.  
 PD 30-JAN-2003.  
 PA (FRAS/) FRASER C C.  
 PA (BARN/) BARNES T M.  
 PA (SHAR/) SHARP J D.  
 PA (KIRS/) KIRST S J.  
 PA (MYER/) MYERS P S.  
 PA (LEIB/) LEIBY K R.  
 PA (HOLT/) HOLTZMAN D A.  
 PA (MCCA/) MCCARTHY S A.  
 PA (WRIG/) WRIGHTON N.  
 PA (MACK/) MACKAY C R.  
 PA (GOOD/) GOODEARL A D J.  
 Best Local Similarity: 24.88% Mismatches: 97  
 Query Match: 12.04% Indels: 30  
 RESULT 379  
 ID ADB90788 standard; cDNA; 3153 BP.  
 DE Mouse cDNA encoding brevin protein.  
 PN US2003082586-A1.  
 PD 01-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Best Local Similarity: 24.88% Mismatches: 97  
 Query Match: 12.04% Indels: 30  
 RESULT 380  
 ID ADF71523 standard; cDNA; 3153 BP.  
 DE Murine brevidin protein cDNA.  
 PN US200317573-A1.  
 PD 18-SEP-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Best Local Similarity: 24.88% Mismatches: 97  
 Query Match: 12.04% Indels: 30  
 RESULT 381  
 ID ADQ10339 standard; cDNA; 3153 BP.  
 DE Human polynucleotide #61.  
 PN US2004121396-A1.  
 PD 24-JUN-2004.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Best Local Similarity: 24.88% Mismatches: 97  
 Query Match: 12.04% Indels: 30  
 RESULT 382  
 ID AAD48132 standard; DNA; 3366 BP.  
 DE Rat CD441 DNA.  
 PN WO200276510-A1.  
 PD 03-OCT-2002.  
 PA (AGYT-) AGY THERAPEUTICS INC.  
 Best Local Similarity: 28.02% Mismatches: 62  
 Query Match: 11.91% Indels: 47

RESULT 383  
 ID ABS70406 standard; cDNA; 1734 BP.  
 DE Human bone remodelling gene #63.  
 PN US6426186-B1.  
 PD 30-JUL-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 30.00% Mismatches: 61  
 Query Match: 11.87% Indels: 14  
 RESULT 384  
 ID ACN42826 standard; cDNA; 7678 BP.  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1701.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 27.43% Mismatches: 54  
 Query Match: 11.78% Indels: 59  
 RESULT 385  
 ID ACN42825 standard; cDNA; 7975 BP.  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1700.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 27.43% Mismatches: 54  
 Query Match: 11.78% Indels: 59  
 RESULT 386  
 ID AB281727 standard; cDNA; 2652 BP.  
 DE Rat mutant brain-enriched hyaluronan binding protein coding sequence.  
 PN WO2003007880-A2.  
 PD 30-JAN-2003.  
 PA (UYVA) UNIV YALE.  
 PA (HOCK/) HOCKFIELD S.  
 PA (MATT/) MATTHEWS R T.  
 Best Local Similarity: 24.26% Mismatches: 81  
 Query Match: 11.69% Indels: 39  
 RESULT 387  
 ID ADK67780 standard; DNA; 2652 BP.  
 DE Rat brain-enriched hyaluronan binding (BEHAB) mutant coding sequence.  
 PN WO2004013356-A1.  
 PD 12-FEB-2004.  
 PA (UYVA) UNIV YALE.  
 Best Local Similarity: 24.26% Mismatches: 81  
 Query Match: 11.69% Indels: 39  
 RESULT 388  
 ID ABA04648 standard; cDNA; 4706 BP.  
 DE Rat Hyaluronic Acid Receptor for Endocytosis, HARE, coding sequence.  
 PN WO200181544-A2.  
 PD 01-NOV-2001.  
 PA (WEIG/) WEIGEL P A.  
 PA (ZHOU/) ZHOU B.  
 PA (WEIG/) WEIGEL J A.  
 Best Local Similarity: 24.75% Mismatches: 91  
 Query Match: 11.69% Indels: 32  
 RESULT 389  
 ID ABX13821 standard; cDNA; 4706 BP.  
 DE cDNA encoding rat 175KDa Hyaluronan receptor for endocytosis (HARE).  
 PN WO200286093-A2.  
 PD 31-OCT-2002.  
 PA (WEIG/) WEIGEL P H.  
 PA (WEIG/) WEIGEL J A.  
 Best Local Similarity: 24.75% Mismatches: 91  
 Query Match: 11.69% Indels: 32  
 RESULT 390  
 ID ADL13490 standard; DNA; 6951 BP.  
 DE Osteoarthritis-associated polymorphic nucleotide #22.  
 PN WO2003054166-A2.  
 PD 03-JUL-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 27.43% Mismatches: 55  
 Query Match: 11.60% Indels: 59  
 RESULT 391  
 ID ADL13489 standard; DNA; 7137 BP.  
 DE Osteoarthritis-associated polymorphic nucleotide #21.  
 PN WO2003054166-A2.

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PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 27.43% Mismatches: 55
Query Match: 11.60% Indels: 59
RESULT 392
ID ADP65694 standard; DNA; 7137 BP.
DE Human aggrecan 1 (chondroitin sulfate proteoglycan 1, large DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Best Local Similarity: 27.43% Mismatches: 55
Query Match: 11.60% Indels: 59
RESULT 393
ID ADP65777 standard; DNA; 7137 BP.
DE Human large aggregating cartilage proteoglycan core protein mRNA, DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Best Local Similarity: 27.43% Mismatches: 55
Query Match: 11.60% Indels: 59
RESULT 394
ID ACH15082 standard; cDNA; 488 BP.
DE Human adult brain cDNA #2294.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 395
ID ADP07636 standard; DNA; 859 BP.
DE Human secreted protein encoding DNA, seq id 119.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 396
ID AAI58121 standard; cDNA; 1365 BP.
DE Human polynucleotide SEQ ID NO 324.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 397
ID ADL91792 standard; cDNA; 1844 BP.
DE Human PRO271 encoding cDNA SEQ ID NO:13.
PN WO2004042076-A2.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 398
ID ADQ23710 standard; DNA; 1925 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6530.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 399
ID AAX52252 standard; DNA; 1984 BP.
DE Protein PRO271 cDNA clone DNA39423-1182.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 400
ID ADC78532 standard; cDNA; 1984 BP.
DE Human PRO271 cDNA.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 401
ID ADR18008 standard; cDNA; 1984 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 402
ID AAF72410 standard; cDNA; 1985 BP.
DE Human PRO271 cDNA.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 403
ID AAS45938 standard; cDNA; 1985 BP.
DE Human DNA encoding PRO polypeptide sequence #14.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 404
ID ACA60174 standard; cDNA; 1985 BP.
DE Human cDNA for secreted/transmembrane protein PRO271.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 405
ID ACA89388 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003036141-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 406
ID ACA73398 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036146-A1.

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PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 407  
ID ACA05713 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 408  
ID ACA66547 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO protein #14.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 409  
ID ACP007574 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein (PRO) cDNA #14.  
PN US2002197671-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 410  
ID ACP20122 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 411  
ID ACP19508 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 412  
ID ACP21796 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 413  
ID ACP12961 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 414  
ID ACP25064 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 415  
ID ACP00113 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 416  
ID ACA72170 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein (PRO) cDNA #14.  
PN US2003036118-A1.  
DE Novel human secreted and transmembrane protein (PRO) cDNA.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 417  
ID ACD04694 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein (PRO) cDNA.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 418  
ID ACD18155 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 419  
ID ACD08162 standard; cDNA; 1985 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO271.  
PN US2002132240-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 420  
ID ABX71622 standard; cDNA; 1985 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO271.  
PN US2002132240-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 421  
ID ACA88596 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 422  
ID ACA70038 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 423  
ID ACD12260 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 424  
ID ACC74175 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 425  
ID ACD15803 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 426  
ID ACD25371 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036118-A1.

PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 427  
ID ACD17848 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 428  
ID ACC8135 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 429  
ID ACD21489 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 430  
ID ACD18556 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 431  
ID ACH06954 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane polypeptide PRO271 cDNA.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 432  
ID ABX98166 standard; cDNA; 1985 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 27.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 433  
ID ACD13917 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 434  
ID ACD06997 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 435  
ID ACC88442 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 436  
ID ACD21182 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054483-A1.  
PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 437  
ID ABX75554 standard; cDNA; 1985 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO271.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 438  
ID ABX97757 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 439  
ID ACA97233 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 440  
ID ACA57696 standard; cDNA; 1985 BP.  
DE Human PRO271 cDNA.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 441  
ID ACD14224 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 442  
ID ACC91007 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 443  
ID ACC8749 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 444  
ID ACD06946 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 445  
ID ACA67397 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 446  
ID ACC81452 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032137-A1.  
PD 13-FEB-2003.



Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 447  
ID ACC89056 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 448  
ID ACC86412 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 449  
ID ACC89670 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 450  
ID ACC92849 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 451  
ID ACA72477 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 452  
ID ACA88995 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 453  
ID ACA69731 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 454  
ID ACA96874 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 455  
ID ACA90870 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 456  
ID ACA70652 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4

RESULT 457  
ID ACA95162 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 458  
ID ACC86105 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 459  
ID ACC89977 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 460  
ID ACD12585 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 461  
ID ACF19815 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 462  
ID ABX76759 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 463  
ID ABX96191 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2002160374-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 464  
ID ACA73091 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 465  
ID ACA05512 standard; cDNA; 1985 BP.  
DE cDNA encoding human secreted protein PRO271.  
PN US2003023054-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 466  
ID ACA68634 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4

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RESULT 467
ID ACA74478 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003036138-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 468
ID ACA70345 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032109-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 469
ID ACD14531 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003040066-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 470
ID ACD20179 standard; cDNA; 1985 BP.
DE Human secreted / transmembrane polypeptide PRO271 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 471
ID ACA68203 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 472
ID ABX98668 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 473
ID ACC81145 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032120-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 474
ID ACA95469 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 475
ID ACD04387 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 476
ID ACC87828 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 477
ID ACC85798 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 478
ID ACA96205 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003017540-A1.
PD 23-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 479
ID ACA64979 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032106-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 480
ID ACA73705 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032129-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 481
ID ACA74117 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 482
ID ACA96512 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032103-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 483
ID ACD10618 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003032107-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 484
ID ACC91314 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032139-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 485
ID ACD02649 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003022301-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 486
ID ACC87214 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 487
ID ACC85798 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
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PN US2003027262-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 488
ID ACA65286 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032110-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 489
ID ACA94103 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036142-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 490
ID ACA97847 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003036145-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 491
ID ACA91349 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 492
ID ACA90563 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 493
ID ACD16110 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044931-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 494
ID ACD17271 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036150-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 495
ID AC91928 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040069-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 496
ID ACA74785 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003022293-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 497
ID ACA91656 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032128-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 498
ID ACA71300 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032116-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 499
ID ACC90700 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032122-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 500
ID ACA65710 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO protein #14.
PN US2003036139-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 501
ID ACA54982 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 502
ID ACA94855 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003017541-A1.
PD 23-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 503
ID ACD16417 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003017543-A1.
PD 23-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 504
ID ACD15496 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036152-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 505
ID ABX16599 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein #14.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 506
ID ACA97540 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032115-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 507
ID ACA98989 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
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RESULT 508
ID ACC91621 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040076-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 509
ID ACD11032 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003008352-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 510
ID ACD14882 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044922-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 511
ID ACD19817 standard; cDNA; 1985 BP.
DE Human secreted / transmembrane polypeptide PRO271 cDNA.
PN US2003027143-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 512
ID ACD11646 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032118-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 513
ID ACC93775 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036135-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 514
ID ACF16338 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054455-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 515
ID ACF02456 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049741-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 516
ID ACF02763 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049743-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 517
ID ACF21350 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049769-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 518
ID ACF10034 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068743-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 519
ID ACF77927 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054479-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 520
ID ACD46632 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068685-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 521
ID ACD49395 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068725-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 522
ID ACF28162 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003088752-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 523
ID ACD88852 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068682-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 524
ID ACD84247 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068701-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 525
ID ACD99021 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003088755-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 526
ID ADA77779 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073180-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
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PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 527  
ID ACF48763 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104539-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 528  
ID ADB29417 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003092002-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 529  
ID ACD09083 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036131-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 530  
ID ACF11876 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040075-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 531  
ID ACF41110 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054459-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 532  
ID ACF15724 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003044930-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 533  
ID ACF16031 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040071-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 534  
ID ACD31858 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054471-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 535  
ID ACF18666 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064452-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 536  
ID ACF09113 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003065159-A1.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068705-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 537  
ID ACF78234 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054473-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 538  
ID ACF51833 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064440-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 539  
ID ACF26320 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068704-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 540  
ID ACF24113 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068722-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 541  
ID ACF63424 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073183-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 542  
ID ACF50298 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104549-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 543  
ID ACH07769 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049749-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 544  
ID ACF13575 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064462-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 545  
ID ACD41501 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003065159-A1.

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PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 546
ID ACF31914 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 547
ID ACF23192 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 548
ID ACF39882 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 549
ID ACD45404 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 550
ID ACF53061 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 551
ID ACF27241 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 552
ID ACF45079 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 553
ID ACF29697 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 554
ID ACD89773 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 555
ID ACD84554 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 556
ID ACD98714 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 557
ID ACF77006 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 558
ID ACF78699 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 559
ID ACF49684 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 560
ID ACF49991 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 561
ID ACD09390 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 562
ID ACD08469 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 563
ID ACF12183 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 564
ID ACC94691 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054468-A1.
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PD 20-MAR-2003.	Query Match: 11.33%	Indels: 4
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 565		
ID ACD22410 standard; cDNA; 1985 BP.		
DE Human secreted/transmembrane protein (PRO) cDNA #14.		
PN US2003054470-A1.		
PD 20-MAR-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 566		
ID ACF15110 standard; cDNA; 1985 BP.		
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.		
PN US2003044917-A1.		
PD 06-MAR-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 567		
ID ACC97205 standard; cDNA; 1985 BP.		
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.		
PN US2003044929-A1.		
PD 06-MAR-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 568		
ID ADA18273 standard; cDNA; 1985 BP.		
DE Human secreted/transmembrane protein cDNA, #42.		
PN US2003039971-A1.		
PD 27-FEB-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 569		
ID ACP66964 standard; cDNA; 1985 BP.		
DE Human cDNA encoding secreted/transmembrane protein PRO271.		
PN US2003045693-A1.		
PD 06-MAR-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 570		
ID ACC92235 standard; cDNA; 1985 BP.		
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.		
PN US2003059880-A1.		
PD 27-MAR-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 571		
ID ACF13882 standard; cDNA; 1985 BP.		
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.		
PN US2003064465-A1.		
PD 03-APR-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 572		
ID ACF14189 standard; cDNA; 1985 BP.		
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.		
PN US2003054478-A1.		
PD 20-MAR-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 573		
ID ACF09420 standard; cDNA; 1985 BP.		
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.		
PN US2003068718-A1.		
PD 10-APR-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 574		
ID ACD45711 standard; cDNA; 1985 BP.		
DE Human secreted/transmembrane protein (PRO) cDNA #14.		
PN US2003064454-A1.		
PD 03-APR-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 575		
ID ACD47860 standard; cDNA; 1985 BP.		
DE Human secreted/transmembrane protein (PRO) cDNA #14.		
PN US2003064461-A1.		
PD 03-APR-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 576		
ID ACD67591 standard; cDNA; 1985 BP.		
DE cDNA encoding human PRO polypeptide #14.		
PN US2003068724-A1.		
PD 10-APR-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 577		
ID ACF25399 standard; cDNA; 1985 BP.		
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.		
PN US2003068727-A1.		
PD 10-APR-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 578		
ID ACF29083 standard; cDNA; 1985 BP.		
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.		
PN US2003068772-A1.		
PD 10-APR-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 579		
ID ACD84861 standard; cDNA; 1985 BP.		
DE Human secreted/transmembrane protein (PRO) cDNA #14.		
PN US2003068714-A1.		
PD 10-APR-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 580		
ID ACD83940 standard; cDNA; 1985 BP.		
DE Human PRO polynucleotide #14.		
PN US2003068758-A1.		
PD 10-APR-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 581		
ID ACD87931 standard; cDNA; 1985 BP.		
DE Human secreted/transmembrane protein (PRO) cDNA #14.		
PN US2003068776-A1.		
PD 10-APR-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		
RESULT 582		
ID ACF30618 standard; cDNA; 1985 BP.		
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.		
PN US2003069407-A1.		
PD 10-APR-2003.		
PA (GETH ) GENENTECH INC.		
Best Local Similarity: 35.56%		
Query Match: 11.33%		

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RESULT 583
ID ACF32221 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US200304555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 584
ID ACH11881 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 585
ID ACH11881 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 586
ID ACD40580 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 587
ID ACF18052 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 588
ID ACF08499 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 589
ID ACF31300 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 590
ID ACF52140 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 591
ID ACD50009 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 592
ID ACF38712 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049777-A1.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 593
ID ACF26627 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 594
ID ACF24727 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 595
ID ACF46307 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 596
ID ACF27855 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 597
ID ACD89159 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 598
ID ACF63731 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 599
ID ACF60371 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 600
ID ACH12495 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 601
ID ACH09918 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049777-A1.
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PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 602  
ID ACD03773 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 603  
ID ACD10311 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 604  
ID ACD11953 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 605  
ID ACD83125 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #38.  
PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 606  
ID ACF42338 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 607  
ID ADAL6248 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 608  
ID ACF18359 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 609  
ID ACF02149 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 610  
ID ACF21657 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4

RESULT 611  
ID ACF10341 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 612  
ID ACF33793 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 613  
ID ACF44755 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 614  
ID ACD90387 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 615  
ID ACD91000 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 616  
ID ACF30311 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 617  
ID ACD87010 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 618  
ID ACF60064 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 619  
ID ACF46614 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 620  
ID ACF75471 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

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PN US2003096353-A1.
PD 22-MAY-2003.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 621
ID ADA79571 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073173-A1.
PD 17-APR-2003.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 622
ID ACF17131 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054458-A1.
PD 20-MAR-2003.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 623
ID ACF22885 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 624
ID ACF07885 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 625
ID ACF08192 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 626
ID ACF40496 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 627
ID ACF53675 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 628
ID ACD46939 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 629
ID ACF47842 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 630
ID ACF47228 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 631
ID ACF46000 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 632
ID ACD86089 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 633
ID ACF52447 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082715-A1.
PD 01-MAY-2003.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 634
ID ACF52754 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082716-A1.
PD 01-MAY-2003.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 635
ID ACF64747 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 636
ID ACF76392 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 637
ID ACF61292 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 638
ID ACF61599 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatches: 39
Indels: 4
RESULT 639
ID ACD30630 standard; cDNA; 1985 BP.
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DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 640  
ID ACD31151 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 641  
ID ACD32472 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 642  
ID ACF17438 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 643  
ID ACF07271 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 644  
ID ACF20429 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 645  
ID ACF21043 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 646  
ID ACF20736 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 647  
ID ACD47553 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 648  
ID ACF47535 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39

Query Match: 11.33% Indels: 4  
RESULT 649  
ID ACF53368 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 650  
ID ACD86703 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 651  
ID ACH04951 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 652  
ID ACF44448 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 653  
ID ADA42393 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003054401-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 654  
ID ADA81298 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 655  
ID ACD22103 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003072726-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 656  
ID ACD24450 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 657  
ID ACD39653 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003072726-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 658  
ID ACD39960 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.

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PN US2003054461-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 659
ID ACF13268 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 660
ID ACF03070 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 661
ID ACD23303 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 662
ID ACF78541 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 663
ID ACF11262 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 664
ID ACF50605 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 665
ID ACF34100 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 666
ID ACD46325 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 667
ID ACD48167 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 668
ID ACF27548 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 669
ID ACF24420 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 670
ID ACD85475 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 671
ID ACD90080 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 672
ID ACD83633 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 673
ID ACF49070 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 674
ID ACH07155 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 675
ID ACH07462 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 676
ID ACH08076 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
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RESULT 677
ID ACH11267 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PD US2003049766-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 678
ID ACF48149 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003064441-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 679
ID ACH11574 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PD US2003049767-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 680
ID ACF01228 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003040059-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 681
ID ACF40803 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003040078-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 682
ID ACD24143 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PD US2003044918-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 683
ID ACD31244 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PD US2003032132-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 684
ID ACF17745 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003054462-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 685
ID ACF32528 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003064445-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 686
ID ACF40189 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003064449-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 687
ID ACF48149 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003064441-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 688
ID ACF38098 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003068696-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 689
ID ACF25034 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003068712-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 690
ID ACF26934 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003068730-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 691
ID ACF29390 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003073174-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 692
ID ACD87624 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PD US2003068775-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 693
ID ACF76085 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003104545-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 694
ID ACF49377 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003104541-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
RESULT 695
ID ACF43834 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD US2003104554-A1.
PA (GETH ) GENENTECH INC.
Query Match: 39
Mismatchatches: 39
Indels: 4
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RESULT 696
ID ACH06179 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 697
ID ACH06486 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 698
ID ADA83096 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 699
ID ACC92542 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 700
ID ACC93156 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 701
ID ACF19201 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 702
ID ACD12892 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 703
ID ACF06350 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 704
ID ACC94384 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 705
ID ACC97812 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 706
ID ACC94077 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 707
ID ACF42031 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 708
ID ACD30937 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 709
ID ACD42966 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 710
ID ACD43273 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 711
ID ACF14803 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 712
ID ACF01535 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 713
ID ACF31607 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 714
ID ACD67284 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Indels: 4
Mismatches: 39
Indels: 4
RESULT 715
ID ACD48474 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
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PD US2003064466-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 716  
ID ACD48781 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PD US2003064468-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 717  
ID ACF51219 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PD US2003068760-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 718  
ID ACF53982 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PD US2003068769-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 719  
ID ACF25706 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PD US2003045700-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 720  
ID ACF39019 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PD US2003068698-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 721  
ID ACF28776 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PD US2003068759-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 722  
ID ACD90693 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PD US2003049748-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 723  
ID ACD86396 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PD US2003068765-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 724  
ID ACH05258 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PD US2003049754-A1.  
PA (GETH ) GENENTECH INC.

PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 725  
ID ACF65054 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PD US2003068688-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 726  
ID ADB20139 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PD US2003082767-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 727  
ID ACF43527 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PD US2003104552-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 728  
ID ACH08997 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PD US2003049774-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 729  
ID ACH09304 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PD US2003049775-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 730  
ID ADA78391 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PD US2003073181-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 731  
ID ACF09727 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PD US2003068720-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 732  
ID ACF50912 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PD US2003068739-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 733  
ID ACF23806 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PD US2003068763-A1.  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 734  
ID ACD88238 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 735  
ID ACH09611 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 736  
ID ACH10532 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 737  
ID ACD11339 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 738  
ID ACC96389 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 739  
ID ACC98419 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 740  
ID ADA16672 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 741  
ID ACF41724 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 742  
ID ACF16645 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 743  
ID ADA13101 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003049622-A1.

PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 744  
ID ACD32165 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 745  
ID ACD30323 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 746  
ID ACD41194 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 747  
ID ACF07578 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 748  
ID ACF30993 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 749  
ID ACF77313 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 750  
ID ACF10955 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073170-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 751  
ID ACF32835 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 752  
ID ACF26013 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39



Query Match: 11.33% Indels: 4  
RESULT 753  
ID ACD83326 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003068728-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 754  
ID ACF23499 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068764-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 755  
ID ACF42913 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104550-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 756  
ID ACF43220 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104551-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 757  
ID ACH05872 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003049761-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 758  
ID ACH08690 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049757-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 759  
ID ADA41969 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003082540-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 760  
ID ACC90284 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027273-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 761  
ID ACF10648 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036119-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 762  
ID ACC93463 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064443-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 763  
ID ACC96082 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036161-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 764  
ID ACD24757 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044921-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 765  
ID ADA17316 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003017498-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 766  
ID ACF01942 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049739-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 767  
ID ACF21964 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003059882-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 768  
ID ACF22578 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003059884-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 769  
ID ACF08806 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068687-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 770  
ID ACF33142 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073186-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 771  
ID ACF54596 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064443-A1.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 772  
ID ACC93463 standard; cDNA; 1985 BP.

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PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 772
ID ACF48456 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064444-A1.
Best Local Similarity: 35.56% Mismatches: 39
PD 03-APR-2003. Indels: 4
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 773
ID ACD47246 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US200308697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 774
ID ACD49088 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 775
ID ACF37791 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 776
ID ACF30004 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 777
ID ACD87317 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 778
ID ACF61906 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104538-A1.
PD 05-JUN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 779
ID ACH10839 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 780
ID ADA42819 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
, Best Local Similarity: 35.56% Mismatches: 39

Query Match: 11.33% Indels: 4
RESULT 781
ID ACD10004 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036158-A1.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 782
ID ACD16729 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003036151-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 783
ID ACC99026 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040067-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 784
ID ACF00420 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054456-A1.
PD 20-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 785
ID ACD40887 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 786
ID ACF14496 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 787
ID ACF22271 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 788
ID ACF78848 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 789
ID ACF11569 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 790
ID ACF51526 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064442-A1.
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PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 791
ID ACF33449 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064450-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 792
ID ACD49702 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 793
ID ACF37484 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068683-A1.
PD 10-APR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 794
ID ACF28469 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 795
ID ACD88545 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068681-A1.
PD 10-APR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 796
ID ACF75164 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 797
ID ACF60985 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 798
ID ACF4141 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 799
ID ACH08383 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 800
ID ACC93770 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036122-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 801
ID ACD20875 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 802
ID ACF06657 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040065-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 803
ID ACD20568 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044919-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 804
ID ACD22717 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040077-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 805
ID ACF41417 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044928-A1.
PD 06-MAR-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 806
ID ACF06964 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 807
ID ACD23665 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #38.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 808
ID ACF77620 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 809
ID ACD46018 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064459-A1.
PD 03-APR-2003.
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PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 810  
ID ACF45921 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 811  
ID ACF54289 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 812  
ID ACF45693 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 813  
ID ACF45386 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 814  
ID ACF38405 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 815  
ID ACD89466 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 816  
ID ACD85168 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 817  
ID ACD85782 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 818  
ID ACF75778 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 819  
ID ACF60678 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 820  
ID ACH05565 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 821  
ID ADA82462 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 822  
ID ACF55824 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 823  
ID ACF55210 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 824  
ID ADB77738 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 825  
ID ADB74874 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 826  
ID ADB85770 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 827  
ID ACF56131 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4

RESULT 828  
ID ACP56438 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 829  
ID ACP55517 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 830  
ID ACP54903 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 831  
ID ADC28520 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003059772-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 832  
ID ADC39720 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003059828-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 833  
ID ADC40234 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003059829-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 834  
ID ADC19058 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003036061-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 835  
ID ADC34358 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003036094-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 836  
ID ADC29413 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003049676-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 837  
ID ADC28944 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003049677-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 838  
ID ADC40829 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003054400-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 839  
ID ADC19486 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003054441-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 840  
ID ADC33934 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003073077-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 841  
ID ADC13004 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003073079-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 842  
ID ADC12456 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003082541-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 843  
ID ADD05500 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 844  
ID ADD05011 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003104469-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 845  
ID ADD04017 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003104381-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 846  
ID ADD03593 standard; cDNA; 1985 BP.

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DE Human secreted/transmembrane protein cdNA, #42.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 847
ID ADE34845 standard; cdNA; 1985 BP.
DE Human secreted/transmembrane protein cdNA, #42.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 848
ID AG02495 standard; cdNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cdNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 849
ID ADG01202 standard; cdNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cdNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 850
ID ADP95377 standard; cdNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cdNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 851
ID ADG12192 standard; cdNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cdNA.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 852
ID ADH08852 standard; cdNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 853
ID ADH59328 standard; cdNA; 1985 BP.
DE Human secreted/transmembrane protein cdNA, #42.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 854
ID ADI38107 standard; cdNA; 1985 BP.
DE Human secreted/transmembrane protein cdNA, #42.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 855
ID ABX78541 standard; cdNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003027272-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 856
ID ACA59070 standard; cdNA; 1985 BP.
DE Human PRO polynucleotide #38.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 857
ID ACA75513 standard; cdNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cdNA.
PN US2003032127-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 858
ID ACA70993 standard; cdNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cdNA #14.
PN US2003032112-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 859
ID ACC87521 standard; cdNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cdNA, SEQ ID NO:27.
PN US2003027278-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 860
ID ACC86907 standard; cdNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cdNA, SEQ ID NO:27.
PN US2003036159-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 861
ID ADC04080 standard; cdNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cdNA #14.
PN US2003040070-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 862
ID ACA69411 standard; cdNA; 1985 BP.
DE CDNA encoding human PRO polypeptide #14.
PN US2003032113-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 863
ID ACA90256 standard; cdNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cdNA.
PN US2003036147-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 864
ID ACA58467 standard; cdNA; 1985 BP.
DE CDNA encoding human PRO polypeptide #38.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 865
ID ACC89363 standard; cdNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cdNA, SEQ ID NO:27.
PN US2003027264-A1.
PD 06-FEB-2003.

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Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 866  
ID ACA98154 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 867  
ID ACA93796 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 868  
ID ACD15189 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 869  
ID ACD08776 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 870  
ID ACC96696 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 871  
ID ACF15417 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 872  
ID ACA72784 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 873  
ID ACD02956 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 874  
ID ACD01771 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 875  
ID ACA91963 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4

RESULT 876  
ID ADJ26375 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003054349-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 877  
ID ADL32633 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 878  
ID ADM30167 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 879  
ID ADE79290 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003135025-A1.  
PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 880  
ID ADE79714 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003130489-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 881  
ID ADE73390 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003129592-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 882  
ID ADE74164 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 883  
ID ADE73925 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003148370-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 884  
ID ADE74776 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 11.33% Indels: 4  
RESULT 885  
ID ADE99479 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.

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PN US2003211576-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 886
ID ADE98598 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cdNA, #42.
PN US2003211569-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 887
ID ADE99025 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cdNA, #42.
PN US2003211568-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 888
ID ADG40495 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cdNA, #42.
PN US200325253-A1.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 889
ID ADF73889 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cdNA, #42.
PN US2003180312-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 890
ID ADF95989 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cdNA.
PN US2003215909-A1.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 891
ID ADF73465 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cdNA, #42.
PN US2003166051-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 892
ID ADG04260 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cdNA.
PN US2003215912-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 893
ID ADG00420 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cdNA.
PN US2003215911-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 894
ID ADG82676 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003215910-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 895
ID ADG92308 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cdNA, #42.
PN US2003027145-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 896
ID ADG92735 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cdNA, #42.
PN US2003027146-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 897
ID ADH25957 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cdNA.
PN US2003068770-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 898
ID ADH32926 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068768-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 899
ID ADH20524 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cdNA, #42.
PN US2004005553-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 900
ID ADH07379 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cdNA, #42.
PN US2004006211-A1.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 901
ID ADH59924 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cdNA, #42.
PN US2003215904-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 11.33% Indels: 4
RESULT 902
ID ADH06952 standard; cDNA; 1985 BP.

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DE Human secreted/transmembrane protein cDNA, #42.
PN US2004005655-A1.
PD 08-JAN-2004.
PA (DESN//) DESNOYERS L.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GURN//) GURNEY A L.
PA (MATH//) MATHUR J P.
PA (WILL//) WILLIAMS P M.
PA (WOOD//) WOOD W I.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatch: 39
Indel: 4
RESULT 903
ID AD118694 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH//) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatch: 39
Indel: 4
RESULT 904
ID AD165414 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH//) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatch: 39
Indel: 4
RESULT 905
ID AD137677 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH//) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatch: 39
Indel: 4
RESULT 906
ID ADH97473 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH//) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatch: 39
Indel: 4
RESULT 907
ID AD165841 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH//) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatch: 39
Indel: 4
RESULT 908
ID ADH60584 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN//) DESNOYERS L.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GURN//) GURNEY A L.
PA (MATH//) MATHUR J P.
PA (WILL//) WILLIAMS P M.
PA (WOOD//) WOOD W I.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatch: 39
Indel: 4
RESULT 909
ID ADJ99641 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH//) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatch: 39
Indel: 4
RESULT 910
ID ADL08834 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH//) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatch: 39
Indel: 4
RESULT 911
ID ADJ54665 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH//) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatch: 39
Indel: 4
RESULT 912
ID ADM25175 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH//) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatch: 39
Indel: 4
RESULT 913
ID ADM29925 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH//) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatch: 39
Indel: 4
RESULT 914
ID ADJ64436 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH//) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatch: 39
Indel: 4
RESULT 915
ID ADM31332 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH//) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatch: 39
Indel: 4
RESULT 916
ID ADM36379 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH//) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatch: 39
Indel: 4
RESULT 917
ID ADM40184 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH//) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatch: 39
Indel: 4
RESULT 918
ID ADO06247 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #40.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH//) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 11.33%
Mismatch: 39
Indel: 4

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RESULT 919	PA (LEIB//) LEIBY K R.	
ID ADN37792 standard; cDNA; 1985 BP.	PA (HOLT//) HOLTZMAN D A.	
DE Novel human secreted and transmembrane protein PRO271 cDNA.	PA (MCCA//) MCCARTHY S A.	
PN US2004091959-A1.	PA (WRIGHT//) WRIGHTON N.	
PD 13-MAY-2004.	PA (WACK//) WACKAY C R.	
PA (GETH ) GENENTECH INC.	PA (GOOD//) GOODEARL A D J.	
Best Local Similarity: 35.56%	Best Local Similarity: 24.65%	Mismatches: 76
Query Match: 11.33%	Query Match: 11.33%	Indels: 53
RESULT 920		
ID ADR11099 standard; cDNA; 1985 BP.	ID ADB90775 standard; cDNA; 2013 BP.	
DE Human secreted/transmembrane protein cDNA, #42.	DE Human TANGO 332 open reading frame.	
PN US2004137561-A1.	PN US2003082586-A1.	
PD 15-JUL-2004.	PD 01-MAY-2003.	
PA (GETH ) GENENTECH INC.	PA (MILL-) MILLENNIUM PHARM INC.	
Best Local Similarity: 35.56%	Best Local Similarity: 24.65%	Mismatches: 76
Query Match: 11.33%	Query Match: 11.33%	Indels: 53
RESULT 921		
ID AUT03684 standard; cDNA; 1985 BP.	ID ADF71510 standard; cDNA; 2013 BP.	
DE Human secreted/transmembrane protein cDNA, #42.	DE Human TANGO 332 CDS.	
PN US2003152922-A1.	PN US2003175733-A1.	
PD 14-AUG-2003.	PD 18-SEP-2003.	
PA (GETH ) GENENTECH INC.	PA (MILL-) MILLENNIUM PHARM INC.	
Best Local Similarity: 35.56%	Best Local Similarity: 24.65%	Mismatches: 76
Query Match: 11.33%	Query Match: 11.33%	Indels: 53
RESULT 922		
ID ADS74647 standard; cDNA; 1985 BP.	ID ADQ10328 standard; cDNA; 2013 BP.	
DE Human secreted/transmembrane cDNA #42.	DE Human polynucleotide #58.	
PN US2004185531-A1.	PN US2004121396-A1.	
PD 23-SEP-2004.	PD 24-JUN-2004.	
PA (ASHK//) ASHKENAZI A.	PA (MILL-) MILLENNIUM PHARM INC.	
PA (BOTS//) BOTSTEIN D.	Best Local Similarity: 24.65%	Mismatches: 76
PA (DESN//) DESNOYERS L.	Query Match: 11.33%	Indels: 53
PA (EATO//) EATON D L.	RESULT 927	
PA (FERR//) FERRARA N.	ID ABZ81728 standard; cDNA; 2652 BP.	
PA (FILV//) FILVAROFF E.	DE Rat brain-enriched hyaluronan binding protein coding sequence.	
PA (FONG//) FONG S.	PN WO2003007880-A2.	
PA (GAOW//) GAO W.	PD 30-JAN-2003.	
PA (GERB//) GERBER H.	PA (UYVA ) UNIV YALE.	
PA (GERR//) GERRITSEN M E.	PA (HOCK//) HOCKFIELD S.	
PA (GODD//) GODDARD A.	PA (WATT//) MATTHEWS R T.	
PA (GODO//) GODOWSKI P J.	Best Local Similarity: 23.00%	Mismatches: 91
PA (GRIM//) GRIMALDI C J.	Query Match: 11.33%	Indels: 33
PA (GURN//) GURNEY A L.	RESULT 929	
PA (HILL//) HILLAN K J.	ID ADK67781 standard; DNA; 2652 BP.	
PA (KLJA//) KLJAVIN I J.	DE Rat glycosylation-variant BEHAV isoform coding sequence.	
PA (MATH//) MATHER J P.	PN WO2004013356-A1.	
PA (PANJ//) PAN J.	PD 12-FEB-2004.	
PA (PAON//) PAONI N F.	PA (UYVA ) UNIV YALE.	
PA (ROYM//) ROY M A.	Best Local Similarity: 23.00%	Mismatches: 91
PA (STEW//) STEWART T A.	Query Match: 11.33%	Indels: 33
PA (TUMA//) TUMAS D.	RESULT 930	
PA (WILL//) WILLIAMS P M.	ID AAF29459 standard; cDNA; 2730 BP.	
PA (WOOD//) WOOD W I.	DE Human TANGO 332 cDNA.	
Best Local Similarity: 35.56%	PN WO200100638-A2.	
Query Match: 11.33%	PD 04-JAN-2001.	
RESULT 923	PA (MILL-) MILLENNIUM PHARM INC.	
ID AAF29460 standard; cDNA; 2013 BP.	Best Local Similarity: 24.65%	Mismatches: 76
DE Human TANGO 332 cDNA open reading frame.	Query Match: 11.33%	Indels: 53
PN WO200100638-A2.	RESULT 931	
PD 04-JAN-2001.	ID ACD66766 standard; cDNA; 2730 BP.	
PA (MILL-) MILLENNIUM PHARM INC.	DE Secreted polypeptide-related cDNA #50.	
Best Local Similarity: 24.65%	PN US2003022279-A1.	
Query Match: 11.33%	PD 30-JAN-2003.	
RESULT 924	PA (FRAS//) FRASER C C.	
ID ACD66767 standard; cDNA; 2013 BP.	PA (BARN//) BARNES T M.	
DE Secreted polypeptide-related cDNA #51.	PA (SHAR//) SHARP J D.	
PN US2003022279-A1.	PA (KIRS//) KIRST S J.	
PD 30-JAN-2003.	PA (MYER//) MYERS P S.	
PA (FRAS//) FRASER C C.	PA (LEIB//) LEIBY K R.	
PA (BARN//) BARNES T M.	PA (HOLT//) HOLTZMAN D A.	
PA (SHAR//) SHARP J D.	PA (MCCA//) MCCARTHY S A.	
PA (KIRS//) KIRST S J.	PA (WRIGHT//) WRIGHTON N.	
PA (MYER//) MYERS P S.	PA (WACK//) WACKAY C R.	

PA (GOOD/) GOODEARL A D J.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatch: 76  
Indel: 53  
RESULT 932  
ID ADB90774 standard; cDNA; 2730 BP.  
DE Human cDNA encoding TANGO 332.  
PN US2003082586-A1.  
PD 01-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatch: 76  
Indel: 53  
RESULT 933  
ID ADF71509 standard; cDNA; 2730 BP.  
DE Human TANGO 332 cDNA.  
PN US2003175733-A1.  
PD 18-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatch: 76  
Indel: 53  
RESULT 934  
ID ADQ10327 standard; cDNA; 2730 BP.  
DE Human polynucleotide #57.  
PN US2004121396-A1.  
PD 24-JUN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatch: 76  
Indel: 53  
RESULT 935  
ID AAD48133 standard; DNA; 2878 BP.  
DE Human chondroitin sulphate proteoglycan BEHAB/brevican DNA.  
PN WO200276510-A1.  
PD 03-OCT-2002.  
PA (AGYT-) AGY THERAPEUTICS INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatch: 76  
Indel: 53  
RESULT 936  
ID ADN38941 standard; cDNA; 2878 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:259.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatch: 76  
Indel: 53  
RESULT 937  
ID ADK67783 standard; DNA; 2878 BP.  
DE Human glycosylation-variant BEHAB isoform coding sequence.  
PN WO2004013356-A1.  
PD 12-FEB-2004.  
PA (UYA) UNIV YALE.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatch: 76  
Indel: 53  
RESULT 938  
ID ADB59097 standard; DNA; 3077 BP.  
DE Toxicity-related gene, SEQ ID 4123.  
PN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 23.00%  
Query Match: 11.33%  
Mismatch: 91  
Indel: 33  
RESULT 939  
ID ADP72861 standard; DNA; 3077 BP.  
DE Renal toxin progression gene marker #1450.  
PN WO2004048598-A2.  
PD 10-JUN-2004.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 23.00%  
Query Match: 11.33%  
Mismatch: 91  
Indel: 33  
RESULT 940  
ID ACN37482 standard; cDNA; 3275 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA323924, SEQ ID NO:394.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH-) GENENTECH INC.

Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatch: 76  
Indel: 53  
RESULT 941  
ID ADH18923 standard; cDNA; 3293 BP.  
DE Human cell adhesion and extracellular matrix CADECM-19 cDNA - SEQ 50.  
PN WO2003094843-A2.  
PD 20-NOV-2003.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatch: 76  
Indel: 53  
RESULT 942  
ID ADI28068 standard; cDNA; 3438 BP.  
DE ECMAD gene clone 6755002CB1.  
PN WO200202634-A2.  
PD 10-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatch: 76  
Indel: 53  
RESULT 943  
ID ADQ83194 standard; cDNA; 3467 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #8.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH-) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatch: 76  
Indel: 53  
RESULT 944  
ID ADQ85107 standard; cDNA; 3467 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1921.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH-) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatch: 76  
Indel: 53  
RESULT 945  
ID AAA91017 standard; DNA; 3476 BP.  
DE Human secreted protein PRO6018 coding sequence.  
PN WO200075317-A2.  
PD 14-DEC-2000.  
PA (GETH-) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatch: 76  
Indel: 53  
RESULT 946  
ID ASK69986 standard; DNA; 3476 BP.  
DE cDNA encoding human Pro peptide #26.  
PN WO200224888-A2.  
PD 28-MAR-2002.  
PA (GETH-) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatch: 76  
Indel: 53  
RESULT 947  
ID ADA01319 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003068779-A1.  
PD 10-APR-2003.  
PA (GETH-) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatch: 76  
Indel: 53  
RESULT 948  
ID ADA43748 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003064474-A1.  
PD 03-APR-2003.  
PA (GETH-) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatch: 76  
Indel: 53  
RESULT 949  
ID ADA43516 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.

PN US2003073196-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 950  
ID ADA01191 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003068782-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 951  
ID ADA01075 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003068780-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 952  
ID ADA43632 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003073190-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 953  
ID ADA06894 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003068781-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 954  
ID ADA08382 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003068783-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 955  
ID ADB99675 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide SEQ ID 51.  
PN US2003082728-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 956  
ID ADB86958 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003082726-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 957  
ID ADB66113 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003082729-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 958  
ID ADB99791 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide SEQ ID 51.  
PN US2003073192-A1.

PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 959  
ID ADB99446 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003082731-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 960  
ID ADB65997 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003082732-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 961  
ID ADC23395 standard; cDNA; 3476 BP.  
DE Human cDNA clone (seqid 51) encoding the transmembrane PRO protein.  
PN US2003073193-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 962  
ID ADC26088 standard; cDNA; 3476 BP.  
DE Human PRO6018 cDNA.  
PN US2003073194-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 963  
ID ADE04915 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003088778-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 964  
ID ADE11221 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003073191-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 965  
ID ADD88152 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003082733-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 966  
ID ADD95447 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003064473-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 967  
ID ADE06377 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003073195-A1.  
PD 17-APR-2003.

PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 968  
ID ADE38152 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119120-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 969  
ID ADD88268 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003073189-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 970  
ID ADD90849 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003073188-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 971  
ID ADF99404 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003078401-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 972  
ID ADG06497 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003077742-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 973  
ID ADG05448 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003077741-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 974  
ID ADG82449 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003077744-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 975  
ID ADE51702 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104560-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 976  
ID ADE51818 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104561-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 977  
ID ADE37676 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104564-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 978  
ID ADE37560 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104565-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 979  
ID ADD95331 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003138901-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 980  
ID ADE38031 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003104566-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 981  
ID ADE76120 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003124665-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 982  
ID ADE39443 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119117-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 983  
ID ADE04247 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003096364-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 984  
ID ADE39844 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138896-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53  
RESULT 985  
ID ADE19709 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138903-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65%  
Query Match: 11.33%  
Mismatches: 76  
Indels: 53

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Query Match: 11.33% Indels: 53
RESULT 986
ID ADE77287 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 987
ID ADE66395 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 988
ID ADE76004 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 989
ID ADE37915 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 990
ID ADE64525 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 991
ID ADE38860 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 992
ID ADE51934 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 993
ID ADD09965 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 994
ID ADE38744 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 995
ID ADE37444 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 996
ID ADE08261 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 997
ID ADD90120 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 998
ID ADE38628 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 999
ID ADE39559 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1000
ID ADD89164 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1001
ID ADD88931 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1002
ID ADE19825 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1003
ID ADE77403 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 24.65% Mismatches: 76
Query Match: 11.33% Indels: 53
RESULT 1004
```

ID AD565279 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119113-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1005

ID AD539327 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119115-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1006

ID AD538512 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104559-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1007

ID ADG11065 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003170809-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1008

ID ADG10949 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003077743-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1009

ID ADH31477 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119139-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1010

ID ADH38725 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119140-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1011

ID ADH29360 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119137-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1012

ID ADH23663 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119143-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1013

ID ADH26993 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119135-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1014

ID ADH38261 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119124-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1015

ID ADH26877 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119134-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1016

ID ADH38145 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119123-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1017

ID ADH38841 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119141-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1018

ID ADH23779 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119142-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1019

ID ADH40155 standard; cDNA; 3476 BP.  
DE Human PRO6018 cDNA.  
PN US2003119132-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1020

ID ADH40039 standard; cDNA; 3476 BP.  
DE Human PRO6018 cDNA.  
PN US2003119133-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1021

ID ADH31361 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119138-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1022

ID ADH29239 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.

PN US2003119136-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1023  
ID ADH49454 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119127-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1024  
ID ADH51918 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119125-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1025  
ID ADH49773 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119128-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1026  
ID ADH52374 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119130-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1027  
ID ADH52490 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119129-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1028  
ID ADH58487 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119121-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1029  
ID ADH51802 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119126-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1030  
ID ADH58363 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119122-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1031  
ID ADH13560 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119131-A1.

PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1032  
ID ADK00816 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003186373-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1033  
ID ADL08557 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003186372-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1034  
ID ACN42086 standard; cDNA; 4353 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:961.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1035  
ID ACN42083 standard; cDNA; 4545 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:958.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1036  
ID ACN42082 standard; cDNA; 4659 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:957.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 24.65% Mismatches: 76  
Query Match: 11.33% Indels: 53  
RESULT 1037  
ID ASK62593 standard; cDNA; 2465 BP.  
DE Rat sequence differentially expressed in response to a hepatotoxin #500.  
PN WO200210453-A2.  
PD 07-FEB-2002.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 27.14% Mismatches: 69  
Query Match: 11.29% Indels: 11  
RESULT 1038  
ID ADQ45337 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 7000.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.65% Mismatches: 30  
Query Match: 11.20% Indels: 2  
RESULT 1039  
ID ADB63670 standard; cDNA; 2160 BP.  
DE Human cDNA encoding clone THYMU20143230.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
Best Local Similarity: 24.64% Mismatches: 92  
Query Match: 11.16% Indels: 40  
RESULT 1040  
ID ACF04000 standard; cDNA; 7879 BP.  
DE Human CLEVER-1 encoding cDNA SEQ ID NO:1.  
PN WO2003057130-A2.



PD 17-JUL-2003.  
PA (JALK/) JALKANEN S.  
PA (IRJA/) IRJALA H.  
PA (SALM/) SALMI M.  
Best Local Similarity: 24.64% Mismatches: 92  
Query Match: 11.16% Indels: 40  
RESULT 1041  
ID ADQ22919 standard; DNA; 8038 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5739.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Best Local Similarity: 24.64% Mismatches: 92  
Query Match: 11.16% Indels: 40  
RESULT 1042  
ID ADQ45257 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6920.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.65% Mismatches: 30  
Query Match: 11.11% Indels: 2  
RESULT 1043  
ID ADQ45308 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6971.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.65% Mismatches: 30  
Query Match: 11.11% Indels: 2  
RESULT 1044  
ID ADQ45241 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6904.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.65% Mismatches: 30  
Query Match: 11.11% Indels: 2  
RESULT 1045  
ID ADQ45225 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6888.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.65% Mismatches: 30  
Query Match: 11.11% Indels: 2  
RESULT 1046  
ID ADQ45323 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6986.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.65% Mismatches: 30  
Query Match: 11.11% Indels: 2  
RESULT 1047  
ID ADQ45215 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6878.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.65% Mismatches: 30  
Query Match: 11.11% Indels: 2  
RESULT 1048  
ID ADQ45264 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6927.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.65% Mismatches: 30  
Query Match: 11.11% Indels: 2  
RESULT 1049  
ID ADQ45280 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6943.

PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.65% Mismatches: 30  
Query Match: 11.11% Indels: 2  
RESULT 1050  
ID ADQ45298 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6961.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.65% Mismatches: 30  
Query Match: 11.11% Indels: 2  
RESULT 1051  
ID ADL13960 standard; DNA; 834 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #492.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 32.97% Mismatches: 39  
Query Match: 11.11% Indels: 8  
RESULT 1052  
ID ABL68341 standard; DNA; 1414 BP.  
DE Kidney cancer related gene sequence SEQ ID NO:6678.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Best Local Similarity: 32.97% Mismatches: 39  
Query Match: 11.11% Indels: 8  
RESULT 1053  
ID ABK83989 standard; cDNA; 1414 BP.  
DE Human cDNA differentially expressed in granulocytic cells #560.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 32.97% Mismatches: 39  
Query Match: 11.11% Indels: 8  
RESULT 1054  
ID ABX76383 standard; DNA; 1414 BP.  
DE Lung cancer-associated polynucleotide #247.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 32.97% Mismatches: 39  
Query Match: 11.11% Indels: 8  
RESULT 1055  
ID ACC72679 standard; cDNA; 1414 BP.  
DE Human cancer related protein encoding cDNA SEQ ID NO:18.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 32.97% Mismatches: 39  
Query Match: 11.11% Indels: 8  
RESULT 1056  
ID ADL13959 standard; DNA; 1414 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #491.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 32.97% Mismatches: 39  
Query Match: 11.11% Indels: 8  
RESULT 1057  
ID ADN38975 standard; cDNA; 1414 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:293.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 32.97% Mismatches: 39  
Query Match: 11.11% Indels: 8  
RESULT 1058  
ID ADO24484 standard; cDNA; 1414 BP.  
DE Human PRO87343 encoding cDNA SEQ ID NO:123.  
PD 22-MAY-2003.

PD 27-MAY-2004.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 32.97% Mismatches: 39  
 Query Match: 11.11% Indels: 8  
 RESULT 1059  
 ID ADO24438 standard; cDNA; 1414 BP.  
 DE Human PRO87335 encoding cDNA SEQ ID NO:77.  
 PN W02004043397-A2.  
 PD 27-MAY-2004.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 32.97% Mismatches: 39  
 Query Match: 11.11% Indels: 8  
 RESULT 1060  
 ID ADR14116 standard; DNA; 1414 BP.  
 DE Human NF-kappaB pathway-associated gene SeqID117.  
 PN W02004065577-A2.  
 PD 03-AUG-2004.  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 Best Local Similarity: 32.97% Mismatches: 39  
 Query Match: 11.11% Indels: 8  
 RESULT 1061  
 ID AA57363 standard; DNA; 1522 BP.  
 DE DNA encoding a human hyaluronan-binding protein, designated WF-HABP.  
 PN W0200039166-A1.  
 PD 06-JUL-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (AMNA-) AMERICAN NAT RED CROSS.  
 Best Local Similarity: 24.15% Mismatches: 92  
 Query Match: 11.07% Indels: 40  
 RESULT 1062  
 ID ABL90758 standard; cDNA; 3681 BP.  
 DE Human polynucleotide SEQ ID NO 1320.  
 PN W0200190304-A2.  
 PD 29-NOV-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 24.15% Mismatches: 92  
 Query Match: 11.07% Indels: 40  
 RESULT 1063  
 ID AA57362 standard; DNA; 6761 BP.  
 DE DNA encoding a human hyaluronan-binding protein, designated WF-HABP.  
 PN W0200039166-A1.  
 PD 06-JUL-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (AMNA-) AMERICAN NAT RED CROSS.  
 Best Local Similarity: 24.15% Mismatches: 92  
 Query Match: 11.07% Indels: 40  
 RESULT 1064  
 ID ACN37944 standard; cDNA; 7871 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA324323, SEQ ID NO:11163.  
 PN W02004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 24.15% Mismatches: 92  
 Query Match: 11.07% Indels: 40  
 RESULT 1065  
 ID ACH45565 standard; cDNA; 474 BP.  
 DE Human foetal brain cDNA #6290.  
 PN US2003073623-A1.  
 PD 17-APR-2003.  
 PA (DRMA/) DRMANAC R T.  
 PA (LABA/) LABAT I.  
 PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.  
 Best Local Similarity: 34.52% Mismatches: 41  
 Query Match: 11.02% Indels: 2  
 RESULT 1066  
 ID ADM80846 standard; cDNA; 795 BP.  
 DE Human CADECM-33 encoding cDNA SEQ ID NO:75.  
 PN W02004015396-A2.  
 PD 19-FEB-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 34.94% Mismatches: 37

Query Match: 10.80% Indels: 3  
 RESULT 1067  
 ID AAV41923 standard; cDNA; 1587 BP.  
 DE Nucleotide sequence of the cDNA clone BEF (HSXCK41).  
 PN W09831800-A2.  
 PD 23-JUL-1998.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (AUCK-) AUCKLAND UNISERVICES LTD.  
 Best Local Similarity: 24.06% Mismatches: 81  
 Query Match: 10.76% Indels: 48  
 RESULT 1068  
 ID ADB47730 standard; cDNA; 2753 BP.  
 DE Novel human secreted protein cDNA #3.  
 PN US2003054443-A1.  
 PD 20-MAR-2003.  
 PA (RUBE/) RUBEN S M.  
 PA (SOPP/) SOPPET D R.  
 PA (EBNE/) EBNER R.  
 PA (OLSE/) OLSEN H S.  
 PA (YOUN/) YOUNG P E.  
 PA (GREE/) GREENE J M.  
 PA (FERR/) FERRIE A M.  
 PA (YUGG/) YU G.  
 PA (NIJJ/) NI J.  
 PA (ROSE/) ROSEN C A.  
 PA (BREW/) BREWER L A.  
 PA (JANA/) JANAT F.  
 PA (BIRS/) BIRSE C E.  
 Best Local Similarity: 24.15% Mismatches: 93  
 Query Match: 10.71% Indels: 40  
 RESULT 1069  
 ID ADJ55285 standard; cDNA; 2753 BP.  
 DE Novel human secreted protein cDNA #3.  
 PN US20040423283-A1.  
 PD 05-FEB-2004.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 24.15% Mismatches: 93  
 Query Match: 10.71% Indels: 40  
 RESULT 1070  
 ID AAT05627 standard; cDNA; 3259 BP.  
 DE Bovine brevicain core protein cDNA.  
 PN W09526201-A1.  
 PD 05-OCT-1995.  
 PA (LJOL-) LA JOLLA CANCER RES FOUND.  
 Best Local Similarity: 24.64% Mismatches: 81  
 Query Match: 10.71% Indels: 47  
 RESULT 1071  
 ID ABL62702 standard; DNA; 11185 BP.  
 DE Colon adenocarcinoma related gene sequence SEQ ID NO:1039.  
 PN W0200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Best Local Similarity: 25.47% Mismatches: 69  
 Query Match: 10.53% Indels: 27  
 RESULT 1072  
 ID ABN96814 standard; DNA; 11185 BP.  
 DE Gene #3312 used to diagnose liver cancer.  
 PN W0200229103-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Best Local Similarity: 25.47% Mismatches: 69  
 Query Match: 10.53% Indels: 27  
 RESULT 1073  
 ID ADN95527 standard; DNA; 11185 BP.  
 DE Human BEC/LSC-related gene sequence SeqID450.  
 PN W02003080640-A1.  
 PD 02-OCT-2003.  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 PA (LICN ) LICENTIA LTD.  
 Best Local Similarity: 25.47% Mismatches: 69  
 Query Match: 10.53% Indels: 27  
 RESULT 1074  
 ID ADJ75063 standard; DNA; 11185 BP.

DE Marker gene SEQ ID NO:315.  
PN EPI394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Best Local Similarity: 25.47% Mismatches: 69  
Query Match: 10.53% Indels: 27  
RESULT 1075  
ID ADN04530 standard; cDNA; 11185 BP.  
DE Antiprosclerotic cDNA sequence #467.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 25.47% Mismatches: 69  
Query Match: 10.53% Indels: 27  
RESULT 1076  
ID ADP23737 standard; cDNA; 11185 BP.  
DE PRO polypeptide encoding cDNA SEQ ID NO:915.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 25.47% Mismatches: 69  
Query Match: 10.53% Indels: 27  
RESULT 1077  
ID AAS94985 standard; DNA; 12319 BP.  
DE Human DNA sequence #240 expressed during foam cell differentiation.  
PN WO200177389-A2.  
PD 18-OCT-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 25.47% Mismatches: 69  
Query Match: 10.53% Indels: 27  
RESULT 1078  
ID ADJ75926 standard; DNA; 7375 BP.  
DE Marker gene SEQ ID NO:1178.  
PN EPI394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Best Local Similarity: 28.93% Mismatches: 57  
Query Match: 10.49% Indels: 11  
RESULT 1079  
ID ABT08487 standard; cDNA; 8444 BP.  
DE Human novel protein NOVIA coding sequence SEQ ID NO: 1.  
PN WO200259315-A2.  
PD 01-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 24.00% Mismatches: 84  
Query Match: 10.31% Indels: 21  
RESULT 1080  
ID ADO09835 standard; cDNA; 8444 BP.  
DE Human NOVIA cDNA.  
PN US2004018970-A1.  
PD 29-JAN-2004.  
PA (SHIM/) SHIMKETS R A.  
PA (PATT/) PATTURAJAN M.  
PA (VERN/) VERNET C A M.  
PA (CASM/) CASMAN S J.  
PA (MALY/) MALYANKAR U M.  
PA (SHEN/) SHENOY S G.  
PA (SPYT/) SPYTEK K A.  
PA (GANG/) GANGOLLI E A.  
PA (MILL/) MILLER C E.  
PA (BOLD/) BOLDOS F L.  
PA (LILL/) LI L.  
PA (TAUP/) TAUPIER R J.  
PA (KEKU/) KEKUDA R.  
PA (SMIT/) SMITHSON G.  
PA (ZERH/) ZERHUSEN B D.  
PA (LLOX/) LIU X.  
PA (COLM/) COLMAN S D.  
PA (TCHE/) TCHERNEV V T.  
PA (SIJJ/) SI J.  
PA (EDIN/) EDINGER S R.  
PA (STON/) STONE D J.  
PA (SCIO/) SCIORE P.  
Mismatches: 82  
Indels: 27

PA (MILL/) MILLET I.  
PA (ROTH/) ROTHENBERG M E.  
Best Local Similarity: 24.00% Mismatches: 84  
Query Match: 10.31% Indels: 21  
RESULT 1081  
ID ACH29430 standard; cDNA; 410 BP.  
DE Human adult spleen cDNA #449.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Best Local Similarity: 32.39% Mismatches: 32  
Query Match: 10.27% Indels: 1  
RESULT 1082  
ID ABX34625 standard; cDNA; 1761 BP.  
DE Human mddt cDNA SEQ ID 186.  
PN WO200279449-A2.  
PD 10-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 23.79% Mismatches: 90  
Query Match: 10.27% Indels: 47  
RESULT 1083  
ID ADQ83195 standard; cDNA; 1771 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #9.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Best Local Similarity: 23.79% Mismatches: 90  
Query Match: 10.27% Indels: 47  
RESULT 1084  
ID AAQ57710 standard; DNA; 5191 BP.  
DE Neurocan DNA.  
PN WO9403601-A2.  
PD 17-FEB-1994.  
PA (UVNY) UNIV NEW YORK STATE.  
Best Local Similarity: 24.16% Mismatches: 74  
Query Match: 10.27% Indels: 39  
RESULT 1085  
ID ADQ38685 standard; DNA; 7291 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 348.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 24.18% Mismatches: 82  
Query Match: 10.27% Indels: 27  
RESULT 1086  
ID ADQ38687 standard; DNA; 7358 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 350.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 24.18% Mismatches: 82  
Query Match: 10.27% Indels: 27  
RESULT 1087  
ID ADQ38681 standard; DNA; 12553 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 344.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 24.18% Mismatches: 82  
Query Match: 10.27% Indels: 27  
RESULT 1088  
ID ADQ38682 standard; DNA; 12620 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 345.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 24.18% Mismatches: 82  
Query Match: 10.27% Indels: 27

Query Match: 10.27% Indels: 27  
RESULT 1089  
ID ADH87060 standard; cDNA; 1783 BP.  
DE Human protein encoding cDNA SEQ ID NO:153.  
PN WO2004009834-A2.  
PD 29-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Best Local Similarity: 22.49% Mismatches: 63  
Query Match: 10.13% Indels: 82  
RESULT 1090  
ID AAA63526 standard; DNA; 285 BP.  
DE DNA encoding the domain of hyaluronic acid which interacts with CD44.  
PN WO200047163-A2.  
PD 17-AUG-2000.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
Best Local Similarity: 27.10% Mismatches: 36  
Query Match: 10.09% Indels: 27  
RESULT 1091  
ID ABA02881 standard; cDNA; 2087 BP.  
DE Human versican isoform V3 encoding cDNA SEQ ID NO 1.  
PN WO200179284-A2.  
PD 25-OCT-2001.  
PA (WIGH/) WIGHT T N.  
PA (MERR/) MERRILLES M.  
Best Local Similarity: 29.75% Mismatches: 57  
Query Match: 10.04% Indels: 11  
RESULT 1092  
ID ADQ38683 standard; DNA; 4330 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 346.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 29.75% Mismatches: 57  
Query Match: 10.04% Indels: 11  
RESULT 1093  
ID ACH04002 standard; cDNA; 7182 BP.  
DE Human cDNA differentially expressed in lung cancer #207.  
PN US2003065157-A1.  
PD 03-APR-2003.  
PA (LASE/) LASEK A W.  
Best Local Similarity: 29.75% Mismatches: 57  
Query Match: 10.04% Indels: 11  
RESULT 1094  
ID AAQ12261 standard; cDNA; 8224 BP.  
DE Versican gene.  
PN WO9108230-A.  
PD 13-JUN-1991.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
Best Local Similarity: 29.75% Mismatches: 57  
Query Match: 10.04% Indels: 11  
RESULT 1095  
ID ABT11088 standard; cDNA; 8224 BP.  
DE Human breast cancer associated coding sequence SEQ ID NO: 1222.  
PN WO200259271-A2.  
PD 01-AUG-2002.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 29.75% Mismatches: 57  
Query Match: 10.04% Indels: 11  
RESULT 1096  
ID ACC50121 standard; cDNA; 8224 BP.  
DE Breast cancer associated cDNA sequence SEQ ID NO:89.  
PN WO2003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Best Local Similarity: 29.75% Mismatches: 57  
Query Match: 10.04% Indels: 11  
RESULT 1097  
ID ADO38686 standard; DNA; 9592 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 349.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.

Best Local Similarity: 29.75% Mismatches: 57  
Query Match: 10.04% Indels: 11  
RESULT 1098  
ID ACN89856 standard; DNA; 9647 BP.  
DE Breast cancer related marker, seq id 11006.  
PN US200309974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Best Local Similarity: 29.75% Mismatches: 57  
Query Match: 10.04% Indels: 11  
RESULT 1099  
ID ADQ38684 standard; DNA; 9659 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 347.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 29.75% Mismatches: 57  
Query Match: 10.04% Indels: 11  
RESULT 1100  
ID ADP71272 standard; DNA; 573 BP.  
DE Human LP2 B-B' domain gene region SeqID7.  
PN JP2004154038-A.  
PD 03-JUN-2004.  
PA (SEKG) SEIKAGAKU KOGYO CO LTD.  
Best Local Similarity: 26.62% Mismatches: 58  
Query Match: 10.00% Indels: 29  
RESULT 1101  
ID ABA08490 standard; cDNA; 972 BP.  
DE Human cDNA SEQ ID NO: 156.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 25.66% Mismatches: 66  
Query Match: 10.00% Indels: 25  
RESULT 1102  
ID ABV83827 standard; cDNA; 972 BP.  
DE Human polynucleotide SEQ ID NO 156.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Best Local Similarity: 25.66% Mismatches: 66  
Query Match: 10.00% Indels: 25  
RESULT 1103  
ID ADO09967 standard; cDNA; 3256 BP.  
DE Human NOVIC cDNA.  
PN US2004018970-A1.  
PD 29-JAN-2004.  
PA (SHIM/) SHINKETS R A.  
PA (PATT/) PATTURAJAN M.  
PA (VERN/) VERNET C A M.  
PA (CASM/) CASMAN S J.  
PA (MALY/) MALYANKAR U M.  
PA (SHEN/) SHENOY S G.  
PA (SPYT/) SPYTEK K A.  
PA (GANG/) GANGOLLI E A.  
PA (MILL/) MILLER C E.  
PA (BOLD/) BOLDOG F L.  
PA (LILL/) LI L.  
PA (TAUP/) TAUPIER R J.  
PA (KEKU/) KEKUDA R.  
PA (SMIT/) SMITHSON G.  
PA (ZERH/) ZERHUSEN B D.  
PA (LIUX/) LIU X.  
PA (COLM/) COLMAN S D.  
PA (TCHE/) TCHERNEV V T.  
PA (SIJJ/) SI J.  
PA (EDIN/) EDINGER S R.  
PA (STON/) STONE D J.  
PA (SCIO/) SCIORE P.  
PA (MILL/) MILLET I.  
PA (ROTH/) ROTHENBERG M E.

Best Local Similarity: 25.15% Mismatches: 84  
Query Match: 10.00% Indels: 20  
RESULT 1104  
ID ABO08489 standard; cDNA; 3260 BP.  
DE Human novel protein NOV9c coding sequence SEQ ID NO: 210.  
PN WO200259315-A2.  
PD 01-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 25.15% Mismatches: 84  
Query Match: 10.00% Indels: 20  
RESULT 1105  
ID ADH71311 standard; DNA; 3260 BP.  
DE Human gene of the invention NOV9a SEQ ID NO:207.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 25.15% Mismatches: 84  
Query Match: 10.00% Indels: 20  
RESULT 1106  
ID ADH71355 standard; DNA; 4527 BP.  
DE Human gene of the invention NOV9w SEQ ID NO:251.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 25.15% Mismatches: 84  
Query Match: 10.00% Indels: 20  
RESULT 1107  
ID ABA04662 standard; cDNA; 4576 BP.  
DE Human Hyaluronic Acid Receptor for Endocytosis, HARE, coding sequence.  
PN WO200181544-A2.  
PD 01-NOV-2001.  
PA (WEIG/) WEIGEL P A.  
PA (ZHOU/) ZHOU B.  
PA (WEIG/) WEIGEL J A.  
Best Local Similarity: 25.15% Mismatches: 84  
Query Match: 10.00% Indels: 20  
RESULT 1108  
ID ABX13822 standard; cDNA; 4642 BP.  
DE cDNA encoding human 190kDa Hyaluronan receptor for endocytosis #1.  
PN WO200286093-A2.  
PD 31-OCT-2002.  
PA (WEIG/) WEIGEL P H.  
PA (WEIG/) WEIGEL J A.  
Best Local Similarity: 25.15% Mismatches: 84  
Query Match: 10.00% Indels: 20  
RESULT 1109  
ID ABX13823 standard; cDNA; 4962 BP.  
DE cDNA encoding human 190kDa Hyaluronan receptor for endocytosis #2.  
PN WO200286093-A2.  
PD 31-OCT-2002.  
PA (WEIG/) WEIGEL P H.  
PA (WEIG/) WEIGEL J A.  
Best Local Similarity: 25.15% Mismatches: 84  
Query Match: 10.00% Indels: 20  
RESULT 1110  
ID ADH71357 standard; DNA; 5416 BP.  
DE Human gene of the invention NOV9x SEQ ID NO:253.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 25.15% Mismatches: 84  
Query Match: 10.00% Indels: 20  
RESULT 1111  
ID ADM90626 standard; DNA; 5688 BP.  
DE Human DNA encoding a pharmaceutically useful protein SeqID 19.  
PN WO2004020595-A2.  
PD 11-MAR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.  
PA (DNAF-) DNAFORM KK.  
Best Local Similarity: 25.15% Mismatches: 84  
Query Match: 10.00% Indels: 20  
RESULT 1112

ID ADM91044 standard; DNA; 5688 BP.  
DE Human DNA encoding a pharmaceutically useful protein SeqID 437.  
PN WO2004020595-A2.  
PD 11-MAR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.  
PA (DNAF-) DNAFORM KK.  
Best Local Similarity: 25.15% Mismatches: 84  
Query Match: 10.00% Indels: 20  
RESULT 1113  
ID ADH71359 standard; DNA; 7670 BP.  
DE Human gene of the invention NOV9y SEQ ID NO:255.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 25.15% Mismatches: 84  
Query Match: 10.00% Indels: 20  
RESULT 1114  
ID ADF71270 standard; DNA; 600 BP.  
DE Human aggrecan B-B' domain gene region SeqID5.  
PN JP2004154038-A.  
PD 03-JUN-2004.  
PA (SEK) SEIKAGAKU KOGYO CO LTD.  
Best Local Similarity: 37.36% Mismatches: 35  
Query Match: 9.87% Indels: 14  
RESULT 1115  
ID AAV34196 standard; DNA; 1720 BP.  
DE Human secreted protein gene 43 clone HSXCK41.  
PN WO9839446-A2.  
PD 11-SEP-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 23.94% Mismatches: 80  
Query Match: 9.87% Indels: 49  
RESULT 1116  
ID ACD08067 standard; cDNA; 1720 BP.  
DE cDNA encoding novel human secreted protein #43.  
PN US2003027132-A1.  
PD 06-FEB-2003.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (FISC/) FISCHER C L.  
PA (SOPP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D R.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN R.  
PA (HUJJ/) HU J.  
PA (FLOR/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
PA (SHIY/) SHI Y.  
Best Local Similarity: 23.94% Mismatches: 80  
Query Match: 9.87% Indels: 49  
RESULT 1117  
ID AAF87120 standard; DNA; 3625 BP.  
DE NOV9 coding sequence.  
PN WO200136638-A2.  
PD 25-MAY-2001.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 24.87% Mismatches: 93  
Query Match: 9.87% Indels: 28  
RESULT 1118  
ID ADH71325 standard; DNA; 3625 BP.  
DE Human gene of the invention NOV9h SEQ ID NO:221.  
PN WO2003102155-A2.  
PD 11-DEC-2003.

PA (CURA-) CURAGEN CORP. Mismatches: 93  
 Best Local Similarity: 24.87% Indels: 28  
 Query Match: 9.87%  
 RESULT 1119  
 ID ABT08488 standard; cDNA; 8495 BP.  
 DE Human novel protein NOV1b coding sequence SEQ ID NO: 3.  
 PN WO200259315-A2.  
 PD 01-AUG-2002.  
 PA (CURA-) CURAGEN CORP. Mismatches: 93  
 Best Local Similarity: 24.87% Indels: 28  
 Query Match: 9.87%  
 RESULT 1120  
 ID ADH71331 standard; DNA; 8495 BP.  
 DE Human Gene of the invention NOV9k SEQ ID NO:227.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP. Mismatches: 93  
 Best Local Similarity: 24.87% Indels: 28  
 Query Match: 9.87%  
 RESULT 1121  
 ID ADO09837 standard; cDNA; 8495 BP.  
 DE Human NOV1b cDNA.  
 PN US2004018970-A1.  
 PD 29-JAN-2004.  
 PA (SHIM/) SHIMKETS R A.  
 PA (PATT/) PATTURAJAN M.  
 PA (VERN/) VERNET C A M.  
 PA (CASM/) CASMAN S J.  
 PA (MALY/) MALYANKAR U M.  
 PA (SHEN/) SHENOY S G.  
 PA (SPY/) SPYTEK K A.  
 PA (GANG/) GANGOLLI E A.  
 PA (MILL/) MILLER C E.  
 PA (BOLD/) BOLDOG F L.  
 PA (LILL/) LI L.  
 PA (TAUP/) TAUPIER R J.  
 PA (KEKU/) KEKUDA R.  
 PA (SMIT/) SMITHSON G.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (LIUX/) LIU X.  
 PA (COLM/) COLMAN S D.  
 PA (TCHE/) TCHERNEV V T.  
 PA (SIJJ/) SI J.  
 PA (EDIN/) EDINGER S R.  
 PA (STON/) STONE D J.  
 PA (SCIO/) SCIORE P.  
 PA (MILL/) MILLET I.  
 PA (ROTH/) ROTHENBERG M E.  
 Best Local Similarity: 24.87% Mismatches: 93  
 Query Match: 9.87% Indels: 28  
 RESULT 1122  
 ID AA57365 standard; DNA; 1259 BP.  
 DE DNA encoding a human hyaluronan-binding protein, designated BM-HABP.  
 PN WO200039166-A1.  
 PD 06-JUL-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (AMNA-) AMERICAN NAT RED CROSS.  
 Best Local Similarity: 24.56% Mismatches: 85  
 Query Match: 9.73% Indels: 20  
 RESULT 1123  
 ID AAD08974 standard; cDNA; 1354 BP.  
 DE Alternative version of human TNF stimulated gene-6 (TSG-6) cDNA.  
 PN US6210905-B1.  
 PD 03-APR-2001.  
 PA (UUNY) UNIV NEW YORK STATE.  
 Best Local Similarity: 26.79% Mismatches: 78  
 Query Match: 9.73% Indels: 16  
 RESULT 1124  
 ID ABT42226 standard; DNA; 5191 BP.  
 DE Toxicity modelling related rat gene SEQ ID No 1928.  
 PN WO200295000-A2.  
 PD 28-NOV-2002.  
 PA (GENE-) GENE LOGIC INC. Mismatches: 74

Best Local Similarity: 23.60% Mismatches: 75  
 Query Match: 9.73% Indels: 39  
 RESULT 1125  
 ID ADO31199 standard; DNA; 5191 BP.  
 DE Rat neurocan gene for glucosaminoglycan reduction in glial scars.  
 PN WO2004041197-A2.  
 PD 21-MAY-2004.  
 PA (UYCA-) UNIV CASE WESTERN RESERVE.  
 Best Local Similarity: 23.60% Mismatches: 75  
 Query Match: 9.73% Indels: 39  
 RESULT 1126  
 ID ACC49518 standard; cDNA; 6310 BP.  
 DE Tumour-associated antigenic target protein TAT185 cDNA SEQ ID NO:26.  
 PN WO2003024392-A2.  
 PD 27-MAR-2003.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 21.43% Mismatches: 92  
 Query Match: 9.69% Indels: 54  
 RESULT 1127  
 ID ADN38943 standard; cDNA; 6310 BP.  
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:261.  
 PN WO2003042661-A2.  
 PD 22-MAY-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Best Local Similarity: 21.43% Mismatches: 92  
 Query Match: 9.69% Indels: 54  
 RESULT 1128  
 ID ADO31195 standard; DNA; 6310 BP.  
 DE Human neurocan gene for glucosaminoglycan reduction in glial scars.  
 PN WO2004041197-A2.  
 PD 21-MAY-2004.  
 PA (UYCA-) UNIV CASE WESTERN RESERVE.  
 Best Local Similarity: 21.43% Mismatches: 92  
 Query Match: 9.69% Indels: 54  
 RESULT 1129  
 ID ADP71268 standard; DNA; 585 BP.  
 DE Human LP1 B-B' domain gene region SeqID3.  
 PN JP2004154038-A.  
 PD 03-JUN-2004.  
 PA (SEKG) SEIKAGAKU KOGYO CO LTD.  
 Best Local Similarity: 33.33% Mismatches: 44  
 Query Match: 9.60% Indels: 7  
 RESULT 1130  
 ID ADL13630 standard; DNA; 1065 BP.  
 DE Osteoarthritis-associated polymorphic nucleotide #162.  
 PN WO2003054166-A2.  
 PD 03-JUL-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 28.57% Mismatches: 52  
 Query Match: 9.60% Indels: 8  
 RESULT 1131  
 ID AET43880 standard; DNA; 1492 BP.  
 DE 15IP3D4 v-1 DNA clone-1 from placenta.  
 PN WO200283860-A2.  
 PD 24-OCT-2002.  
 PA (AGEN-) AGENSYS INC.  
 Best Local Similarity: 28.57% Mismatches: 52  
 Query Match: 9.60% Indels: 8  
 RESULT 1132  
 ID ABT43881 standard; DNA; 1492 BP.  
 DE DNA derived from mRNA of human cartilage link protein.  
 PN WO200283860-A2.  
 PD 24-OCT-2002.  
 PA (AGEN-) AGENSYS INC.  
 Best Local Similarity: 28.57% Mismatches: 52  
 Query Match: 9.60% Indels: 8  
 RESULT 1133  
 ID AAS28787 standard; cDNA; 1640 BP.  
 DE Human immunoglobulin encoding cDNA SEQ ID No 33.  
 PN WO200155315-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 74  
 Best Local Similarity: 25.83%

Query Match:	9.60%	Indels:	22
RESULT 1134			
ID ABA06583 standard; cDNA; 1640 BP.			
DE Human cDNA SEQ ID NO: 249.			
PN WO200154474-A2.			
PD 02-AUG-2001.			
PA (HUMA-) HUMAN GENOME SCI INC.			
Best Local Similarity: 25.83%		Mismatches:	74
Query Match:	9.60%	Indels:	22
RESULT 1135			
ID ABV83920 standard; cDNA; 1640 BP.			
DE Human polynucleotide SEQ ID NO 249.			
PN US2002090672-A1.			
PD 11-JUL-2002.			
PA (ROSE/) ROSEN C A.			
PA (RUBE/) RUBEN S M.			
PA (BARA/) BARASH S C.			
Best Local Similarity: 25.83%		Mismatches:	74
Query Match:	9.60%	Indels:	22
RESULT 1136			
ID ADB31512 standard; cDNA; 1640 BP.			
DE Human cDNA encoding a novel protein SEQ ID NO 33.			
PN US2003077606-A1.			
PD 24-APR-2003.			
PA (HUMA-) HUMAN GENOME SCI INC.			
Best Local Similarity: 25.83%		Mismatches:	74
Query Match:	9.60%	Indels:	22
RESULT 1137			
ID AAS28848 standard; cDNA; 1641 BP.			
DE Human immunoglobulin encoding cDNA SEQ ID NO 94.			
PN WO200155315-A2.			
PD 02-AUG-2001.			
PA (HUMA-) HUMAN GENOME SCI INC.			
Best Local Similarity: 25.83%		Mismatches:	74
Query Match:	9.60%	Indels:	22
RESULT 1138			
ID ABA06754 standard; cDNA; 1641 BP.			
DE Human cDNA SEQ ID NO: 420.			
PN WO200154474-A2.			
PD 02-AUG-2001.			
PA (HUMA-) HUMAN GENOME SCI INC.			
Best Local Similarity: 25.83%		Mismatches:	74
Query Match:	9.60%	Indels:	22
RESULT 1139			
ID ABV84091 standard; cDNA; 1641 BP.			
DE Human polynucleotide SEQ ID NO 420.			
PN US2002090672-A1.			
PD 11-JUL-2002.			
PA (ROSE/) ROSEN C A.			
PA (RUBE/) RUBEN S M.			
PA (BARA/) BARASH S C.			
Best Local Similarity: 25.83%		Mismatches:	74
Query Match:	9.60%	Indels:	22
RESULT 1140			
ID ADB31573 standard; cDNA; 1641 BP.			
DE Human cDNA encoding a novel protein SEQ ID NO 94.			
PN US2003077606-A1.			
PD 24-APR-2003.			
PA (HUMA-) HUMAN GENOME SCI INC.			
Best Local Similarity: 25.83%		Mismatches:	74
Query Match:	9.60%	Indels:	22
RESULT 1141			
ID ADH71347 standard; DNA; 1668 BP.			
DE Human gene of the invention NOV9s SEQ ID NO:243.			
PN WO2003102155-A2.			
PD 11-DEC-2003.			
PA (CURA-) CURAGEN CORP.			
Best Local Similarity: 29.21%		Mismatches:	44
Query Match:	9.60%	Indels:	2
RESULT 1142			
ID ADL13629 standard; DNA; 1759 BP.			
DE Osteoarthritis-associated polymorphic nucleotide #161.			
PN WO2003054166-A2.			

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PD 03-JUL-2003.			
PA (INCY-) INCYTE GENOMICS INC.			
Best Local Similarity: 28.57%		Mismatches:	52
Query Match:	9.60%	Indels:	8
RESULT 1143			
ID ABT43866 standard; DNA; 1957 BP.			
DE DNA of transcript variant 151P3D4 v-1.			
PN WO200283860-A2.			
PD 24-OCT-2002.			
PA (AGEN-) AGENSYS INC.			
Best Local Similarity: 28.57%		Mismatches:	52
Query Match:	9.60%	Indels:	8
RESULT 1144			
ID ABT43869 standard; cDNA; 1957 BP.			
DE 151P3D4 v-1 cDNA clone-1 from placenta.			
PN WO200283860-A2.			
PD 24-OCT-2002.			
PA (AGEN-) AGENSYS INC.			
Best Local Similarity: 28.57%		Mismatches:	52
Query Match:	9.60%	Indels:	8
RESULT 1145			
ID ABT43878 standard; cDNA; 1957 BP.			
DE 151P3D4 v-10 cDNA clone-1 from placenta.			
PN WO200283860-A2.			
PD 24-OCT-2002.			
PA (AGEN-) AGENSYS INC.			
Best Local Similarity: 28.57%		Mismatches:	52
Query Match:	9.60%	Indels:	8
RESULT 1146			
ID ABT43877 standard; cDNA; 1957 BP.			
DE 151P3D4 v-9 cDNA clone-1 from placenta.			
PN WO200283860-A2.			
PD 24-OCT-2002.			
PA (AGEN-) AGENSYS INC.			
Best Local Similarity: 28.57%		Mismatches:	52
Query Match:	9.60%	Indels:	8
RESULT 1147			
ID ABT43879 standard; cDNA; 1957 BP.			
DE 151P3D4 v-11 cDNA clone-1 from placenta.			
PN WO200283860-A2.			
PD 24-OCT-2002.			
PA (AGEN-) AGENSYS INC.			
Best Local Similarity: 28.57%		Mismatches:	52
Query Match:	9.60%	Indels:	8
RESULT 1148			
ID ABT43874 standard; cDNA; 1957 BP.			
DE 151P3D4 v-6 cDNA clone-1 from placenta.			
PN WO200283860-A2.			
PD 24-OCT-2002.			
PA (AGEN-) AGENSYS INC.			
Best Local Similarity: 28.57%		Mismatches:	52
Query Match:	9.60%	Indels:	8
RESULT 1149			
ID ABT43876 standard; cDNA; 1957 BP.			
DE 151P3D4 v-8 cDNA clone-1 from placenta.			
PN WO200283860-A2.			
PD 24-OCT-2002.			
PA (AGEN-) AGENSYS INC.			
Best Local Similarity: 28.57%		Mismatches:	52
Query Match:	9.60%	Indels:	8
RESULT 1150			
ID ABT43871 standard; cDNA; 1957 BP.			
DE 151P3D4 v-3 cDNA clone-1 from placenta.			
PN WO200283860-A2.			
PD 24-OCT-2002.			
PA (AGEN-) AGENSYS INC.			
Best Local Similarity: 28.57%		Mismatches:	52
Query Match:	9.60%	Indels:	8
RESULT 1151			
ID ABT43872 standard; cDNA; 1957 BP.			
DE 151P3D4 v-4 cDNA clone-1 from placenta.			
PN WO200283860-A2.			
PD 24-OCT-2002.			

PA (AGEN-) AGENSYS INC.					
Best Local Similarity: 28.57%	Mismatches: 52				
Query Match: 9.60%	Indels: 8				
RESULT 1152					
ID ABT43873 standard; cDNA; 1957 BP.					
DE 151P3D4 v-5 cDNA clone-1 from placenta.					
PN WO200283860-A2.					
PD 24-OCT-2002.					
PA (AGEN-) AGENSYS INC.					
Best Local Similarity: 28.57%	Mismatches: 52				
Query Match: 9.60%	Indels: 8				
RESULT 1153					
ID ABT43875 standard; cDNA; 1957 BP.					
DE 151P3D4 v-7 cDNA clone-1 from placenta.					
PN WO200283860-A2.					
PD 24-OCT-2002.					
PA (AGEN-) AGENSYS INC.					
Best Local Similarity: 28.57%	Mismatches: 52				
Query Match: 9.60%	Indels: 8				
RESULT 1154					
ID ABT43870 standard; cDNA; 2166 BP.					
DE 151P3D4 v-2 cDNA clone-1 from placenta.					
PN WO200283860-A2.					
PD 24-OCT-2002.					
PA (AGEN-) AGENSYS INC.					
Best Local Similarity: 28.57%	Mismatches: 52				
Query Match: 9.60%	Indels: 8				
RESULT 1155					
ID ABT43865 standard; DNA; 2166 BP.					
DE DNA of transcript variant 151P3D4 v-2.					
PN WO200283860-A2.					
PD 24-OCT-2002.					
PA (AGEN-) AGENSYS INC.					
Best Local Similarity: 28.57%	Mismatches: 52				
Query Match: 9.60%	Indels: 8				
RESULT 1156					
ID ABT43867 standard; DNA; 2166 BP.					
DE DNA of transcript variant 151P3D4 v-2.					
PN WO200283860-A2.					
PD 24-OCT-2002.					
PA (AGEN-) AGENSYS INC.					
Best Local Similarity: 28.57%	Mismatches: 52				
Query Match: 9.60%	Indels: 8				
RESULT 1157					
ID AQD24054 standard; DNA; 2538 BP.					
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6874.					
PN WO2004048938-A2.					
PD 10-JUN-2004.					
PA (PROT-) PROTEIN DESIGN LABS INC.					
Best Local Similarity: 28.57%	Mismatches: 52				
Query Match: 9.60%	Indels: 8				
RESULT 1158					
ID ADH71333 standard; DNA; 1599 BP.					
DE Human gene of the invention NOV91 SEQ ID NO:229.					
PN WO2003102155-A2.					
PD 11-DEC-2003.					
PA (CURA-) CURAGEN CORP.					
Best Local Similarity: 29.21%	Mismatches: 45				
Query Match: 9.51%	Indels: 2				
RESULT 1159					
ID ADH71335 standard; DNA; 1611 BP.					
DE Human gene of the invention NOV9m SEQ ID NO:231.					
PN WO2003102155-A2.					
PD 11-DEC-2003.					
PA (CURA-) CURAGEN CORP.					
Best Local Similarity: 29.21%	Mismatches: 45				
Query Match: 9.51%	Indels: 2				
RESULT 1160					
ID ADH71313 standard; DNA; 1668 BP.					
DE Human gene of the invention NOV9b SEQ ID NO:209.					
PN WO2003102155-A2.					
PD 11-DEC-2003.					
PA (CURA-) CURAGEN CORP.					

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Best Local Similarity: 29.21%	Mismatches: 45				
Query Match: 9.51%	Indels: 2				
RESULT 1161					
ID ADH71353 standard; DNA; 1668 BP.					
DE Human gene of the invention NOV9v SEQ ID NO:249.					
PN WO2003102155-A2.					
PD 11-DEC-2003.					
PA (CURA-) CURAGEN CORP.					
Best Local Similarity: 29.21%	Mismatches: 45				
Query Match: 9.51%	Indels: 2				
RESULT 1162					
ID ADH71341 standard; DNA; 1668 BP.					
DE Human gene of the invention NOV9p SEQ ID NO:237.					
PN WO2003102155-A2.					
PD 11-DEC-2003.					
PA (CURA-) CURAGEN CORP.					
Best Local Similarity: 29.21%	Mismatches: 45				
Query Match: 9.51%	Indels: 2				
RESULT 1163					
ID ADH71345 standard; DNA; 1668 BP.					
DE Human gene of the invention NOV9r SEQ ID NO:241.					
PN WO2003102155-A2.					
PD 11-DEC-2003.					
PA (CURA-) CURAGEN CORP.					
Best Local Similarity: 29.21%	Mismatches: 45				
Query Match: 9.51%	Indels: 2				
RESULT 1164					
ID ADH71339 standard; DNA; 1668 BP.					
DE Human gene of the invention NOV9o SEQ ID NO:235.					
PN WO2003102155-A2.					
PD 11-DEC-2003.					
PA (CURA-) CURAGEN CORP.					
Best Local Similarity: 29.21%	Mismatches: 45				
Query Match: 9.51%	Indels: 2				
RESULT 1165					
ID ADH71349 standard; DNA; 1668 BP.					
DE Human gene of the invention NOV9t SEQ ID NO:245.					
PN WO2003102155-A2.					
PD 11-DEC-2003.					
PA (CURA-) CURAGEN CORP.					
Best Local Similarity: 29.21%	Mismatches: 45				
Query Match: 9.51%	Indels: 2				
RESULT 1166					
ID ADH71343 standard; DNA; 1668 BP.					
DE Human gene of the invention NOV9q SEQ ID NO:239.					
PN WO2003102155-A2.					
PD 11-DEC-2003.					
PA (CURA-) CURAGEN CORP.					
Best Local Similarity: 29.21%	Mismatches: 45				
Query Match: 9.51%	Indels: 2				
RESULT 1167					
ID ABA83182 standard; DNA; 1851 BP.					
DE HOST-4 ovarian tumour marker gene sequence, SEQ ID NO:144.					
PN WO200175177-A2.					
PD 11-OCT-2001.					
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.					
Best Local Similarity: 33.71%	Mismatches: 41				
Query Match: 9.51%	Indels: 4				
RESULT 1168					
ID AAF87113 standard; DNA; 2011 BP.					
DE NOV2 coding sequence.					
PN WO200136638-A2.					
PD 25-MAY-2001.					
PA (CURA-) CURAGEN CORP.					
Best Local Similarity: 25.14%	Mismatches: 84				
Query Match: 9.51%	Indels: 22				
RESULT 1169					
ID ADH71315 standard; DNA; 2011 BP.					
DE Human gene of the invention NOV9c SEQ ID NO:211.					
PN WO2003102155-A2.					
PD 11-DEC-2003.					
PA (CURA-) CURAGEN CORP.					
Best Local Similarity: 25.14%	Mismatches: 84				



Query Match: 9.51% Indels: 22  
RESULT 1170  
ID AD031201 standard; DNA; 5259 BP.  
DE Mouse neurocan gene for glucosaminoglycan reduction in glial scars.  
PN WO2004041197-A2.  
PD 21-MAY-2004.  
PA (UYCA-) UNIV CASE WESTERN RESERVE.  
Best Local Similarity: 26.21% Mismatches: 44  
Query Match: 9.51% Indels: 16  
RESULT 1171  
ID AD045269 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6932.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.86% Mismatches: 24  
Query Match: 9.42% Indels: 2  
RESULT 1172  
ID AD045261 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6924.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.86% Mismatches: 24  
Query Match: 9.42% Indels: 2  
RESULT 1173  
ID AD045247 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6910.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.86% Mismatches: 24  
Query Match: 9.42% Indels: 2  
RESULT 1174  
ID AD045220 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6883.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.86% Mismatches: 24  
Query Match: 9.42% Indels: 2  
RESULT 1175  
ID AD045210 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6873.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.86% Mismatches: 24  
Query Match: 9.42% Indels: 2  
RESULT 1176  
ID AD045303 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6966.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.86% Mismatches: 24  
Query Match: 9.42% Indels: 2  
RESULT 1177  
ID AD045335 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6998.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.86% Mismatches: 24  
Query Match: 9.42% Indels: 2  
RESULT 1178  
ID AD045230 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6893.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.86% Mismatches: 24  
Query Match: 9.42% Indels: 2

RESULT 1179  
ID AD045293 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6956.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.86% Mismatches: 24  
Query Match: 9.42% Indels: 2  
RESULT 1180  
ID AD045313 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6976.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 42.86% Mismatches: 24  
Query Match: 9.42% Indels: 2  
RESULT 1181  
ID ADP71266 standard; DNA; 600 BP.  
DE Human versican B-B' domain gene region SeqID1.  
PN JP2004154038-A.  
PD 03-JUN-2004.  
PA (SEK) SEIKAGAKU KOGYO CO LTD.  
Best Local Similarity: 32.63% Mismatches: 43  
Query Match: 9.42% Indels: 9  
RESULT 1182  
ID ADH71337 standard; DNA; 1668 BP.  
DE Human gene of the invention NOV9n SEQ ID NO:233.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 29.21% Mismatches: 46  
Query Match: 9.42% Indels: 2  
RESULT 1183  
ID AAA61263 standard; DNA; 1308 BP.  
DE Human secreted protein gene 4 clone HFXHC41.  
PN WO200029422-A1.  
PD 25-MAY-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 28.87% Mismatches: 50  
Query Match: 9.38% Indels: 35  
RESULT 1184  
ID ADQ38559 standard; DNA; 3858 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 222.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 22.28% Mismatches: 91  
Query Match: 9.38% Indels: 31  
RESULT 1185  
ID ACN44758 standard; DNA; 172569 BP.  
DE Human genomic sequence hCG20145.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 34.21% Mismatches: 35  
Query Match: 9.29% Indels: 1  
RESULT 1186  
ID ADR24283 standard; DNA; 484 BP.  
DE Breast cancer prognosis marker #144.  
PN WO2004065545-A2.  
PD 03-AUG-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
PA (NECA-) NETHERLANDS CANCER INST.  
Best Local Similarity: 20.71% Mismatches: 61  
Query Match: 9.24% Indels: 28  
RESULT 1187  
ID ADH71351 standard; DNA; 1668 BP.  
DE Human gene of the invention NOV9u SEQ ID NO:247.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 29.21% Mismatches: 46  
Query Match: 9.24% Indels: 2

RESULT 1188  
ID ADN41609 standard; DNA; 4767 BP.  
DE Novel human secreted protein polynucleotide seqid 731.  
PN US2004044191-A1.  
PD 04-MAR-2004.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) Soppet D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIYY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAFLE/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (OLSE/) OLSEN H.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.  
Best Local Similarity: 33.33% Mismatches: 46  
Query Match: 9.24% Indels: 13  
RESULT 1189  
ID ADN41608 standard; DNA; 4768 BP.  
DE Novel human secreted protein polynucleotide seqid 730.  
PN US2004044191-A1.  
PD 04-MAR-2004.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) Soppet D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIYY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAFLE/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (OLSE/) OLSEN H.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.  
Best Local Similarity: 33.33% Mismatches: 46  
Query Match: 9.24% Indels: 13  
RESULT 1190  
ID ABL27120 standard; DNA; 8433 BP.  
DE Drosophila melanogaster genomic polynucleotide seq ID NO 32833.  
PN WO200171042-A2.  
PD 27-SEP-2001  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 31.01% Mismatches: 39  
Query Match: 9.20% Indels: 42  
RESULT 1191  
ID ADF80106 standard; DNA; 402 BP.  
DE Leukaemia-related DNA sequence #662.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
PA (HAFE/) HAFELACH T.  
PA (SCHO/) SCHOCH C.  
PA (KERN/) KERN W.  
Best Local Similarity: 32.26% Mismatches: 30  
Query Match: 9.16% Indels: 0  
RESULT 1192  
ID AAT01476 standard; cDNA; 1519 BP.  
DE Cat brain-enriched hyaluronan binding protein cDNA.  
PN WO9527785-A1.  
PD 19-OCT-1995.  
PA (UYYA ) UNIV YALE.  
Best Local Similarity: 21.74% Mismatches: 87  
Query Match: 9.16% Indels: 82  
RESULT 1193  
ID ACN42085 standard; cDNA; 4391 BP.  
DE Human diagnostic and therapeutic polynucleotide seq ID NO:960.  
PN WO2004023973-A2.  
PD 25-MAR-2004.

PA (INCY-) INCYTE CORP.  
Best Local Similarity: 25.00% Mismatches: 51  
Query Match: 9.16% Indels: 14  
RESULT 1194  
ID ACN42084 standard; cDNA; 4536 BP.  
DE Human diagnostic and therapeutic polynucleotide seq ID NO:959.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 25.00% Mismatches: 51  
Query Match: 9.16% Indels: 14  
RESULT 1195  
ID ACA55632 standard; cDNA; 1482 BP.  
DE Human signalling pathway polynucleotide probe seq ID NO 230.  
PN US6500938-B1.  
PD 31-DEC-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 24.15% Mismatches: 92  
Query Match: 9.11% Indels: 41  
RESULT 1196  
ID ADI55428 standard; DNA; 1482 BP.  
DE Human polynucleotide probe #230.  
PN US2004010136-A1.  
PD 15-JAN-2004.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 24.15% Mismatches: 92  
Query Match: 9.11% Indels: 41  
RESULT 1197  
ID AAV34254 standard; DNA; 1962 BP.  
DE Human secreted protein gene 43 clone HSXCK41.  
PN WO9839446-A2.  
PD 11-SEP-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 24.88% Mismatches: 81  
Query Match: 9.11% Indels: 48  
RESULT 1198  
ID ACD08125 standard; cDNA; 1962 BP.  
DE cDNA encoding novel human secreted protein #101.  
PN US2003027132-A1.  
PD 08-FEB-2003.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (FISC/) FISCHER C L.  
PA (SOPP/) Soppet D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D R.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJU/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN R.  
PA (HUJU/) HU J.  
PA (FLOR/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
PA (SHIY/) SHI Y.  
Best Local Similarity: 24.88% Mismatches: 81  
Query Match: 9.11% Indels: 48  
RESULT 1199  
ID ACH79577 standard; DNA; 538 BP.  
DE Human genome derived single exon probe #12772.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENNV/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Best Local Similarity: 26.88% Mismatches: 44  
Query Match: 8.98% Indels: 8  
RESULT 1200

ID AAT01475 standard; cDNA; 1084 BP.  
 DE Rat brain-enriched hyaluronan binding protein cDNA.  
 PN WO95227785-A1.  
 PD 19-OCT-1995.  
 PA (UYUA) UNIV YALE.  
 Best Local Similarity: 25.00% Mismatches: 52  
 Query Match: 8.98% Indels: 14  
 RESULT 1201  
 ID ADL13962 standard; DNA; 160198 BP.  
 DE Osteoarthritis-associated polymorphic nucleotide #494.  
 PN WO2003054166-A2.  
 PD 03-JUL-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 34.55% Mismatches: 23  
 Query Match: 8.98% Indels: 2  
 RESULT 1202  
 ID AAS17594 standard; cDNA; 1209 BP.  
 DE DNA encoding novel secreted protein #23.  
 PN WO200179454-A1.  
 PD 25-OCT-2001.  
 PA (SMIK) SMITHKLINE BEECHAM CORP.  
 Best Local Similarity: 30.86% Mismatches: 40  
 Query Match: 8.93% Indels: 3  
 RESULT 1203  
 ID ADF58259 standard; cDNA; 1209 BP.  
 DE Human polynucleotide sequence SEQ ID NO:626.  
 PN WO2003080795-A2.  
 PD 02-OCT-2003.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 30.86% Mismatches: 40  
 Query Match: 8.93% Indels: 3  
 RESULT 1204  
 ID ABK11078 standard; cDNA; 1475 BP.  
 DE cDNA encoding LP polypeptide #1.  
 PN WO200216578-A2.  
 PD 28-FEB-2002.  
 PA (ELIL) LILLY & CO ELI.  
 Best Local Similarity: 30.86% Mismatches: 40  
 Query Match: 8.93% Indels: 3  
 RESULT 1205  
 ID ADF74225 standard; cDNA; 5409 BP.  
 DE Human novel brain/hippocampus cDNA #43.  
 PN JP2003009886-A.  
 PD 14-JAN-2003.  
 PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.  
 Best Local Similarity: 30.86% Mismatches: 40  
 Query Match: 8.93% Indels: 3  
 RESULT 1206  
 ID AAS28917 standard; DNA; 5430 BP.  
 DE Human immunoglobulin encoding genomic DNA SEQ ID No 279.  
 PN WO200155315-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 23.97% Mismatches: 59  
 Query Match: 8.93% Indels: 11  
 RESULT 1207  
 ID ADB31758 standard; DNA; 5430 BP.  
 DE Human novel protein DNA SEQ ID NO 279.  
 PN US2003077606-A1.  
 PD 24-APR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 23.97% Mismatches: 59  
 Query Match: 8.93% Indels: 11  
 RESULT 1208  
 ID AAS56128 standard; DNA; 7596 BP.  
 DE Mouse Notch carcinoma associated (CA) gene coding region.  
 PN WO2003035837-A2.  
 PD 01-MAY-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Best Local Similarity: 25.99% Mismatches: 65  
 Query Match: 8.93% Indels: 47

RESULT 1209  
 ID ADA02491 standard; cDNA; 7596 BP.  
 DE Mouse Notch1 carcinoma associated coding sequence, SEQ ID NO:1009.  
 PN WO2003057146-A2.  
 PD 17-JUL-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Best Local Similarity: 25.99% Mismatches: 65  
 Query Match: 8.93% Indels: 47  
 RESULT 1210  
 ID ADB72229 standard; cDNA; 7596 BP.  
 DE Mouse Notch1 cDNA.  
 PN WO2003008583-A2.  
 PD 30-JAN-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Best Local Similarity: 25.99% Mismatches: 65  
 Query Match: 8.93% Indels: 47  
 RESULT 1211  
 ID AAD56127 standard; DNA; 8064 BP.  
 DE Mouse Notch carcinoma associated (CA) DNA.  
 PN WO2003035837-A2.  
 PD 01-MAY-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Best Local Similarity: 25.99% Mismatches: 65  
 Query Match: 8.93% Indels: 47  
 RESULT 1212  
 ID ADA02490 standard; cDNA; 8064 BP.  
 DE Mouse Notch1 carcinoma associated cDNA, SEQ ID NO:1008.  
 PN WO2003057146-A2.  
 PD 17-JUL-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Best Local Similarity: 25.99% Mismatches: 65  
 Query Match: 8.93% Indels: 47  
 RESULT 1213  
 ID ADB72228 standard; mRNA; 8064 BP.  
 DE Mouse Notch1 mRNA.  
 PN WO2003008583-A2.  
 PD 30-JAN-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Best Local Similarity: 25.99% Mismatches: 65  
 Query Match: 8.93% Indels: 47  
 RESULT 1214  
 ID ADR99037 standard; DNA; 9487 BP.  
 DE Chondroitin sulfate proteoglycan 2 (versican), CSPG2, DNA SEQ ID 43.  
 PN WO2004078035-A2.  
 PD 16-SEP-2004.  
 PA (FARB) BAYER PHARM CORP.  
 Best Local Similarity: 20.09% Mismatches: 98  
 Query Match: 8.89% Indels: 48  
 RESULT 1215  
 ID AAA37671 standard; DNA; 1241 BP.  
 DE Human peptidase, HPEP-15 coding sequence.  
 PN WO200042201-A2.  
 PD 20-JUL-2000.  
 PA (INCY-) INCYTE PHARM INC.  
 Best Local Similarity: 23.33% Mismatches: 74  
 Query Match: 8.84% Indels: 45  
 RESULT 1216  
 ID ABZ59662 standard; cDNA; 2622 BP.  
 DE Human secreted protein SECP-17 encoding cDNA SEQ ID NO:48.  
 PN WO2003004615-A2.  
 PD 16-JAN-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 30.86% Mismatches: 40  
 Query Match: 8.84% Indels: 3  
 RESULT 1217  
 ID ABL27121 standard; DNA; 4287 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32836.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Best Local Similarity: 28.39% Mismatches: 59  
 Query Match: 8.80% Indels: 42

RESULT 1218  
ID AAF86431 standard; DNA; 349980 BP.  
DE Pyrococcus abyssi genomic fragment #1.  
PN FR2792651-A1.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
PA (IFRE-) IFREMER INST FR RECH EXPL MER.  
Best Local Similarity: 23.50%  
Query Match: 8.80%  
Mismatches: 51  
Indels: 80  
RESULT 1219  
ID AAA27366 standard; DNA; 1206 BP.  
DE Sinorhizobium meliloti ribC gene.  
PN WO200029607-A1.  
PA (REGC ) UNIV CALIFORNIA.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Best Local Similarity: 23.61%  
Query Match: 8.76%  
Mismatches: 64  
Indels: 73  
RESULT 1220  
ID ADS48391 standard; cDNA; 3799 BP.  
DE Bacterial polynucleotide #3134.  
PN US2003233675-A1.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Best Local Similarity: 23.61%  
Query Match: 8.76%  
Mismatches: 64  
Indels: 73  
RESULT 1221  
ID AAA27364 standard; DNA; 4248 BP.  
DE Sinorhizobium meliloti ribC/ribD gene complex.  
PN WO200029607-A1.  
PA (REGC ) UNIV CALIFORNIA.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Best Local Similarity: 23.61%  
Query Match: 8.76%  
Mismatches: 64  
Indels: 73  
RESULT 1222  
ID ADM43175 standard; DNA; 35167 BP.  
DE Wild-type adenovirus serotype 24 nucleotide sequence SEQ ID NO:5.  
PN WO2004018627-A2.  
PA (MERI ) MERCK & CO INC.  
PA (MERI ) MERCK & CO INC.  
Best Local Similarity: 23.79%  
Query Match: 8.76%  
Mismatches: 68  
Indels: 63  
RESULT 1223  
ID ADS00140 standard; DNA; 35167 BP.  
DE Wild-type human adenovirus serotype 24 DNA SEQ ID NO:1.  
PN WO2004083418-A1.  
PA (MERI ) MERCK & CO INC.  
PA (MERI ) MERCK & CO INC.  
Best Local Similarity: 23.79%  
Query Match: 8.76%  
Mismatches: 68  
Indels: 63  
RESULT 1224  
ID ABT23334 standard; DNA; 1341 BP.  
DE Cellulohydrolase I activity polynucleotide SEQ ID NO 43.  
PN WO2003000941-A2.  
PA (NOVO ) NOVOZYMES AS.  
PA (NOVO ) NOVOZYMES AS.  
Best Local Similarity: 26.46%  
Query Match: 8.71%  
Mismatches: 56  
Indels: 61  
RESULT 1225  
ID AAH90018 standard; cDNA; 2313 BP.  
DE Human bone marrow cDNA, SEQ ID NO: 262.  
PN WO200153453-A2.  
PA (HYSE-) HYSEQ INC.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 27.44%  
Query Match: 8.71%  
Mismatches: 78  
Indels: 45  
RESULT 1226  
ID ACD05902 standard; cDNA; 2313 BP.  
DE Novel human contig #76.  
PN WO2003023013-A2.

PD 20-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 27.44%  
Query Match: 8.71%  
Mismatches: 78  
Indels: 45  
RESULT 1227  
ID ADE08790 standard; DNA; 2313 BP.  
DE Novel DNA-related contig nucleotide sequence #512.  
PN WO2003054152-A2.  
PA (HYSE-) HYSEQ INC.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 27.44%  
Query Match: 8.71%  
Mismatches: 78  
Indels: 45  
RESULT 1228  
ID ADE07629 standard; DNA; 2514 BP.  
DE Novel coding sequence (useful for identifying genetic disorders) #695.  
PN WO2003054152-A2.  
PA (HYSE-) HYSEQ INC.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 27.44%  
Query Match: 8.71%  
Mismatches: 78  
Indels: 45  
RESULT 1229  
ID AAH14562 standard; cDNA; 3118 BP.  
DE Human cDNA sequence SEQ ID NO:12139.  
PN EP1074617-A2.  
PA (HELI-) HELIX RES INST.  
PA (HELI-) HELIX RES INST.  
Best Local Similarity: 27.44%  
Query Match: 8.71%  
Mismatches: 78  
Indels: 45  
RESULT 1230  
ID AAH14010 standard; cDNA; 3499 BP.  
DE Human cDNA sequence SEQ ID NO:11101.  
PN EP1074617-A2.  
PA (HELI-) HELIX RES INST.  
PA (HELI-) HELIX RES INST.  
Best Local Similarity: 27.44%  
Query Match: 8.71%  
Mismatches: 78  
Indels: 45  
RESULT 1231  
ID ADO00911 standard; cDNA; 4011 BP.  
DE Human homologue of Fruit fly AD-related cDNA CG1103 #2.  
PN US2004067535-A1.  
PA (LIFE-) LIFE SCI DEV CORP.  
PA (LIFE-) LIFE SCI DEV CORP.  
Best Local Similarity: 27.44%  
Query Match: 8.71%  
Mismatches: 78  
Indels: 45  
RESULT 1232  
ID ADR07180 standard; cDNA; 5131 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 686.  
PN EP1447413-A2.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 27.44%  
Query Match: 8.71%  
Mismatches: 78  
Indels: 45  
RESULT 1233  
ID ABL07173 standard; cDNA; 6353 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16001.  
PN WO200171042-A2.  
PA (PEKE ) PE CORP NY.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 25.88%  
Query Match: 8.71%  
Mismatches: 71  
Indels: 34  
RESULT 1234  
ID ABL07172 standard; cDNA; 8429 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15998.  
PN WO200171042-A2.  
PA (PEKE ) PE CORP NY.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 25.88%  
Query Match: 8.71%  
Mismatches: 71  
Indels: 34  
RESULT 1235  
ID ACH93277 standard; DNA; 334 BP.  
DE Human genome derived single exon probe #26472.  
PN US2003194704-A1.  
PD 16-OCT-2003.

PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANK/) HANZEL D K.  
 Best Local Similarity: 27.27% Mismatches: 40  
 Query Match: 8.62% Indels: 8  
 RESULT 1236  
 ID AA051157 standard; DNA; 1190 BP.  
 DE Herpes simplex virus glycoprotein I DNA.  
 PN EP568178-A1.  
 PD 03-NOV-1993.  
 PA (CEDA-) CEDARS SINAI MEDICAL CENT.  
 Best Local Similarity: 28.97% Mismatches: 38  
 Query Match: 8.62% Indels: 20  
 RESULT 1237  
 ID ADS63288 standard; cDNA; 3584 BP.  
 DE Bacterial polynucleotide #15275.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 23.77% Mismatches: 57  
 Query Match: 8.58% Indels: 114  
 RESULT 1238  
 ID ABX77167 standard; DNA; 125653 BP.  
 DE DNA sequence of human BAC clone RP11-8211.  
 PN WO200283897-A1.  
 PD 24-OCT-2002.  
 PA (GENE-) GENE STREAM PTY LTD.  
 Best Local Similarity: 33.68% Mismatches: 31  
 Query Match: 8.58% Indels: 21  
 RESULT 1239  
 ID ADO42013 standard; DNA; 784 BP.  
 DE Human cell adhesion and extracellular matrix protein 1 gene SeqID42.  
 PN WO2004048529-A2.  
 PD 10-JUN-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 28.07% Mismatches: 48  
 Query Match: 8.53% Indels: 14  
 RESULT 1240  
 ID AAX22095 standard; DNA; 1767 BP.  
 DE Cellobiohydrolase CBH B coding sequence.  
 PN WO9906574-A1.  
 PD 11-FEB-1999.  
 PA (KONN) GIST-BROCADES BV.  
 Best Local Similarity: 26.79% Mismatches: 39  
 Query Match: 8.53% Indels: 26  
 RESULT 1241  
 ID AAD17184 standard; DNA; 65140 BP.  
 DE Streptomyces noursei nys1 DNA of nystatin PKS gene cluster.  
 PN WO200159126-A2.  
 PD 16-AUG-2001.  
 PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
 PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.  
 PA (ALPH-) ALPHARMA AS.  
 PA (SINV-) SINVENT AS.  
 PA (DZIE/) DZIEGLEWSKA H.  
 PA (ZOTC/) ZOTCHEV S B.  
 PA (SEKU/) SEKUROVA O N.  
 PA (FJAE/) FJAEVRIK E.  
 PA (BRAU/) BRAUTASET T.  
 PA (STRO/) STROM A R.  
 PA (VALL/) VALLA S.  
 Best Local Similarity: 26.39% Mismatches: 57  
 Query Match: 8.49% Indels: 32  
 RESULT 1242  
 ID AAD17186 standard; DNA; 125401 BP.  
 DE Streptomyces noursei nystatin PKS gene cluster DNA.  
 PN WO200159126-A2.  
 PD 16-AUG-2001.  
 PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.

PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.  
 PA (ALPH-) ALPHARMA AS.  
 PA (SINV-) SINVENT AS.  
 PA (DZIE/) DZIEGLEWSKA H.  
 PA (ZOTC/) ZOTCHEV S B.  
 PA (SEKU/) SEKUROVA O N.  
 PA (FJAE/) FJAEVRIK E.  
 PA (BRAU/) BRAUTASET T.  
 PA (STRO/) STROM A R.  
 PA (VALL/) VALLA S.  
 Best Local Similarity: 26.39% Mismatches: 57  
 Query Match: 8.49% Indels: 32  
 RESULT 1243  
 ID ABL18341 standard; DNA; 1372 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6496.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Best Local Similarity: 34.48% Mismatches: 34  
 Query Match: 8.40% Indels: 17  
 RESULT 1244  
 ID ADH12800 standard; cDNA; 2207 BP.  
 DE Abalone (Haliotis discus hannai) cellulase-encoding cDNA, SEQ ID NO:1.  
 PN JP2003235552-A.  
 PD 26-AUG-2003.  
 PA (HOKK-) HOKKAIDO TLO KK.  
 Best Local Similarity: 24.09% Mismatches: 62  
 Query Match: 8.40% Indels: 78  
 RESULT 1245  
 ID ABL18340 standard; DNA; 4492 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6493.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Best Local Similarity: 34.48% Mismatches: 34  
 Query Match: 8.40% Indels: 17  
 RESULT 1246  
 ID ABL25979 standard; DNA; 5388 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 29410.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Best Local Similarity: 33.01% Mismatches: 56  
 Query Match: 8.40% Indels: 5  
 RESULT 1247  
 ID ABL25978 standard; DNA; 7782 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 29407.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Best Local Similarity: 33.01% Mismatches: 56  
 Query Match: 8.40% Indels: 5  
 RESULT 1248  
 ID ABD13413 standard; DNA; 1179 BP.  
 DE Pseudomonas aeruginosa polynucleotide #12017.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 27.60% Mismatches: 63  
 Query Match: 8.36% Indels: 59  
 RESULT 1249  
 ID AAS80823 standard; cDNA; 7568 BP.  
 DE DNA encoding novel human diagnostic protein #16627.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 21.50% Mismatches: 77  
 Query Match: 8.31% Indels: 55  
 RESULT 1250  
 ID ADL12996 standard; cDNA; 8146 BP.  
 DE Human steroid-induced C3A liver cell cDNA #725.  
 PN US6673549-B1.  
 PD 06-JAN-2004.

PA (INCY-) INCYTE CORP.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 8.31% Indels: 55  
RESULT 1251  
ID ADL61871 standard; DNA; 9169 BP.  
DE Human ovarian cancer DNA marker #20083.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 8.31% Indels: 55  
RESULT 1252  
ID ABV24414 standard; cDNA; 9220 BP.  
DE Human prostate expression marker cDNA 24405.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 8.31% Indels: 55  
RESULT 1253  
ID ABV23265 standard; cDNA; 9220 BP.  
DE Human prostate expression marker cDNA 25256.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 8.31% Indels: 55  
RESULT 1254  
ID ABK83800 standard; cDNA; 9416 BP.  
DE Human cDNA differentially expressed in granulocytic cells #371.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 8.31% Indels: 55  
RESULT 1255  
ID ACF34559 standard; DNA; 9416 BP.  
DE Gene encoding angiogenesis protein BNO382.  
PN WO2003027285-A1.  
PD 03-APR-2003.  
PA (BION-) BIONOMICS LTD.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 8.31% Indels: 55  
RESULT 1256  
ID ADN05259 standard; cDNA; 9416 BP.  
DE Antiposoriatic cDNA sequence #849.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 8.31% Indels: 55  
RESULT 1257  
ID ADR14613 standard; DNA; 9416 BP.  
DE Human NF-kappaB pathway-associated gene SeqID614.  
PN WO2004065577-A2.  
PD 05-AUG-2004.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 8.31% Indels: 55  
RESULT 1258  
ID ADI61664 standard; cDNA; 11917 BP.  
DE Human cDNA downregulated in Alzheimer's disease, INCYTE 475473.1.  
PN US668288-B1.  
PD 27-JAN-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 8.31% Indels: 55  
RESULT 1259  
ID ADE53871 standard; cDNA; 11950 BP.  
DE Human prostate cancer cDNA #218.  
PN US2003190640-A1.  
PD 09-OCT-2003.  
PA (FARI/) FARIS M.

PA (PEAR/) PEARSON C I.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 8.31% Indels: 55  
RESULT 1260  
ID ADF90735 standard; DNA; 11965 BP.  
DE Human hepatic-fibrosis disease marker SEQ ID 197.  
PN JP2003259877-A.  
PD 16-SEP-2003.  
PA (SUMU ) SUMITOMO SEIYAKU KK.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 8.31% Indels: 55  
RESULT 1261  
ID ADN04560 standard; cDNA; 12004 BP.  
DE Antiposoriatic cDNA sequence #484.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 8.31% Indels: 55  
RESULT 1262  
ID ABO81848 standard; DNA; 349980 BP.  
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1104.  
PN EP1227152-A1.  
PD 31-JUL-2002.  
PA (NEST ) SOC PROD NESTLE SA.  
Best Local Similarity: 23.68% Mismatches: 62  
Query Match: 8.31% Indels: 57  
RESULT 1263  
ID AAT29035 standard; cDNA; 1321 BP.  
DE Endoglucanase (60 kDa Family 5 cellulase) cDNA sequence.  
PN WO9611262-A1.  
PD 18-APR-1996.  
PA (NOVO ) NOVO-NORDISK AS.  
Best Local Similarity: 30.00% Mismatches: 32  
Query Match: 8.27% Indels: 22  
RESULT 1264  
ID AAK94215 standard; cDNA; 1995 BP.  
DE Human full-length cDNA, SEQ ID NO: 2788.  
PN EP1130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Best Local Similarity: 26.98% Mismatches: 79  
Query Match: 8.27% Indels: 45  
RESULT 1265  
ID ADL30755 standard; cDNA; 1995 BP.  
DE Full length human cDNA clone SeqID 2788.  
PN EP1396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 26.98% Mismatches: 79  
Query Match: 8.27% Indels: 45  
RESULT 1266  
ID ADP04444 standard; cDNA; 4849 BP.  
DE Sea squirt cDNA with tissue specific expression in development Seq 39.  
PN JP2004057129-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN  
Best Local Similarity: 23.83% Mismatches: 94  
Query Match: 8.27% Indels: 75  
RESULT 1267  
ID ABL25205 standard; DNA; 5931 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27088.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 32.65% Mismatches: 34  
Query Match: 8.27% Indels: 13  
RESULT 1268  
ID ABL25204 standard; DNA; 7931 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27085.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.

Best Local Similarity: 32.65% Mismatches: 34  
Query Match: 8.27% Indels: 13  
RESULT 1269  
ID AAS73740 standard; cDNA; 1365 BP.  
DE DNA encoding novel human diagnostic protein #9544.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC. Mismatches: 53  
Best Local Similarity: 24.46% Indels: 33  
Query Match: 8.22%  
RESULT 1270  
ID ABD15716 standard; DNA; 1665 BP.  
DE Pseudomonas aeruginosa polynucleotide #14320.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP. Mismatches: 70  
Best Local Similarity: 24.90% Indels: 78  
Query Match: 8.22%  
RESULT 1271  
ID AAQ71391 standard; DNA; 2589 BP.  
DE Yeast 2.6 kb agglutination gene FLO1S.  
PN WO9419475-A2.  
PD 01-SEP-1994.  
PA (SAPB) SAPPORO BREWERIES.  
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.  
Best Local Similarity: 27.57% Mismatches: 79  
Query Match: 8.22% Indels: 27  
RESULT 1272  
ID AAQ67360 standard; DNA; 2685 BP.  
DE S. cerevisiae FLO1 gene.  
PN WO9418330-A1.  
PD 18-AUG-1994.  
PA (UNIL) UNILEVER PLC. Mismatches: 79  
PA (UNIL) UNILEVER NV. Indels: 27  
Best Local Similarity: 27.57%  
Query Match: 8.22%  
RESULT 1273  
ID AAQ54029 standard; DNA; 2685 BP.  
DE Flocculation protein coding sequence of Saccharomyces cerevisiae.  
PN WO9401567-A1.  
PD 20-JAN-1994.  
PA (UNIL) UNILEVER PLC. Mismatches: 79  
PA (UNIL) UNILEVER NV. Indels: 27  
Best Local Similarity: 27.57%  
Query Match: 8.22%  
RESULT 1274  
ID AAQ71390 standard; DNA; 4614 BP.  
DE Yeast 4.7 kb agglutination gene FLO1L.  
PN WO9419475-A2.  
PD 01-SEP-1994.  
PA (SAPB) SAPPORO BREWERIES.  
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.  
Best Local Similarity: 27.57% Mismatches: 79  
Query Match: 8.22% Indels: 27  
RESULT 1275  
ID AAA95422 standard; DNA; 4614 BP.  
DE S. cerevisiae FLO1 coding sequence.  
PN WO200058342-A1.  
PD 05-OCT-2000.  
PA (VALW) VALTION TEKNIILINEN TUTKIMUSKESKUS.  
Best Local Similarity: 27.57% Mismatches: 79  
Query Match: 8.22% Indels: 27  
RESULT 1276  
ID ADG46655 standard; cDNA; 4614 BP.  
DE Bacterial polynucleotide #1398.  
PN US200323675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y. Mismatches: 38  
PA (HINK) HINKLE G J. Indels: 7  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Best Local Similarity: 27.57% Mismatches: 79

Query Match: 8.22% Indels: 27  
RESULT 1277  
ID ADR32196 standard; DNA; 5613 BP.  
DE Yeast FLO1 open reading frame fragment, SEQ ID NO:1.  
PN WO2004067565-A1.  
PD 12-AUG-2004.  
PA (OSBO-) OSBORNE DISTRIBUIDORA SA.  
PA (UYDO) UNIV DE OLAVIDE PABLO. Mismatches: 79  
Best Local Similarity: 27.57% Indels: 27  
Query Match: 8.22%  
RESULT 1278  
ID ADP87474 standard; DNA; 5864 BP.  
DE S. cerevisiae glucan synthase pathway gene YAR050W (FLO1) SeqID16.  
PN WO2004057033-A1.  
PD 08-JUL-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC. Mismatches: 79  
Best Local Similarity: 27.57% Indels: 27  
Query Match: 8.22%  
RESULT 1279  
ID AAL56704 standard; DNA; 36604 BP.  
DE Chimpanzee adenovirus serotype Pan6 genomic DNA.  
PN WO2003046124-A2.  
PD 05-JUN-2003.  
PA (UYPE-) UNIV PENNSYLVANIA. Mismatches: 89  
Best Local Similarity: 23.31% Indels: 61  
Query Match: 8.22%  
RESULT 1280  
ID ADH69807 standard; DNA; 684973 BP.  
DE Human Vbeta gene.  
PN US2002150891-A1.  
PD 17-OCT-2002.  
PA (HOOD) HOOD L E. Mismatches: 64  
PA (ROWE) ROWEN L. Indels: 21  
Best Local Similarity: 27.74%  
Query Match: 8.22%  
RESULT 1281  
ID ABL68560 standard; DNA; 267156 BP.  
DE Kidney cancer related gene sequence SEQ ID NO:6897.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM. Mismatches: 64  
Best Local Similarity: 27.74% Indels: 21  
Query Match: 8.22%  
RESULT 1282  
ID ADJ41911 standard; cDNA; 632 BP.  
DE Plant cDNA #2911.  
PN US2004016025-A1.  
PD 22-JAN-2004.  
PA (BUDW) BUDWORTH P. Mismatches: 77  
PA (MOUG) MOUGHAMER T. Indels: 43  
PA (BRIG) BRIGGS S P.  
PA (COOP) COOPER B.  
PA (GLAZ) GLAZEBROOK J.  
PA (GOFF) GOFF S A.  
PA (KATA) KATAGIRI F.  
PA (KREP) KREPS J.  
PA (PROV) PROVANT N.  
PA (RICK) RICK D.  
PA (ZHUT) ZHU T.  
Best Local Similarity: 23.33% Mismatches: 77  
Query Match: 8.13% Indels: 43  
RESULT 1283  
ID AAS28824 standard; cDNA; 697 BP.  
DE Human immunoglobulin encoding cDNA SEQ ID No 70.  
PN WO200155315-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 38  
Best Local Similarity: 31.71% Indels: 7  
Query Match: 8.13%  
RESULT 1284  
ID ABA06691 standard; cDNA; 697 BP.  
DE Human cDNA SEQ ID NO: 357.  
PN WO200154474-A2.

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PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 31.71% Mismatches: 38
Query Match: 8.13% Indels: 7
RESULT 1285
ID ABV84028 standard; cDNA; 697 BP.
DE Human polynucleotide SEQ ID NO 357.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Best Local Similarity: 31.71% Mismatches: 38
Query Match: 8.13% Indels: 7
RESULT 1286
ID AB31549 standard; cDNA; 697 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 70.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 31.71% Mismatches: 38
Query Match: 8.13% Indels: 7
RESULT 1287
ID ADS5917 standard; cDNA; 1386 BP.
DE Bacterial polynucleotide #7904.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 27.04% Mismatches: 78
Query Match: 8.13% Indels: 45
RESULT 1288
ID ABQ14764 standard; DNA; 3034 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1355.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 31.82% Mismatches: 36
Query Match: 8.13% Indels: 24
RESULT 1289
ID ABQ14765 standard; DNA; 3034 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1356.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 31.82% Mismatches: 36
Query Match: 8.13% Indels: 24
RESULT 1290
ID ABL25807 standard; DNA; 3381 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28894.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE/) PE CORP NY.
Best Local Similarity: 32.32% Mismatches: 41
Query Match: 8.13% Indels: 15
RESULT 1291
ID AAQ22986 standard; DNA; 3502 BP.
DE Sequence of ILTV gp60 gene.
PN WO9203554-A.
PD 05-MAR-1992.
PA (WEBS-) WEBSTER A PTY LTD.
Best Local Similarity: 28.49% Mismatches: 58
Query Match: 8.13% Indels: 46
RESULT 1292
ID ADS49082 standard; cDNA; 3873 BP.
DE Bacterial polynucleotide #3825.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 25.12% Mismatches: 65
Query Match: 8.13% Indels: 66
RESULT 1293
ID ABL25806 standard; DNA; 5381 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28891.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE/) PE CORP NY.
Best Local Similarity: 32.32% Mismatches: 41
Query Match: 8.13% Indels: 15
RESULT 1294
ID AAD08215 standard; DNA; 114793 BP.
DE Human genome from BAC clone, hbm168.
PN WO200142434-A1.
PD 14-JUN-2001.
PA (MERI/) MERCK & CO INC.
Best Local Similarity: 28.68% Mismatches: 70
Query Match: 8.13% Indels: 15
RESULT 1295
ID ACAS1121 standard; DNA; 1374 BP.
DE Prokaryotic essential gene #32778.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 26.40% Mismatches: 44
Query Match: 8.09% Indels: 30
RESULT 1296
ID ABT42440 standard; DNA; 2636 BP.
DE Toxicity modelling related rat gene SEQ ID NO 2142.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 36.84% Mismatches: 43
Query Match: 8.09% Indels: 11
RESULT 1297
ID AAAS3800 standard; DNA; 7720 BP.
DE Genomic DNA encoding M68 TNF receptor related protein.
PN WO200046247-A1.
PD 10-AUG-2000.
PA (MERI/) MERCK & CO INC.
Best Local Similarity: 26.67% Mismatches: 80
Query Match: 8.09% Indels: 16
RESULT 1298
ID AA121781 standard; DNA; 1075 BP.
DE Probe #11714 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88% Mismatches: 44
Query Match: 8.04% Indels: 9
RESULT 1299
ID ABA66852 standard; DNA; 1075 BP.
DE Human foetal liver single exon nucleic acid probe #15157.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88% Mismatches: 44
Query Match: 8.04% Indels: 9
RESULT 1300
ID AA147064 standard; DNA; 1075 BP.
DE Probe #15750 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 26.88% Mismatches: 44
Query Match: 8.04% Indels: 9
RESULT 1301
ID ABA48937 standard; DNA; 1075 BP.
DE Human breast cell single exon nucleic acid probe #7632.
PN WO200157271-A2.
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PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 26.88%  
Query Match: 8.04%  
Mismatch: 44  
Indels: 9  
RESULT 1302  
ID ABA33921 standard; DNA; 1075 BP.  
DE Probe #12387 for gene expression analysis in human heart cell sample.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 26.88%  
Query Match: 8.04%  
Mismatch: 44  
Indels: 9  
RESULT 1303  
ID AAK41011 standard; DNA; 1075 BP.  
DE Human bone marrow expressed single exon probe SEQ ID NO: 15568.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 26.88%  
Query Match: 8.04%  
Mismatch: 44  
Indels: 9  
RESULT 1304  
ID AAK15288 standard; DNA; 1075 BP.  
DE Human brain expressed single exon probe SEQ ID NO: 15279.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 26.88%  
Query Match: 8.04%  
Mismatch: 44  
Indels: 9  
RESULT 1305  
ID ABS40603 standard; DNA; 1075 BP.  
DE Human liver single exon probe, SEQ ID No 15593.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 26.88%  
Query Match: 8.04%  
Mismatch: 44  
Indels: 9  
RESULT 1306  
ID AA107466 standard; DNA; 1075 BP.  
DE Probe #7457 used to measure gene expression in human breast sample.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 26.88%  
Query Match: 8.04%  
Mismatch: 44  
Indels: 9  
RESULT 1307  
ID ABS14983 standard; DNA; 1075 BP.  
DE Human genome-derived single exon probe ORF from lung SEQ ID No 14974.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 26.88%  
Query Match: 8.04%  
Mismatch: 44  
Indels: 9  
RESULT 1308  
ID AA112593 standard; DNA; 1403 BP.  
DE Probe #2526 for gene expression analysis in human cervical cell sample.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 26.88%  
Query Match: 8.04%  
Mismatch: 44  
Indels: 9  
RESULT 1309  
ID ABA54290 standard; DNA; 1403 BP.  
DE Human foetal liver single exon nucleic acid probe #2595.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 26.88%  
Query Match: 8.04%  
Mismatch: 44  
Indels: 9  
RESULT 1310  
ID AA133941 standard; DNA; 1403 BP.  
DE Probe #2627 used to measure gene expression in human placenta sample.  
PN WO200157272-A2.  
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 26.88%  
Query Match: 8.04%  
Mismatch: 44  
Indels: 9  
RESULT 1311  
ID ABA43834 standard; DNA; 1403 BP.  
DE Human breast cell single exon nucleic acid probe #2529.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 26.88%  
Query Match: 8.04%  
Mismatch: 44  
Indels: 9  
RESULT 1312  
ID ABA24047 standard; DNA; 1403 BP.  
DE Probe #2513 for gene expression analysis in human heart cell sample.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 26.88%  
Query Match: 8.04%  
Mismatch: 44  
Indels: 9  
RESULT 1313  
ID AAK28010 standard; DNA; 1403 BP.  
DE Human bone marrow expressed single exon probe SEQ ID NO: 2567.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 26.88%  
Query Match: 8.04%  
Mismatch: 44  
Indels: 9  
RESULT 1314  
ID AAK02574 standard; DNA; 1403 BP.  
DE Human brain expressed single exon probe SEQ ID NO: 2565.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 26.88%  
Query Match: 8.04%  
Mismatch: 44  
Indels: 9  
RESULT 1315  
ID ABS27605 standard; DNA; 1403 BP.  
DE Human liver single exon probe, SEQ ID No 2595.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 26.88%  
Query Match: 8.04%  
Mismatch: 44  
Indels: 9  
RESULT 1316  
ID AA102498 standard; DNA; 1403 BP.  
DE Probe #2489 used to measure gene expression in human breast sample.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 26.88%  
Query Match: 8.04%  
Mismatch: 44  
Indels: 9  
RESULT 1317  
ID ABS02482 standard; DNA; 1403 BP.  
DE Human genome-derived single exon probe from lung SEQ ID No 2473.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 26.88%  
Query Match: 8.04%  
Mismatch: 44  
Indels: 9  
RESULT 1318  
ID ADB58239 standard; DNA; 1548 BP.  
DE Toxicity-related gene, SEQ ID 3265.  
PN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 21.17%  
Query Match: 8.04%  
Mismatch: 96  
Indels: 88  
RESULT 1319  
ID ADB52767 standard; DNA; 1548 BP.  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID No:3309.  
PN WO2003065993-A2.  
PD 14-AUG-2003.  
PA (GENE-) GENE LOGIC INC.

Best Local Similarity: 21.17% Mismatches: 96  
Query Match: 8.04% Indels: 88  
RESULT 1320  
ID ABT41946 standard; DNA; 1548 BP.  
DE Toxicity modelling related rat gene SEQ ID NO 1648.  
PN WO200295000-A2.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 21.17% Mismatches: 96  
Query Match: 8.04% Indels: 88  
RESULT 1321  
ID AAC51572 standard; DNA; 1626 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 69007.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Best Local Similarity: 21.58% Mismatches: 48  
Query Match: 8.04% Indels: 31  
RESULT 1322  
ID ADG73739 standard; CDNA; 2059 BP.  
DE Aspergillus niger Brsa-109 CDNA.  
PN US2003215950-A1.  
PD 20-NOV-2003.  
PA (LASU//) LASURE L L.  
PA (DAIZ//) DAI Z.  
Best Local Similarity: 26.95% Mismatches: 65  
Query Match: 8.04% Indels: 19  
RESULT 1323  
ID AA81515 standard; DNA; 16878 BP.  
DE N. meningitidis partial DNA sequence gnm\_62 SEQ ID NO:62.  
PN WO20022430-A2.  
PD 20-APR-2000.  
PA (CHIR ) CHIRON CORP.  
Best Local Similarity: 18.25% Mismatches: 91  
Query Match: 8.04% Indels: 87  
RESULT 1324  
Best Local Similarity: 18.25% Mismatches: 91  
Query Match: 8.04% Indels: 87  
RESULT 1325  
ID AAF21609 standard; DNA; 349980 BP.  
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:110.  
PN WO200066791-A1.  
PD 09-NOV-2000.  
PA (CHIR ) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Best Local Similarity: 18.25% Mismatches: 91  
Query Match: 8.04% Indels: 87  
RESULT 1326  
ID AAF21608 standard; DNA; 349980 BP.  
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.  
PN WO200066791-A1.  
PD 09-NOV-2000.  
PA (CHIR ) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Best Local Similarity: 18.25% Mismatches: 91  
Query Match: 8.04% Indels: 87  
RESULT 1327  
ID ACA40155 standard; DNA; 1209 BP.  
DE Prokaryotic essential gene #21812.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 22.39% Mismatches: 83  
Query Match: 8.00% Indels: 46  
RESULT 1328  
ID ABL24493 standard; DNA; 1344 BP.  
DE Drosophila melanogaster Genomic polynucleotide SEQ ID NO 24952.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 25.81% Mismatches: 72  
Query Match: 8.00% Indels: 37  
RESULT 1329  
ID AAZ38579 standard; CDNA; 1608 BP.

DE D. farinae mite allergen protein (map) gene nDerf98-1608 coding strand.  
PN WO9954349-A2.  
PD 28-OCT-1999.  
PA (HESK-) HESKA CORP.  
Best Local Similarity: 23.83% Mismatches: 91  
Query Match: 8.00% Indels: 56  
RESULT 1330  
ID AAZ38580 standard; CDNA; 1608 BP.  
DE D. farinae mite allergen protein (map) gene nDerf98-1608 complement.  
PN WO9954349-A2.  
PD 28-OCT-1999.  
PA (HESK-) HESKA CORP.  
Best Local Similarity: 23.83% Mismatches: 91  
Query Match: 8.00% Indels: 56  
RESULT 1331  
ID ABK69575 standard; CDNA; 1608 BP.  
DE Der HMW-map polynucleotide #5.  
PN WO200222807-A2.  
PD 21-MAR-2002.  
PA (HESK-) HESKA CORP.  
Best Local Similarity: 23.83% Mismatches: 91  
Query Match: 8.00% Indels: 56  
RESULT 1332  
ID ABK69576 standard; CDNA; 1608 BP.  
DE Der HMW-map polynucleotide #6.  
PN WO200222807-A2.  
PD 21-MAR-2002.  
PA (HESK-) HESKA CORP.  
Best Local Similarity: 23.83% Mismatches: 91  
Query Match: 8.00% Indels: 56  
RESULT 1333  
ID AAZ38577 standard; CDNA; 1665 BP.  
DE D. farinae mite allergen protein (map) gene nDerf98-1665 coding strand.  
PN WO9954349-A2.  
PD 28-OCT-1999.  
PA (HESK-) HESKA CORP.  
Best Local Similarity: 23.83% Mismatches: 91  
Query Match: 8.00% Indels: 56  
RESULT 1334  
ID AAZ38578 standard; CDNA; 1665 BP.  
DE D. farinae mite allergen protein (map) gene nDerf98-1665 complement.  
PN WO9954349-A2.  
PD 28-OCT-1999.  
PA (HESK-) HESKA CORP.  
Best Local Similarity: 23.83% Mismatches: 91  
Query Match: 8.00% Indels: 56  
RESULT 1335  
ID ABK69573 standard; CDNA; 1665 BP.  
DE Der HMW-map polynucleotide #3.  
PN WO200222807-A2.  
PD 21-MAR-2002.  
PA (HESK-) HESKA CORP.  
Best Local Similarity: 23.83% Mismatches: 91  
Query Match: 8.00% Indels: 56  
RESULT 1336  
ID ABK69574 standard; CDNA; 1665 BP.  
DE Der HMW-map polynucleotide #4.  
PN WO200222807-A2.  
PD 21-MAR-2002.  
PA (HESK-) HESKA CORP.  
Best Local Similarity: 23.83% Mismatches: 91  
Query Match: 8.00% Indels: 56  
RESULT 1337  
ID AAZ38576 standard; CDNA; 1752 BP.  
DE D. farinae mite allergen protein (map) gene nDerf98-1752 complement.  
PN WO9954349-A2.  
PD 28-OCT-1999.  
PA (HESK-) HESKA CORP.  
Best Local Similarity: 23.83% Mismatches: 91  
Query Match: 8.00% Indels: 56  
RESULT 1338  
ID AAZ38575 standard; CDNA; 1752 BP.  
DE D. farinae mite allergen protein (map) gene nDerf98-1752 coding strand.



PA (SLEA/) SLEATH P R. PA (MOSS/) MOSSMAN S. PA (EVAN/) EVANS L. PA (SPIE/) SPIES A G. PA (BOYD/) BOYDSTON J. Best Local Similarity: 23.63% Query Match: 7.91% RESULT 1356 ID ADJ80818 standard; DNA; 1251 BP. DE Wilm's tumor antigen associated DNA #17. PN WO2003037060-A2. PD 08-MAY-2003. PA (CORI-) CORIXA CORP. PA (GAIG/) GAIGER A. Best Local Similarity: 23.63% Query Match: 7.91% RESULT 1357 ID ADJ83738 standard; DNA; 1251 BP. DE Human lysosomal associated membrane protein 1 (LAMP-1) DNA. PN US2003235557-A1. PD 25-DEC-2003. PA (CORI-) CORIXA CORP. Best Local Similarity: 23.63% Query Match: 7.91% RESULT 1358 ID ADL57626 standard; cDNA; 1251 BP. DE Human lysosomal associated membrane protein, LAMP-1, cDNA. PN US2003215458-A1. PD 20-NOV-2003. PA (CORI-) CORIXA CORP. Best Local Similarity: 23.63% Query Match: 7.91% RESULT 1359 ID ADO09181 standard; DNA; 1251 BP. DE Human lysosomal associated membrane protein-1, LAMP-1, DNA. PN US2004018204-A1. PD 29-JAN-2004. PA (CORI-) CORIXA CORP. Best Local Similarity: 23.63% Query Match: 7.91% RESULT 1360 ID AAS76541 standard; cDNA; 1275 BP. DE DNA encoding novel human diagnostic protein #12345. PN WO200175067-A2. PD 11-OCT-2001. PA (HYSE-) HYSEQ INC. Best Local Similarity: 24.12% Query Match: 7.91% RESULT 1361 ID AAZ38628 standard; DNA; 1298 BP. DE Human lysosomal membrane glycoprotein-1 (LAMP-1) DNA. PN WO9958658-A2. PD 18-NOV-1999. PA (EPIM-) EPIMUNE INC. Best Local Similarity: 23.63% Query Match: 7.91% RESULT 1362 ID AAS52636 standard; DNA; 1374 BP. DE E. coli DNA for cellular proliferation protein #358. PN WO200170955-A2. PD 27-SEP-2001. PA (ELIT-) ELITRA PHARM INC. Best Local Similarity: 29.31% Query Match: 7.91% RESULT 1363 ID ACA32668 standard; DNA; 1374 BP. DE Prokaryotic essential gene #14325. PN WO200277183-A2. PD 03-OCT-2002. PA (ELIT-) ELITRA PHARM INC. Best Local Similarity: 29.31% Query Match: 7.91% RESULT 1364	PA (CAOY/) CAO Y. PA (HINK/) HINKLE G J. PA (SLAT/) SLATER S C. PA (CHEN/) CHEN X. PA (GOLD/) GOLDMAN B S. Best Local Similarity: 22.56% Query Match: 7.91% RESULT 1365 ID ADS63675 standard; cDNA; 1515 BP. DE Bacterial polynucleotide #15662. PN US2003233675-A1. PD 18-DEC-2003. PA (CAOY/) CAO Y. PA (HINK/) HINKLE G J. PA (SLAT/) SLATER S C. PA (CHEN/) CHEN X. PA (GOLD/) GOLDMAN B S. Best Local Similarity: 22.56% Query Match: 7.91% RESULT 1366 ID ADS64066 standard; cDNA; 1515 BP. DE Bacterial polynucleotide #16053. PN US2003233675-A1. PD 18-DEC-2003. PA (CAOY/) CAO Y. PA (HINK/) HINKLE G J. PA (SLAT/) SLATER S C. PA (CHEN/) CHEN X. PA (GOLD/) GOLDMAN B S. Best Local Similarity: 22.56% Query Match: 7.91% RESULT 1367 ID AAS89998 standard; cDNA; 1788 BP. DE DNA encoding novel human diagnostic protein #25802. PN WO200175067-A2. PD 11-OCT-2001. PA (HYSE-) HYSEQ INC. Best Local Similarity: 29.31% Query Match: 7.91% RESULT 1368 ID AAS93927 standard; cDNA; 2019 BP. DE DNA encoding novel human diagnostic protein #29731. PN WO200175067-A2. PD 11-OCT-2001. PA (HYSE-) HYSEQ INC. Best Local Similarity: 29.31% Query Match: 7.91% RESULT 1369 ID AAS84011 standard; cDNA; 2019 BP. DE DNA encoding novel human diagnostic protein #19815. PN WO200175067-A2. PD 11-OCT-2001. PA (HYSE-) HYSEQ INC. Best Local Similarity: 29.31% Query Match: 7.91% RESULT 1370 ID AAS82441 standard; cDNA; 2244 BP. DE DNA encoding novel human diagnostic protein #18245. PN WO200175067-A2. PD 11-OCT-2001. PA (HYSE-) HYSEQ INC. Best Local Similarity: 29.31% Query Match: 7.91% RESULT 1371 ID ADO07724 standard; cDNA; 2298 BP. DE Fly polynucleotide #24. PN US2004071700-A1. PD 15-APR-2004. PA (LIFE-) LIFE SCI DEV CORP.	Mismatches: 63 Indels: 52	Mismatches: 70 Indels: 41
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Best Local Similarity: 25.97% Mismatches: 51  
Query Match: 7.91% Indels: 41  
RESULT 1372  
ID AAV19281 standard; DNA; 2409 BP.  
DE H. insolens cellulase NC2 genomic sequence.  
PN JP08126492-A.  
PD 21-MAY-1996.  
PA (MEIJ ) MEIJI SEIKA KAISHA LTD.  
Best Local Similarity: 26.77% Mismatches: 45  
Query Match: 7.91% Indels: 23  
RESULT 1373  
ID AAV19377 standard; DNA; 2409 BP.  
DE Humicola insolens cellulase NCE2 gene.  
PN WO9803667-A1.  
PD 29-JAN-1998.  
PA (MEIJ ) MEIJI SEIKA KAISHA LTD.  
Best Local Similarity: 26.77% Mismatches: 45  
Query Match: 7.91% Indels: 23  
RESULT 1374  
ID AAQ81966 standard; DNA; 2454 BP.  
DE Human lysosomal membrane sialoglycoprotein lamp-1 DNA.  
PN WO9429342-A1.  
PD 22-DEC-1994.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
PA (UNMI ) UNIV MICHIGAN.  
Best Local Similarity: 23.63% Mismatches: 63  
Query Match: 7.91% Indels: 52  
RESULT 1375  
ID ABK83772 standard; cDNA; 2455 BP.  
DE Human cDNA differentially expressed in granulocytic cells #343.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 23.63% Mismatches: 63  
Query Match: 7.91% Indels: 52  
RESULT 1376  
ID ADP65852 standard; DNA; 2455 BP.  
DE Human lysosomal membrane glycoprotein-1 (LAMP1) mRNA, DNA.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Best Local Similarity: 23.63% Mismatches: 63  
Query Match: 7.91% Indels: 52  
RESULT 1377  
ID ADP65085 standard; DNA; 2455 BP.  
DE Human lysosomal-associated membrane protein 1 (LAMP1) DNA sequence.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Best Local Similarity: 23.63% Mismatches: 63  
Query Match: 7.91% Indels: 52  
RESULT 1378  
ID ADN03754 standard; cDNA; 2455 BP.  
DE Antipsoriatic cDNA sequence #75.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 23.63% Mismatches: 63  
Query Match: 7.91% Indels: 52  
RESULT 1379  
ID ADP03003 standard; cDNA; 2455 BP.  
DE Human housekeeping gene cDNA #44.  
PN JP2004135552-A.  
PD 13-MAY-2004.  
PA (NIGA ) NGK INSULATORS LTD.  
Best Local Similarity: 23.63% Mismatches: 63  
Query Match: 7.91% Indels: 52  
RESULT 1380  
ID ADP49319 standard; DNA; 2455 BP.  
DE Human lysosomal associated membrane protein LAMP coding sequence #1.  
PN WO2004048537-A2.  
PD 10-JUN-2004.  
PA (EXEL-) EXELIXIS INC.

Best Local Similarity: 23.63% Mismatches: 63  
Query Match: 7.91% Indels: 52  
RESULT 1381  
ID ADS88501 standard; cDNA; 2455 BP.  
DE Human housekeeping gene cDNA sequence SEQ ID NO:44.  
PN WO2004035785-A1.  
PD 29-APR-2004.  
PA (NIGA ) NGK INSULATORS LTD.  
Best Local Similarity: 23.63% Mismatches: 63  
Query Match: 7.91% Indels: 52  
RESULT 1382  
ID ADP23230 standard; cDNA; 2455 BP.  
DE PRO polypeptide encoding cDNA SEQ ID NO:324.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 23.63% Mismatches: 63  
Query Match: 7.91% Indels: 52  
RESULT 1383  
ID ABU18124 standard; DNA; 3183 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 5845.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 31.63% Mismatches: 43  
Query Match: 7.91% Indels: 16  
RESULT 1384  
ID AAT13688 standard; DNA; 675 BP.  
DE AGNPV ORF 91, residues 78661-77987.  
PN WO9601320-A2.  
PD 18-JAN-1996.  
PA (NATU-) NATURAL ENVIRONMENT RES COUNCIL.  
Best Local Similarity: 31.65% Mismatches: 33  
Query Match: 7.87% Indels: 8  
RESULT 1385  
ID ADK58412 standard; DNA; 1047 BP.  
DE Plant DNA sequence which confers altered metabolic characteristic #5795.  
PN WO2003020936-A1.  
PD 13-MAR-2003.  
PA (DOWC ) DOW CHEM CO.  
PA (DOWC ) DOW AGROSCIENCES LLC.  
Best Local Similarity: 23.50% Mismatches: 70  
Query Match: 7.87% Indels: 76  
RESULT 1386  
ID ADP29126 standard; DNA; 1053 BP.  
DE Human secreted protein encoding sequence SEQ ID #1124.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Best Local Similarity: 19.53% Mismatches: 78  
Query Match: 7.87% Indels: 126  
RESULT 1387  
ID ABD02026 standard; DNA; 1356 BP.  
DE Pseudomonas aeruginosa polynucleotide #630.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 20.68% Mismatches: 84  
Query Match: 7.87% Indels: 95  
RESULT 1388  
ID AA51962 standard; DNA; 2310 BP.  
DE Modified HIV-1 Env gp160, Lys121-Val200; Aen425-Lys432.  
PN WO200039303-A2.  
PD 06-JUL-2000.  
PA (CHIR ) CHIRON CORP.  
Best Local Similarity: 24.15% Mismatches: 67  
Query Match: 7.87% Indels: 78  
RESULT 1389  
ID AA51954 standard; DNA; 2535 BP.  
DE Modified HIV-1 Env gp160, Aen425-Lys432.  
PN WO200039303-A2.  
PD 06-JUL-2000.  
PA (CHIR ) CHIRON CORP.

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Best Local Similarity: 24.15% Mismatches: 67
Query Match: 7.87% Indels: 78
RESULT 1390
ID ABL28110 standard; DNA; 2665 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35803.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Best Local Similarity: 24.15% Mismatches: 66
Query Match: 7.87% Indels: 66
RESULT 1391
ID ABD2080 standard; DNA; 2955 BP.
DE Pseudomonas aeruginosa polynucleotide #684.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 20.68% Mismatches: 84
Query Match: 7.87% Indels: 95
RESULT 1392
ID ABD2123 standard; DNA; 3150 BP.
DE Pseudomonas aeruginosa polynucleotide #727.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 20.68% Mismatches: 84
Query Match: 7.87% Indels: 95
RESULT 1393
ID AAT13635 standard; DNA; 133894 BP.
DE AcNPV genomic DNA clone 6.
PN WO9601320-A2.
PD 18-JAN-1996.
PA (NATU-) NATURAL ENVIRONMENT RES COUNCIL.
Best Local Similarity: 31.65% Mismatches: 33
Query Match: 7.87% Indels: 8
RESULT 1394
ID AQO7766 standard; cDNA; 1701 BP.
DE Nucleotide sequence of serine protease INTP039.
PN WO2004053117-A2.
PD 24-JUN-2004.
PA (INPH-) INPHARMATICA LTD.
Best Local Similarity: 25.77% Mismatches: 54
Query Match: 7.82% Indels: 53
RESULT 1395
ID ABK99974 standard; cDNA; 1738 BP.
DE Human CADPKL cDNA #2.
PN WO200254939-A2.
PD 18-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 24.23% Mismatches: 55
Query Match: 7.82% Indels: 66
RESULT 1396
ID ABL12433 standard; cDNA; 1946 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31781.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Best Local Similarity: 23.26% Mismatches: 59
Query Match: 7.82% Indels: 52
RESULT 1397
ID AAS57123 standard; cDNA; 1946 BP.
DE cDNA encoding Drosophila G-protein coupled receptor, GCPR #26.
PN WO200170980-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Best Local Similarity: 23.26% Mismatches: 59
Query Match: 7.82% Indels: 52
RESULT 1398
ID ADC35825 standard; cDNA; 1946 BP.
DE Drosophila G protein coupled receptor cDNA seq id 27.
PN US2003092124-A1.
PD 15-MAY-2003.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 23.26% Mismatches: 59
Query Match: 7.82% Indels: 52
RESULT 1399
ID ADM01511 standard; cDNA; 1955 BP.
DE Human cDNA of the invention SEQ ID NO.196.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 22.31% Mismatches: 88
Query Match: 7.82% Indels: 78
RESULT 1400
ID AAI60703 standard; cDNA; 1956 BP.
DE Human polynucleotide SEQ ID NO 4692.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 24.23% Mismatches: 55
Query Match: 7.82% Indels: 66
RESULT 1401
ID AAI58917 standard; cDNA; 2165 BP.
DE Human polynucleotide SEQ ID NO 1120.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 24.23% Mismatches: 55
Query Match: 7.82% Indels: 66
RESULT 1402
ID ADQ99139 standard; cDNA; 2165 BP.
DE DNA encoding human GPCR-like protein seqid 809.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 24.23% Mismatches: 55
Query Match: 7.82% Indels: 66
RESULT 1403
ID ADB48899 standard; cDNA; 2165 BP.
DE Novel human cDNA SEQ ID NO 809.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
Best Local Similarity: 24.23% Mismatches: 55
Query Match: 7.82% Indels: 66
RESULT 1404
ID AAD36140 standard; DNA; 2447 BP.
DE Human calmodulin kinase, CAMK-XI gene.
PN WO200224947-A2.
PD 28-MAR-2002.
PA (KINE-) KINETEK PHARM INC.
PA (UYBR-) UNIV BRITISH COLUMBIA.
Best Local Similarity: 24.23% Mismatches: 55
Query Match: 7.82% Indels: 66
RESULT 1405
ID ABL12432 standard; cDNA; 3946 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31778.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Best Local Similarity: 20.58% Mismatches: 91
Query Match: 7.82% Indels: 88
RESULT 1406
ID AAS57122 standard; DNA; 3946 BP.
DE DNA encoding Drosophila G-protein coupled receptor, GCPR #26.
PN WO200170980-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Best Local Similarity: 20.58% Mismatches: 91
Query Match: 7.82% Indels: 88
RESULT 1407
ID ADC35824 standard; DNA; 3946 BP.
DE Drosophila G protein coupled receptor genomic DNA seq id 26.
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PN US2003092124-A1.  
PD 15-MAY-2003.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 20.58%  
Query Match: 7.82%  
Mismatch: 91  
Indel: 88  
RESULT 1408  
ID AD853355 standard; DNA; 4238 BP.  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3897.  
PN WO2003065993-A2.  
PD 14-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 25.23%  
Query Match: 7.82%  
Mismatch: 83  
Indel: 50  
RESULT 1409  
ID AC42734 standard; DNA; 6210 BP.  
DE Geldanamycin PKS module 1 DNA sequence, SEQ ID 1.  
PN WO2003013430-A2.  
PD 20-FEB-2003.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Best Local Similarity: 32.04%  
Query Match: 7.82%  
Mismatch: 47  
Indel: 10  
RESULT 1410  
ID AAD61810 standard; DNA; 6210 BP.  
DE Streptomyces geldanus polyketide synthase (PKS) gene #1.  
PN US2003114450-A1.  
PD 19-JUN-2003.  
PA (SANT/) SANTI D.  
PA (MYLE/) MYLES D C.  
PA (TIAN/) TIAN Z.  
PA (HUTC/) HUTCHINSON C R.  
PA (JOHN/) JOHNSON R.  
PA (ZHOU/) ZHOU Y.  
PA (FENG/) FENG L.  
Best Local Similarity: 32.04%  
Query Match: 7.82%  
Mismatch: 47  
Indel: 10  
RESULT 1411  
ID ACA37577 standard; DNA; 31263 BP.  
DE Prokaryotic essential gene #19234.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 28.21%  
Query Match: 7.82%  
Mismatch: 57  
Indel: 60  
RESULT 1412  
ID ADI39159 standard; DNA; 85692 BP.  
DE Streptomyces hygroscopicus geldanamycin gene cluster, SEQ ID NO:1.  
PN WO2003106653-A2.  
PD 24-DEC-2003.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
PA (REID/) REID R C.  
Best Local Similarity: 32.04%  
Query Match: 7.82%  
Mismatch: 47  
Indel: 10  
RESULT 1413  
ID AB081845 standard; DNA; 349980 BP.  
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1101.  
PN EPI227152-A1.  
PD 31-JUL-2002.  
PA (NEST) SOC PROD NESTLE SA.  
Best Local Similarity: 35.06%  
Query Match: 7.82%  
Mismatch: 35  
Indel: 8  
RESULT 1414  
ID ADC72389 standard; DNA; 515 BP.  
DE DNA Seq ID101 related to herbicide resistance and tolerance.  
PN WO2003020956-A2.  
PD 13-MAR-2003.  
PA (DOWC) DOW CHEM CO.  
Best Local Similarity: 28.70%  
Query Match: 7.78%  
Mismatch: 32  
Indel: 39  
RESULT 1415  
ID ADC76620 standard; DNA; 515 BP.  
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1889.  
PN WO2003020905-A2.  
PD 13-MAR-2003.

PA (DOWC) DOW CHEM CO.  
Best Local Similarity: 28.70%  
Query Match: 7.78%  
Mismatch: 32  
Indel: 39  
RESULT 1416  
ID ADK59253 standard; DNA; 515 BP.  
DE Plant DNA sequence which confers altered metabolic characteristic #6636.  
PN WO2003020936-A1.  
PD 13-MAR-2003.  
PA (DOWC) DOW CHEM CO.  
Best Local Similarity: 28.70%  
Query Match: 7.78%  
Mismatch: 32  
Indel: 39  
RESULT 1417  
ID AAV53721 standard; cDNA; 759 BP.  
DE The ORF of the cloned duplicate of human aggrecan G1-B domain.  
PN EP861903-A1.  
PD 02-SEP-1998.  
PA (UHLE/) UHLENKUEKEN J.  
PA (SCHM/) SCHMIDT G.  
Best Local Similarity: 21.02%  
Query Match: 7.78%  
Mismatch: 77  
Indel: 36  
RESULT 1418  
ID AAV53720 standard; cDNA; 770 BP.  
DE Cloned duplicate of human aggrecan G1-B domain.  
PN EP861903-A1.  
PD 02-SEP-1998.  
PA (UHLE/) UHLENKUEKEN J.  
PA (SCHM/) SCHMIDT G.  
Best Local Similarity: 21.02%  
Query Match: 7.78%  
Mismatch: 77  
Indel: 36  
RESULT 1419  
ID ABD05199 standard; DNA; 795 BP.  
DE Pseudomonas aeruginosa polynucleotide #3803.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 24.30%  
Query Match: 7.78%  
Mismatch: 74  
Indel: 58  
RESULT 1420  
ID AB080359 standard; DNA; 1149 BP.  
DE A. fumigatus AfFGU3 DNA.  
PN WO2003012071-A2.  
PD 13-FEB-2003.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 23.24%  
Query Match: 7.78%  
Mismatch: 74  
Indel: 76  
RESULT 1421  
ID AAX27948 standard; DNA; 1422 BP.  
DE H. insolens Cel6A fungal cellulase coding sequence.  
PN WO9901544-A1.  
PD 14-JAN-1999.  
PA (NOVO) NOVO-NORDISK AS.  
Best Local Similarity: 27.86%  
Query Match: 7.78%  
Mismatch: 43  
Indel: 8  
RESULT 1422  
ID AAX27958 standard; DNA; 1437 BP.  
DE H. insolens Cel6A fungal cellulase coding sequence.  
PN WO9901544-A1.  
PD 14-JAN-1999.  
PA (NOVO) NOVO-NORDISK AS.  
Best Local Similarity: 27.66%  
Query Match: 7.78%  
Mismatch: 43  
Indel: 8  
RESULT 1423  
ID ADG76370 standard; cDNA; 1471 BP.  
DE Human incyte cDNA encoding an enzyme (SeqID 62).  
PN WO2003083082-A2.  
PD 09-OCT-2003.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 22.04%  
Query Match: 7.78%  
Mismatch: 57  
Indel: 59  
RESULT 1424

ID ABD05240 standard; DNA; 1623 BP.	PA (NPSP-) NPS PHARM INC.	
DE Pseudomonas aeruginosa polynucleotide #3844.	PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.	
PN US6551795-B1.	Best Local Similarity: 22.75%	Mismatches: 113
PD 22-APR-2003.	Query Match: 7.78%	Indels: 49
PA (GENO-) GENOME THERAPEUTICS CORP.	RESULT 1433	
Best Local Similarity: 24.30%	ID AAI72120 standard; cDNA to mRNA; 5275 BP.	
Query Match: 7.78%	DE cDNA encoding BopCar1.	
RESULT 1425	PN US6313146-B1.	
ID ADQ85383 standard; cDNA; 2529 BP.	PD 06-NOV-2001.	
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2197.	PA (NPSP-) NPS PHARM INC.	
PN WQ2004060270-A2.	Best Local Similarity: 22.75%	Mismatches: 113
PD 22-JUL-2004.	Query Match: 7.78%	Indels: 49
PA (GETH ) GENENTECH INC.	RESULT 1434	
PA (WUO/) WU T D.	ID AAX91461 standard; DNA; 867 BP.	
PA (ZHOU/) ZHOU Y.	DE T. gondii nTg867 reverse complement sequence.	
Best Local Similarity: 26.44%	PN W09932633-A1.	
Query Match: 7.78%	PD 01-JUL-1999.	
RESULT 1426	PA (HESK-) HESKA CORP.	
ID ADI21801 standard; cDNA; 2539 BP.	Best Local Similarity: 29.67%	Mismatches: 47
DE Novel human protein cDNA #60.	Query Match: 7.73%	Indels: 6
PN W02003025148-A2.	RESULT 1435	
PD 27-MAR-2003.	ID AAX91460 standard; DNA; 867 BP.	
PA (HYSE-) HYSEQ INC.	DE T. gondii immunogenic protein encoding DNA.	
Best Local Similarity: 26.44%	PN W09932633-A1.	
Query Match: 7.78%	PD 01-JUL-1999.	
RESULT 1427	PA (HESK-) HESKA CORP.	
ID AAL42738 standard; DNA; 2578 BP.	Best Local Similarity: 29.67%	Mismatches: 47
DE Human membrane protein coding sequence.	Query Match: 7.73%	Indels: 6
PN JP2002085074-A.	RESULT 1436	
PD 26-MAR-2002.	ID AAS42783 standard; cDNA; 867 BP.	
PA (KIRI ) KIRIN BREWERY KK.	DE T. gondii cDNA encoding immunogenic protein PTg288.	
Best Local Similarity: 26.44%	PN US2001014447-A1.	
Query Match: 7.78%	PD 16-AUG-2001.	
RESULT 1428	PA (MILH/) MILHAUSEN M J.	
ID ABD05062 standard; DNA; 4167 BP.	Best Local Similarity: 29.67%	Mismatches: 47
DE Pseudomonas aeruginosa polynucleotide #3666.	Query Match: 7.73%	Indels: 6
PN US6551795-B1.	RESULT 1437	
PD 22-APR-2003.	ID AAS42784 standard; cDNA; 867 BP.	
PA (GENO-) GENOME THERAPEUTICS CORP.	DE Reverse complement of T. gondii cDNA nTg288.	
Best Local Similarity: 24.30%	PN US2001014447-A1.	
Query Match: 7.78%	PD 16-AUG-2001.	
RESULT 1429	PA (MILH/) MILHAUSEN M J.	
ID AAV26962 standard; cDNA to mRNA; 5275 BP.	Best Local Similarity: 29.67%	Mismatches: 47
DE Bovine parathyroid calcium receptor 1 gene 5Kb fragment.	Query Match: 7.73%	Indels: 6
PN US5763569-A.	RESULT 1438	
PD 09-JUN-1998.	ID ADG17392 standard; DNA; 867 BP.	
PA (NPSP-) NPS PHARM INC.	DE T. gondii protein DNA #86.	
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.	PN US2003194393-A1.	
Best Local Similarity: 22.75%	PD 16-OCT-2003.	
Query Match: 7.78%	PA (MILH/) MILHAUSEN M J.	
RESULT 1430	Best Local Similarity: 29.67%	Mismatches: 47
ID AA225053 standard; cDNA to mRNA; 5275 BP.	Query Match: 7.73%	Indels: 6
DE Bovine parathyroid calcium receptor 1 nucleotide sequence.	RESULT 1439	
PN US5962314-A.	ID ADG17390 standard; cDNA; 867 BP.	
PD 05-OCT-1999.	DE T. gondii protein cDNA #6.	
PA (NPSP-) NPS PHARM INC.	PN US2003194393-A1.	
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.	PD 16-OCT-2003.	
Best Local Similarity: 22.75%	PA (MILH/) MILHAUSEN M J.	
Query Match: 7.78%	Best Local Similarity: 29.67%	Mismatches: 47
RESULT 1431	Query Match: 7.73%	Indels: 6
ID AAV82483 standard; cDNA to mRNA; 5275 BP.	RESULT 1440	
DE Bovine parathyroid calcium receptor BopCar 1 encoding cDNA.	ID AAS92828 standard; cDNA; 1200 BP.	
PN US5858684-A.	DE DNA encoding novel human diagnostic protein #28632.	
PD 12-JAN-1999.	PN W0200175067-A2.	
PA (NPSP-) NPS PHARM INC.	PD 11-OCT-2001.	
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.	PA (HYSE-) HYSEQ INC.	
Best Local Similarity: 22.75%	Best Local Similarity: 22.22%	Mismatches: 77
Query Match: 7.78%	Query Match: 7.73%	Indels: 40
RESULT 1432	RESULT 1441	
ID AAZ89296 standard; cDNA to mRNA; 5275 BP.	ID ADS57193 standard; cDNA; 1272 BP.	
DE Bovine calcium receptor BopCar1 cDNA.	DE Bacterial polynucleotide #9180.	
PN US6031003-A.	PD US2003233675-A1.	
PD 29-FEB-2000.	PD 18-DEC-2003.	



PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 28.12% Mismatches: 56  
 Query Match: 7.73% Indels: 40  
 RESULT 1442  
 ID ADM1029 standard; DNA; 1359 BP.  
 DE Clostridium botulinum neurotoxin A light chain nucleic acid.  
 PN WO2004031355-A2.  
 PD 15-APR-2004.  
 PA (UTMA-) UNIV MARYLAND BALTIMORE.  
 Best Local Similarity: 25.95% Mismatches: 61  
 Query Match: 7.73% Indels: 69  
 RESULT 1443  
 ID AAX91462 standard; DNA; 1397 BP.  
 DE T. gondii immunogenic protein encoding DNA.  
 PN WO9932633-A1.  
 PD 01-JUL-1999.  
 PA (HESK-) HESKA CORP.  
 Best Local Similarity: 29.67% Mismatches: 47  
 Query Match: 7.73% Indels: 6  
 RESULT 1444  
 ID AAX91463 standard; DNA; 1397 BP.  
 DE T. gondii ntG1397 reverse complement sequence.  
 PN WO9932633-A1.  
 PD 01-JUL-1999.  
 PA (HESK-) HESKA CORP.  
 Best Local Similarity: 29.67% Mismatches: 47  
 Query Match: 7.73% Indels: 6  
 RESULT 1445  
 ID AAS42786 standard; cDNA; 1397 BP.  
 DE Reverse complement of T. gondii cDNA ntG1397.  
 PN US2001014447-A1.  
 PD 16-AUG-2001.  
 PA (MILH/) MILHAUSEN M J.  
 Best Local Similarity: 29.67% Mismatches: 47  
 Query Match: 7.73% Indels: 6  
 RESULT 1446  
 ID AAS42785 standard; cDNA; 1397 BP.  
 DE T. gondii cDNA encoding immunogenic protein Ptg1397.  
 PN US2001014447-A1.  
 PD 16-AUG-2001.  
 PA (MILH/) MILHAUSEN M J.  
 Best Local Similarity: 29.67% Mismatches: 47  
 Query Match: 7.73% Indels: 6  
 RESULT 1447  
 ID ADG17395 standard; DNA; 1397 BP.  
 DE T. gondii protein DNA #87.  
 PN US2003194393-A1.  
 PD 16-OCT-2003.  
 PA (MILH/) MILHAUSEN M J.  
 Best Local Similarity: 29.67% Mismatches: 47  
 Query Match: 7.73% Indels: 6  
 RESULT 1448  
 ID ADG17393 standard; cDNA; 1397 BP.  
 DE T. gondii protein cDNA #7.  
 PN US2003194393-A1.  
 PD 16-OCT-2003.  
 PA (MILH/) MILHAUSEN M J.  
 Best Local Similarity: 29.67% Mismatches: 47  
 Query Match: 7.73% Indels: 6  
 RESULT 1449  
 ID ADF44597 standard; cDNA; 1493 BP.  
 DE Corn fructokinase cDNA #1.  
 PN US2003088882-A1.  
 PD 08-MAY-2003.  
 PA (HARV/) HARVELL L T.  
 PA (RAGG/) RAGGHIANI J J.  
 Best Local Similarity: 28.68% Mismatches: 49  
 Query Match: 7.73% Indels: 33  
 RESULT 1450

ID ADR85486 standard; DNA; 1536 BP.  
 DE Aspergillus fumigatus essential gene open reading frame #123.  
 PN WO2004067709-A2.  
 PD 12-AUG-2004.  
 PA (ELIT-) ELITRA PHARM INC.  
 PA (ELIT-) ELITRA CANADA LTD.  
 Best Local Similarity: 25.00% Mismatches: 63  
 Query Match: 7.73% Indels: 51  
 RESULT 1451  
 ID AAS89605 standard; cDNA; 1750 BP.  
 DE DNA encoding novel human diagnostic protein #25409.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 25.97% Mismatches: 79  
 Query Match: 7.73% Indels: 18  
 RESULT 1452  
 ID AAC41495 standard; DNA; 2469 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 32093.  
 PN EPI033405-A2.  
 PD 06-SEP-2000.  
 Best Local Similarity: 21.57% Mismatches: 62  
 Query Match: 7.73% Indels: 32  
 RESULT 1453  
 ID AAQ02831 standard; DNA; 2716 BP.  
 DE Sequence encoding tumour necrosis factor.  
 PN JP01285191-A.  
 PD 16-NOV-1989.  
 PA (GREC) GREEN CROSS CORP.  
 Best Local Similarity: 23.63% Mismatches: 64  
 Query Match: 7.73% Indels: 52  
 RESULT 1454  
 ID ADL90420 standard; DNA; 3393 BP.  
 DE Clostridial neurotoxin nucleotide sequence SEQ ID NO:138.  
 PN WO2004024909-A2.  
 PD 25-MAR-2004.  
 PA (HEAL-) HEALTH PROTECTION AGENCY.  
 Best Local Similarity: 23.25% Mismatches: 76  
 Query Match: 7.73% Indels: 65  
 RESULT 1455  
 ID ABL16368 standard; DNA; 7417 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 577.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Best Local Similarity: 37.50% Mismatches: 28  
 Query Match: 7.73% Indels: 23  
 RESULT 1456  
 ID ABL07608 standard; cDNA; 12713 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17306.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Best Local Similarity: 25.13% Mismatches: 76  
 Query Match: 7.73% Indels: 45  
 RESULT 1457  
 ID ABV94393 standard; cDNA; 813 BP.  
 DE Breast carcinoma related nucleotide sequence SEQ ID NO:384.  
 PN WO200246467-A2.  
 PD 13-JUN-2002.  
 PA (IPSO-) IPSOGEN.  
 Best Local Similarity: 27.52% Mismatches: 41  
 Query Match: 7.69% Indels: 23  
 RESULT 1458  
 ID ADR47322 standard; DNA; 1297 BP.  
 DE Periconia gene encoding a serine protease.  
 PN WO2004072279-A2.  
 PD 26-AUG-2004.  
 PA (NOVO) NOVOZYMES AS.  
 Best Local Similarity: 25.13% Mismatches: 62  
 Query Match: 7.69% Indels: 62  
 RESULT 1459  
 ID AAN91235 standard; DNA; 1368 BP.

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DE DNA sequence of preprospasmolysin.
PN DE3808456-A.
PD 28-SEP-1989.
PA (PLAC ) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.
Best Local Similarity: 30.77% Mismatches: 44
Query Match: 7.69% Indels: 5
RESULT 1460
ID ACA26216 standard; DNA; 1629 BP.
DE Prokaryotic essential gene #7873.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 24.31% Mismatches: 93
Query Match: 7.69% Indels: 40
RESULT 1461
ID ABZ41778 standard; DNA; 1728 BP.
DE N. gonorrhoeae nucleotide sequence SEQ ID 8145.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Best Local Similarity: 23.90% Mismatches: 71
Query Match: 7.69% Indels: 62
RESULT 1462
ID AAZ54260 standard; DNA; 1731 BP.
DE Neisseria gonorrhoeae ORF 730 partial DNA sequence SEQ ID NO:2469.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR ) CHIRON CORP.
Best Local Similarity: 23.90% Mismatches: 71
Query Match: 7.69% Indels: 62
RESULT 1463
ID ADA71387 standard; DNA; 1815 BP.
DE Rice gene, SEQ ID 4710.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
Best Local Similarity: 28.39% Mismatches: 43
Query Match: 7.69% Indels: 50
RESULT 1464
ID ABZ39678 standard; DNA; 1815 BP.
DE N. gonorrhoeae nucleotide sequence SEQ ID 3945.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Best Local Similarity: 23.90% Mismatches: 71
Query Match: 7.69% Indels: 62
RESULT 1465
ID ABD11870 standard; DNA; 1929 BP.
DE Pseudomonas aeruginosa polynucleotide #10474.
PN US6551795-B1..
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 23.85% Mismatches: 77
Query Match: 7.69% Indels: 63
RESULT 1466
ID ADA48491 standard; DNA; 2015 BP.
DE Rice gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
Best Local Similarity: 28.39% Mismatches: 43
Query Match: 7.69% Indels: 50
RESULT 1467
ID AAAS1960 standard; DNA; 2322 BP.
DE Modified HIV-1 Env gp160, Arg426-Lys432.
PN WO200039303-A2.
PD 06-JUL-2000.
PA (CHIR ) CHIRON CORP.
Best Local Similarity: 23.73% Mismatches: 70
Query Match: 7.69% Indels: 76
RESULT 1468
ID ADS57996 standard; cDNA; 2328 BP.
DE

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DE Bacterial polynucleotide #9983.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 24.69% Mismatches: 48
Query Match: 7.69% Indels: 51
RESULT 1469
ID AAAS1953 standard; DNA; 2541 BP.
DE Modified HIV-1 Env gp160, Arg426-Lys432.
PN WO200039303-A2.
PD 06-JUL-2000.
PA (CHIR ) CHIRON CORP.
Best Local Similarity: 23.73% Mismatches: 70
Query Match: 7.69% Indels: 76
RESULT 1470
ID ABL16369 standard; DNA; 2607 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 580.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Best Local Similarity: 32.93% Mismatches: 34
Query Match: 7.69% Indels: 9
RESULT 1471
ID AAX60539 standard; DNA; 4435 BP.
DE C. trachomatis LGV L2 HMW protein encoding DNA.
PN WO9917741-A1.
PD 15-APR-1999.
PA (ANTE-) ANTEX BIOLOGICS INC.
Best Local Similarity: 23.36% Mismatches: 61
Query Match: 7.69% Indels: 79
RESULT 1472
ID ABK91474 standard; DNA; 6658 BP.
DE Modified HIV protein-encoding plasmid DNA #26.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Best Local Similarity: 28.16% Mismatches: 66
Query Match: 7.69% Indels: 40
RESULT 1473
ID ABK91509 standard; DNA; 6730 BP.
DE Modified HIV protein-encoding plasmid DNA #61.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Best Local Similarity: 28.16% Mismatches: 66
Query Match: 7.69% Indels: 40
RESULT 1474
ID ABK91468 standard; DNA; 6736 BP.
DE Modified HIV protein-encoding plasmid DNA #20.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Best Local Similarity: 28.16% Mismatches: 66
Query Match: 7.69% Indels: 40
RESULT 1475
ID ABK91503 standard; DNA; 6808 BP.
DE Modified HIV protein-encoding plasmid DNA #55.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Best Local Similarity: 28.16% Mismatches: 66
Query Match: 7.69% Indels: 40
RESULT 1476
ID ABK91489 standard; DNA; 7909 BP.
DE Modified HIV protein-encoding plasmid DNA #41.
DE

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PN WO200232943-A2.  
PD 25-APR-2002.  
PA (USH) US DEPT HEALTH & HUMAN SERVICES.  
PA (CHAD/) CHADABARTI B K.  
Best Local Similarity: 28.16% Mismatches: 66  
Query Match: 7.69% Indels: 40  
RESULT 1477  
ID ABK91483 standard; DNA; 7987 BP.  
DE Modified HIV protein-encoding plasmid DNA #35.  
PN WO200232943-A2.  
PD 25-APR-2002.  
PA (USH) US DEPT HEALTH & HUMAN SERVICES.  
PA (CHAD/) CHADABARTI B K.  
Best Local Similarity: 28.16% Mismatches: 66  
Query Match: 7.69% Indels: 40  
RESULT 1478  
Best Local Similarity: 23.36% Mismatches: 61  
Query Match: 7.69% Indels: 79  
RESULT 1479  
Best Local Similarity: 23.42% Mismatches: 83  
Query Match: 7.69% Indels: 19  
RESULT 1480  
ID ABQ34166 standard; DNA; 593 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20757.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 27.52% Mismatches: 36  
Query Match: 7.64% Indels: 28  
RESULT 1481  
ID ABQ34167 standard; DNA; 593 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20758.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 27.52% Mismatches: 36  
Query Match: 7.64% Indels: 28  
RESULT 1482  
ID ADR85331 standard; DNA; 1110 BP.  
DE Aspergillus fumigatus essential gene with introns #555.  
PN WO2004067709-A2.  
PD 12-AUG-2004.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 23.56% Mismatches: 85  
Query Match: 7.64% Indels: 58  
RESULT 1483  
ID ABT06525 standard; DNA; 1150 BP.  
DE HOXA5 gene promoter sequence.  
PN WO200259347-A2.  
PD 01-AUG-2002.  
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
Best Local Similarity: 32.91% Mismatches: 27  
Query Match: 7.64% Indels: 14  
RESULT 1484  
ID ADM83708 standard; DNA; 1150 BP.  
DE Human homeobox gene A5 (HOXA5) promoter DNA #1.  
PN US2003138783-A1.  
PD 24-JUL-2003.  
PA (SUKU/) SUKUMAR S.  
PA (EVRO/) EVRON E.  
PA (DOOL/) DOOLEY W C.  
PA (SACC/) SACCCHI N.  
PA (DAVI/) DAVIDSON N.  
PA (FACK/) FACKLER M J.  
Best Local Similarity: 32.91% Mismatches: 27  
Query Match: 7.64% Indels: 14  
RESULT 1485  
ID ADR83433 standard; DNA; 1332 BP.  
DE Human homeo box A5 DNA, target gene of miRNA.  
PN WO2004076622-A2.  
PD 10-SEP-2004.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

Best Local Similarity: 32.91% Mismatches: 27  
Query Match: 7.64% Indels: 14  
RESULT 1486  
ID ADB69782 standard; DNA; 1371 BP.  
DE C. neoformans open reading frame SEQ ID NO:2187.  
PN WO2003052076-A2.  
PD 26-JUN-2003.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 24.51% Mismatches: 37  
Query Match: 7.64% Indels: 20  
RESULT 1487  
ID ADA69648 standard; DNA; 1518 BP.  
DE Rice gene. SEQ ID 2971.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Best Local Similarity: 23.58% Mismatches: 78  
Query Match: 7.64% Indels: 71  
RESULT 1488  
ID ADQ25471 standard; DNA; 1544 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8291.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Best Local Similarity: 32.91% Mismatches: 27  
Query Match: 7.64% Indels: 14  
RESULT 1489  
ID AAL26527 standard; cDNA; 1574 BP.  
DE Human breast cancer expressed polynucleotide 18984.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Best Local Similarity: 32.91% Mismatches: 27  
Query Match: 7.64% Indels: 14  
RESULT 1490  
ID AAL26465 standard; cDNA; 1574 BP.  
DE Human breast cancer expressed polynucleotide 18922.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Best Local Similarity: 32.91% Mismatches: 27  
Query Match: 7.64% Indels: 14  
RESULT 1491  
ID AAL26532 standard; cDNA; 1574 BP.  
DE Human breast cancer expressed polynucleotide 18989.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Best Local Similarity: 32.91% Mismatches: 27  
Query Match: 7.64% Indels: 14  
RESULT 1492  
ID ADF81842 standard; DNA; 1636 BP.  
DE Leukaemia-related DNA sequence #2398.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
PA (HAPE/) HAERLACH T.  
PA (SCHO/) SCHOCH C.  
PA (KERN/) KERN W.  
Best Local Similarity: 32.91% Mismatches: 27  
Query Match: 7.64% Indels: 14  
RESULT 1493  
ID ADF38056 standard; cDNA; 2089 BP.  
DE Synchronised tobacco BY2 cDNA sequence SEQ ID NO:115.  
PN WO2003085115-A2.  
PD 16-OCT-2003.  
PA (CROP-) CROPDISEIGN NV.  
Best Local Similarity: 23.63% Mismatches: 104  
Query Match: 7.64% Indels: 47  
RESULT 1494  
ID ACN41796 standard; cDNA; 2167 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:671.

PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 32.14% Mismatches: 41  
Query Match: 7.64% Indels: 8  
RESULT 1495  
ID ACN41509 standard; cDNA; 2167 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:384.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 32.14% Mismatches: 41  
Query Match: 7.64% Indels: 8  
RESULT 1496  
ID ADA70158 standard; DNA; 2664 BP.  
DE Rice gene, SEQ ID 3481.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Best Local Similarity: 26.87% Mismatches: 51  
Query Match: 7.64% Indels: 28  
RESULT 1497  
ID ADR84744 standard; DNA; 3110 BP.  
DE Aspergillus fumigatus essential gene genomic sequence #555.  
PN WO2004067709-A2.  
PD 12-AUG-2004.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 23.56% Mismatches: 85  
Query Match: 7.64% Indels: 58  
RESULT 1498  
ID ABL27410 standard; DNA; 3289 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 33703.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 24.12% Mismatches: 60  
Query Match: 7.64% Indels: 70  
RESULT 1499  
ID ABZ09895 standard; DNA; 3523 BP.  
DE Human 5' and/or regulatory region of HOXA5 DNA SEQ ID NO:35.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 32.91% Mismatches: 27  
Query Match: 7.64% Indels: 14  
RESULT 1500  
ID ADE84042 standard; DNA; 6523 BP.  
DE 5' regulatory region of human gene HOXA5.  
PN WO2003044226-A2.  
PD 30-MAY-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 32.91% Mismatches: 27  
Query Match: 7.64% Indels: 14

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 8, 2005, 16:31:30 ; Search time 4154.4 Seconds  
(without alignments)  
2950.295 Million cell updates/sec

Title: US-10-063-670-6

Perfect score: 1657

Sequence: 1 MARCFSLVLLTSTWTRLL.....NPBESKSPKTVRCLEAEV 322

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2 1/USPTO.spool h/US10063670/runat.06102005.112745.221/app.query.fasta\_1.910  
-DB=EST -OPMT=fastap -SUPFI=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10063670 -CGN 1 4385 @runat.06102005.112745.221 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hc.\*  
4: gb\_hc.\*  
5: gb\_est3.\*  
6: gb\_est4.\*  
7: gb\_est6.\*  
8: gb\_gsl1.\*  
9: gb\_gsl2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1657	100.0	1091	1	AL550279
2	1657	100.0	1781	3	CR598862
3	1657	100.0	1786	3	CR614245
4	1657	100.0	1797	3	CR604450
5	1657	100.0	1820	3	CR612000
6	1657	100.0	1898	3	CR597409
7	1657	100.0	1911	3	CR614790
8	1657	100.0	1925	3	CR595979
9	1657	100.0	1945	3	CR605021

10	1510.5	91.2	1045	1	AL550621
11	1480	89.3	965	1	AL552299
12	1476.5	89.1	1090	1	AL546669
13	1439	86.8	1043	1	AL551020
14	1347.5	81.3	1823	3	CR599107
15	1323.5	79.9	945	1	AL553858
16	1316	79.4	845	5	BA559046
17	1283	77.4	977	5	BA366718
18	1278	77.1	1023	1	AL550911
19	1275	76.9	922	1	AL549512
20	1264	76.3	855	1	AL543874
21	1262	76.2	1056	1	AL547774
22	1253	75.6	1059	1	AL552127
23	1243.5	75.0	1036	5	BA402505
24	1243	75.0	1017	1	AL544430
25	1235	74.5	973	5	BA366589
26	1230	74.2	1033	1	AL552661
27	1225.5	74.0	1064	1	AL550829
28	1213	73.2	769	1	AL546217
29	1207.5	72.9	998	1	AL546623
30	1200	72.4	896	1	AL550615
31	1168	70.5	961	1	AL552777
32	1160	70.0	863	4	BI761420
33	1142	68.9	835	1	AL545331
34	1103	66.6	2607	3	AK004726
35	1054.5	63.6	760	6	CB959809
36	1019	61.5	583	5	BP291949
37	1019	61.5	746	6	CD238639
38	1000	60.4	846	5	BA418211
39	970	58.5	743	1	AL598709
40	961	58.0	580	5	BP339718
41	935.5	56.5	801	4	BA483354
42	929	56.1	1018	1	AL553712
43	926	55.9	794	4	BA566260
44	925	55.8	58	5	BP198472
45	923	55.7	1765	3	CR622723
46	909.5	54.9	898	5	BP159588
47	905	54.6	1023	6	BY704927
48	901	54.4	596	1	AA046671
49	892	53.8	911	6	CB966791
50	874.5	52.8	802	6	CB994314
51	844	50.9	1070	1	AL546565
52	826	49.8	751	7	CO737890
53	822.5	49.6	757	6	CB229605
54	820	49.5	580	5	BP341529
55	812	49.0	581	5	BP197816
56	807	48.7	877	4	BI763579
57	795.5	48.0	964	5	BU504417
58	778	47.0	581	5	BP197366
59	771	46.5	582	5	BP320362
60	766	46.2	895	1	AL553920
61	737	44.5	487	6	CA407758
62	733.5	44.3	1298	7	CF110966
63	732	44.2	696	7	CV111589
64	725.5	43.8	910	6	CA786491
65	712.5	43.0	974	6	CB988195
66	690	41.6	465	7	H69328
67	675	40.7	841	4	BI730362
68	660.5	39.9	670	2	BB611620
69	635.5	38.4	682	5	BP434862
70	634	38.3	584	5	BP345245
71	627	37.8	581	5	BP320205
72	612.5	37.0	579	1	AI391129
73	605	36.5	793	9	AY411057
74	603.5	36.4	556	5	BM935573
75	587	35.4	368	4	EG012717
76	576.5	34.8	499	2	BE198670
77	573	34.6	872	4	EG541447
78	567.5	34.2	1070	6	CB989089
79	564	34.0	473	6	CB269023
80	563	34.0	790	9	AY411058
81	562.5	33.9	581	5	BP344636
82	560	33.8	535	2	BE756611

83	557.5	33.6	735	7	CK364727	CK364727 AGENCOURT	
c	84	530	1130	1	AL574194	AL574194	
85	523.5	31.6	411	7	H02823	Y741h11.r1	
86	517	31.2	437	6	CA406980		
87	511.5	30.9	455	1	A1006667	ue16b07.y	
88	511.5	30.9	883	5	B0239567		
89	509	30.7	409	2	AW961536	EST373608	
90	503	30.4	707	7	CK836545	4061500.B	
91	481.5	29.1	380	1	AA081350	z333h09.f	
92	472.5	28.5	813	5	B0388030		
93	470.5	28.4	474	7	CF791146	879311.MA	
94	470	28.4	581	5	BF338802	BF338802	
95	466.5	28.2	437	1	AJ686473	AJ686473	
96	450	27.2	865	6	CD106276	AGENCOURT	
97	447	27.0	675	7	CK958011	4098647.B	
98	445	26.9	444	7	T96904	ye55g09.r1	
99	443	26.7	673	7	CK949504		
100	438	26.4	776	7	CO567156	AGENCOURT	
101	434.5	26.2	540	5	BQ417943	1k53a10.y	
102	430	26.0	871	4	BG173551	602336969	
103	423	25.5	415	1	AA463325	z271f04.f	
104	417	25.2	656	4	BM426481	pgf2n.pk0	
105	407.5	24.6	569	2	BE627175	uu16h04.y	
106	406.5	24.5	366	7	R24376	yh30e08.r1	
107	397.5	24.0	479	2	BE847124	uw22b07.y	
108	387	23.4	328	1	AA297240	EST112782	
109	386.5	23.3	800	9	AY411059	Mus muscu	
110	382	23.1	807	5	B0125818	603150355	
111	380	22.9	418	6	CB765478	AMGNNUC.N	
112	378	22.8	371	2	BE684197	184504.MA	
113	371.5	22.4	747	5	B0324601	603492075	
114	360.5	21.8	745	7	CF520494	AGENCOURT	
115	353.5	21.3	385	7	W29485	mc02a12.r1	
c	116	351	1007	1	AL552625	AL552625	
117	347.5	21.0	469	2	BF471572	UI-M-BH3-	
c	118	343.5	20.7	993	1	AL575633	
119	333.5	20.1	449	2	BF041814	BP250014B	
c	120	322.5	19.5	1013	1	AL546590	AL546590
121	318	19.2	1010	1	AL571871	AL571871	
c	122	315.5	19.0	351	6	CB780898	AMGNNUC.C
c	123	315	19.0	779	7	CK773274	961895.MA
124	298.5	18.0	353	5	BY318491	BY318491	
125	291.5	17.6	354	5	BY107653	BY107653	
126	288	17.4	529	6	CD671330	fg03c09.y	
c	127	285	17.2	948	1	AL573693	AL573693
c	128	275.5	16.6	1006	1	AL571928	AL571928
129	275	16.6	540	4	BM253102	512458.MA	
c	130	275	16.6	751	7	CK775586	966716.MA
131	274.5	16.6	652	7	CF250037	esa007.f1	
132	259	15.6	974	7	CK404422	AUF IFHdk	
133	254.5	15.4	801	7	CK030244	AGENCOURT	
134	253	15.3	895	6	CA474635	AGENCOURT	
135	250.5	15.1	627	5	B0241066	603321257	
c	136	249	15.0	960	1	AL575514	AL575514
137	248	15.0	811	7	CF285506	AGENCOURT	
138	245	14.8	906	7	CF546586	AGENCOURT	
139	241	14.5	723	7	CF547545	AGENCOURT	
140	240	14.5	242	2	AW318386	um96a08.y	
c	141	239.5	14.5	924	1	AL550876	AL550876
142	238	14.4	390	7	H78909	yul1d03.r1	
143	233.5	14.1	405	6	BY766304	BY766304	
144	233	14.1	305	1	AV749159	AV749159	
145	233	14.1	318	7	R71437	vi51e04.r1	
146	233	14.1	337	7	R81462	yj02f03.r1	
147	232.5	14.0	576	5	BQ400750	NISC.mp11	
148	231.5	14.0	913	7	CK410366	AUF IPHdk	
149	228.5	13.8	600	6	CB512734	sealrqb54	
150	228	13.8	868	7	CF379047	AGENCOURT	
151	226	13.6	2851	3	AK045226	Mus muscu	
152	225.5	13.6	599	6	CB515759	sealrqb51	
153	224	13.5	759	7	CF285642	AGENCOURT	
154	224	13.5	827	7	CK471875	AGENCOURT	
155	224	13.5	833	6	CD361163	AGENCOURT	

c	156	222.5	13.4	954	5	BX418210	BX418210
157	220.5	13.3	431	4	BG657011	dab27a03.	
158	218.5	13.2	423	2	AW419846	fj84c10.y	
159	218.5	13.2	599	6	CB582683	AMGNNUC.N	
160	218.5	13.2	763	7	CO570158	AGENCOURT	
161	218.5	13.2	810	7	CK476032	AGENCOURT	
162	216	13.0	774	5	BP169122	BP169122	
163	216	13.0	905	5	BP166057	BP166057	
164	215.5	13.0	766	5	BP167565	BP167565	
165	215	13.0	825	5	BP157524	BP157524	
166	214.5	12.9	289	5	BY145458	BY145458	
167	214	12.9	598	6	CA367101	642837.NC	
168	212	12.8	1876	3	CR596847	full1-leng	
169	212	12.8	1955	3	CR621045	full1-leng	
170	211	12.7	721	7	CF763972	CES004694	
171	210	12.7	563	5	BQ566621	gi64e12.y	
172	208	12.6	793	7	CN823883	Oa_splbn_	
173	207	12.5	1906	3	AK087472	Mus muscu	
174	206.5	12.5	838	7	CF727499	UI-M-HB0-	
175	206	12.4	642	6	CB442342	692918.MA	
176	206	12.4	821	6	CA846294	haa12a06.	
177	206	12.4	824	7	CK791054	AGENCOURT	
178	204.5	12.3	828	5	EX078167	BX078167	
179	204	12.3	499	6	CD285349	G39163.54	
180	203.5	12.3	810	6	CB314546	AGENCOURT	
181	203	12.3	706	7	CN823877	Oa_splbn	
182	202.5	12.2	592	7	CN660471	A0705G09-	
183	202.5	12.2	615	7	CF907877	A0516A04-	
184	202.5	12.2	619	5	BQ393883	NISC_rg06	
185	202.5	12.2	623	7	CN661635	A0721H04-	
186	202.5	12.2	623	7	CN661701	A0722G02-	
187	202.5	12.2	638	7	CK624682	m124a09.y	
188	202.5	12.2	647	6	CA572928	K0542E07-	
189	202.5	12.2	650	7	CF909697	A05A0A04-	
190	202.5	12.2	666	6	BY731449	BY731449	
191	202.5	12.2	670	4	B1328140	602979293	
192	202	12.2	828	4	BG170766	602323885	
193	201.5	12.2	1085	5	BM913991	AGENCOURT	
194	201	12.1	867	5	BU184888	AGENCOURT	
195	201	12.1	1085	4	BM550721	AGENCOURT	
196	200.5	12.1	864	5	BQ690615	AGENCOURT	
197	200	12.1	820	4	BG760275	602716678	
198	200	12.1	916	5	BU166171	AGENCOURT	
199	200	12.1	1024	5	BM904914	AGENCOURT	
200	199.5	12.0	750	6	CD467776	Leuko81_6	
c	201	199	12.0	578	4	BI008726	QV3-RT007
202	199	12.0	627	5	BP280494	BP280494	
203	199	12.0	834	5	BU150725	AGENCOURT	
204	198.5	12.0	630	2	AW732334	bb03a02.y	
205	198.5	12.0	658	6	CD466155	LeukoN2_2	
206	198.5	12.0	749	6	CD470595	Leuko84_5	
207	198.5	12.0	750	6	CD466893	LeukoN2_8	
208	198.5	12.0	775	7	CN218866	RU0A0G05	
209	198	11.9	821	6	CD559300	AGENCOURT	
210	197.5	11.9	582	2	B8611006	B8611006	
211	197.5	11.9	677	6	BY744790	BY744790	
212	197.5	11.9	735	7	CN347081	170004249	
213	197.5	11.9	731	1	AL548444	AL548444	
214	197.5	11.9	831	4	BI856036	603383421	
215	197	11.9	886	4	CF251786	hdm004.co	
216	197	11.9	976	4	BM562794	AGENCOURT	
217	197	11.9	976	5	BQ957776	AGENCOURT	
218	196.5	11.9	658	6	CD469720	Leuko82_8	
219	196.5	11.9	660	6	CD469535	Leuko85_2	
220	196.5	11.9	669	6	CD470836		
221	196.5	11.9	796	4	BG868920	602784523	
222	196.5	11.9	819	4	B1333992	602997261	
223	196.5	11.9	851	4	BG750268	602709071	
224	196.5	11.9	925	2	BF311255	601898521	
225	196	11.8	588	4	BM742218	K-EST0014	
226	196	11.8	636	7	CV026388	Full1	
227	196	11.8	654	7	CN347082		
228	196	11.8	656	7	CN347074	170005318	
						CN347082	
						170004248	

229	196	11.8	698	7	CN347073	CN347073	170005325	302	191.5	11.6	582	7	CF256984	pha005_c0
230	196	11.8	699	4	BM763301	BM763301	K-EST0044	303	191.5	11.6	608	7	CF257313	pha009_f1
231	196	11.8	709	4	BG539893	BG539893	60256781	304	191.5	11.6	660	6	CD468968	LeukoS3_8
232	196	11.8	728	4	B1769128	B1769128	603053720	305	191.5	11.6	739	1	AJ450624	AJ450624
233	196	11.8	730	7	CN347080	CN347080	170004708	306	191.5	11.6	855	7	CF257095	pha006_g0
234	196	11.8	743	6	CB318661	CB318661	AGENCOURT	307	191.5	11.6	859	7	CF257757	pha015_a1
235	196	11.8	764	4	BG759720	BG759720	602711117	308	191.5	11.6	881	7	CF251803	hdm004_e0
236	196	11.8	791	4	BG485676	BG485676	602505976	309	191	11.5	393	7	CF144025	UI-HF-BP0
237	196	11.8	827	4	B1833320	B1833320	603087916	310	191	11.5	515	4	BM753415	K-EST0030
238	196	11.8	858	5	BQ223902	BQ223902	AGENCOURT	311	191	11.5	536	5	BP162646	BP162646
239	196	11.8	864	1	AL548999	AL548999	AGENCOURT	312	191	11.5	565	5	BP267691	BP267691
240	196	11.8	879	5	BQ962000	BQ962000	AGENCOURT	313	191	11.5	582	5	BP278066	BP278066
241	196	11.8	885	7	CF257093	CF257093	pha006_f1	314	191	11.5	582	5	BP356315	BP356315
242	196	11.8	889	7	CF251893	CF251893	hdm005_f1	315	191	11.5	582	5	BP354072	BP354072
243	196	11.8	890	5	BUI58569	BUI58569	AGENCOURT	316	191	11.5	598	5	BP279982	BP279982
244	196	11.8	894	5	BQ880928	BQ880928	AGENCOURT	317	191	11.5	602	5	BP279073	BP279073
245	196	11.8	903	6	CA455121	CA455121	AGENCOURT	318	191	11.5	625	2	AW732339	bb03b02_Y
246	196	11.8	906	5	BUI49945	BUI49945	AGENCOURT	319	191	11.5	697	4	BG912337	602806886
247	196	11.8	923	5	BQ946450	BQ946450	AGENCOURT	320	190.5	11.5	820	4	BM051234	BM051234
248	196	11.8	940	4	BG747697	BG747697	602705169	321	190.5	11.5	951	4	BG119674	602347092
249	196	11.8	985	5	BUI68480	BUI68480	AGENCOURT	322	190.5	11.5	973	4	B1820251	603036802
250	196	11.8	985	5	BX356719	BX356719	AGENCOURT	323	190	11.5	512	4	BM744870	K-EST0018
251	196	11.8	1004	5	BX439725	BX439725	AL552534	324	190	11.5	545	6	CB135807	CB135807
252	196	11.8	1010	1	AL552534	AL552534	AL552534	325	190	11.5	550	5	BP377364	BP377364
253	195.5	11.8	801	2	BG570280	BG570280	603332944	326	190	11.5	553	4	BM846600	K-EST0125
254	195.5	11.8	832	4	BG114530	BG114530	602884857	327	190	11.5	555	4	BM753425	K-EST0030
255	195.5	11.8	984	5	BQ677018	BQ677018	AGENCOURT	328	190	11.5	556	6	CB141325	K-EST0194
256	195.5	11.8	1054	5	BM918483	BM918483	AGENCOURT	329	190	11.5	556	6	CB141372	K-EST0194
257	195	11.8	476	2	AW501445	AW501445	UI-HF-BP0	330	190	11.5	558	7	CN482614	hw22e06_Y
258	195	11.8	579	5	BP268197	BP268197	AGENCOURT	331	190	11.5	561	4	BM743702	K-EST0016
259	195	11.8	738	5	BUI95946	BUI95946	AGENCOURT	332	190	11.5	563	4	BM840881	K-EST0118
260	195	11.8	928	5	BQ683148	BQ683148	AGENCOURT	333	190	11.5	569	4	BM848299	K-EST0128
261	195	11.8	1067	1	AL544334	AL544334	AL544334	334	190	11.5	569	4	BM853235	K-EST0134
262	194.5	11.7	503	6	CA573126	CA573126	K0546C07-	335	190	11.5	573	1	AU280746	AU280746
263	194.5	11.7	504	5	BQ562475	BQ562475	H4076B11-	336	190	11.5	576	5	BP279188	BP279188
264	194.5	11.7	509	2	AW761944	AW761944	u51f10_Y	337	190	11.5	578	4	BM742678	K-EST0015
265	194.5	11.7	519	6	CA570202	CA570202	K0503C08-	338	190	11.5	579	5	BP363851	BP363851
266	194.5	11.7	521	6	CA570891	CA570891	K0513B10-	339	190	11.5	580	5	BP236550	BP236550
267	194.5	11.7	522	6	CA873377	CA873377	K0924G02-	340	190	11.5	580	5	BP272835	BP272835
268	194.5	11.7	546	6	CA883079	CA883079	B0101A07-	341	190	11.5	581	4	B1824066	603038788
269	194.5	11.7	581	6	CA896005	CA896005	B0196A07-	342	190	11.5	581	5	BP206044	BP206044
270	194.5	11.7	883	5	BQ877431	BQ877431	AGENCOURT	343	190	11.5	581	5	BP221857	BP221857
271	194	11.7	574	4	BM742230	BM742230	K-EST0015	344	190	11.5	581	5	BP221889	BP221889
272	194	11.7	583	5	BP280870	BP280870	BP280870	345	190	11.5	581	5	BP222451	BP222451
273	194	11.7	625	4	BG822513	BG822513	K-EST0591	346	190	11.5	581	5	BP222755	BP222755
274	194	11.7	660	4	BM745022	BM745022	K-EST0018	347	190	11.5	581	5	BP225898	BP225898
275	194	11.7	662	5	BQ109366	BQ109366	imagegc_6	348	190	11.5	581	5	BP237035	BP237035
276	194	11.7	667	6	CB125104	CB125104	K-EST0173	349	190	11.5	581	5	BP252243	BP252243
277	194	11.7	668	4	BG421565	BG421565	602452141	350	190	11.5	581	5	BP252906	BP252906
278	194	11.7	668	4	BM763472	BM763472	K-EST0044	351	190	11.5	581	5	BP278646	BP278646
279	194	11.7	670	6	CB141293	CB141293	K-EST0194	352	190	11.5	581	5	BP280300	BP280300
280	194	11.7	676	4	BG250321	BG250321	602362454	353	190	11.5	581	5	BP280869	BP280869
281	194	11.7	678	6	CB136318	CB136318	K-EST0188	354	190	11.5	581	5	BP285640	BP285640
282	194	11.7	757	4	B1821097	B1821097	603035569	355	190	11.5	581	5	BP295553	BP295553
283	194	11.7	796	5	BUI527984	BUI527984	AGENCOURT	356	190	11.5	581	5	BP297294	BP297294
284	194	11.7	805	4	BG822701	BG822701	602725835	357	190	11.5	581	5	BP323904	BP323904
285	194	11.7	913	4	BG327238	BG327238	602426190	358	190	11.5	581	5	BP354214	BP354214
286	193.5	11.7	634	7	CA662209	CA662209	A0730E09-	359	190	11.5	581	5	BP355784	BP355784
287	193.5	11.7	1036	5	BM908486	BM908486	AGENCOURT	360	190	11.5	582	5	BP215631	BP215631
288	193	11.6	630	6	CD470529	CD470529	LeukoS4_5	361	190	11.5	582	5	BP223379	BP223379
289	193	11.6	635	6	CD468828	CD468828	LeukoS3_7	362	190	11.5	582	5	BP222548	BP222548
290	193	11.6	647	6	CD469564	CD469564	LeukoS2_4	363	190	11.5	582	5	BP223038	BP223038
291	193	11.6	649	6	CD469238	CD469238	LeukoS2_2	364	190	11.5	582	5	BP225812	BP225812
292	193	11.6	668	4	B1855939	B1855939	60338313	365	190	11.5	582	5	BP230984	BP230984
293	193	11.6	889	4	BG679238	BG679238	602672320	366	190	11.5	582	5	BP231716	BP231716
294	192.5	11.6	572	6	CB016588	CB016588	pgn1c_pk0	367	190	11.5	582	5	BP233787	BP233787
295	192.5	11.6	1184	5	BM906074	BM906074	AGENCOURT	368	190	11.5	582	5	BP278171	BP278171
296	192	11.6	582	5	BP236685	BP236685	AGENCOURT	369	190	11.5	582	5	BP278231	BP278231
297	192	11.6	582	5	BP278321	BP278321	BP278321	370	190	11.5	582	5	BP278305	BP278305
298	192	11.6	582	5	BP353372	BP353372	BP353372	371	190	11.5	582	5	BP278475	BP278475
299	192	11.6	959	5	BQ935522	BQ935522	AGENCOURT	372	190	11.5	582	5	BP278491	BP278491
300	191.5	11.6	469	1	AA794029	AA794029	vr37c07_X	373	190	11.5	582	5	BP279295	BP279295
301	191.5	11.6	500	6	CD734509	CD734509	4048585_1	374	190	11.5	582	5	BP279324	BP279324

375	190	11.5	582	5	BP279363	BP279363	448	190	11.5	598	6	CB132093	CB132093 K-EST0182
376	190	11.5	582	5	BP280048	BP280048	449	190	11.5	598	6	CB149427	CB149427 K-EST0205
377	190	11.5	582	5	BP280228	BP280228	450	190	11.5	600	4	BM742193	BM742193 K-EST0014
378	190	11.5	582	5	BP280613	BP280613	451	190	11.5	601	6	CD469117	CD469117 LeukoS2_1
379	190	11.5	582	5	BP280921	BP280921	452	190	11.5	603	5	BP278981	BP278981 LeukoS2_1
380	190	11.5	582	5	BP280955	BP280955	453	190	11.5	608	4	BM846665	BM846665 K-EST0125
381	190	11.5	582	5	BP280957	BP280957	454	190	11.5	613	4	BM846787	BM846787 K-EST0125
382	190	11.5	582	5	BP2809145	BP2809145	455	190	11.5	617	5	BP278547	BP278547 BP278547
383	190	11.5	582	5	BP303210	BP303210	456	190	11.5	625	5	BP280558	BP280558 BP280558
384	190	11.5	582	5	BP335831	BP335831	457	190	11.5	626	2	AW955521	AW955521 EST367591
385	190	11.5	582	5	BP336193	BP336193	458	190	11.5	635	2	AW239286	AW239286 x338d03.y
386	190	11.5	582	5	BP352339	BP352339	459	190	11.5	648	4	BG548953	BG548953 602575790
387	190	11.5	582	5	BP353072	BP353072	460	190	11.5	702	1	AU140087	AU140087 AU140087
388	190	11.5	582	5	BP353576	BP353576	461	190	11.5	835	4	BI161210	BI161210 602865668
389	190	11.5	582	5	BP353566	BP353566	462	190	11.5	837	4	BI161210	BI161210 602865668
390	190	11.5	582	5	BP363182	BP363182	463	190	11.5	929	5	BU501360	BU501360 AGENCOURT
391	190	11.5	582	5	BP363335	BP363335	464	190	11.5	158	4	BG323913	BG323913 60242942
392	190	11.5	582	5	BP365020	BP365020	465	189.5	11.4	548	2	BF039338	BF039338 BP250009A
393	190	11.5	582	5	BP365667	BP365667	466	189.5	11.4	761	1	AA637653	AA637653 v110e10.r
394	190	11.5	582	5	BP365708	BP365708	467	189	11.4	510	4	BM836382	BM836382 K-EST0112
395	190	11.5	582	5	BP365745	BP365745	468	189	11.4	592	5	BP279220	BP279220 BP279220
396	190	11.5	583	5	BP234498	BP234498	469	189	11.4	593	5	BP278114	BP278114 BP278114
397	190	11.5	583	5	BP234878	BP234878	470	189	11.4	583	5	BP279317	BP279317 BP279317
398	190	11.5	583	5	BP236879	BP236879	471	189	11.4	583	5	BP280964	BP280964 BP280964
399	190	11.5	583	5	BP278008	BP278008	472	189	11.4	587	5	BP277775	BP277775 BP277775
400	190	11.5	583	5	BP278196	BP278196	473	189	11.4	588	5	BP277718	BP277718 BP277718
401	190	11.5	583	5	BP278366	BP278366	474	188.5	11.4	359	6	BY788232	BY788232 BY788232
402	190	11.5	583	5	BP278548	BP278548	475	188.5	11.4	442	1	AI226003	AI226003 u108b06.y
403	190	11.5	583	5	BP278697	BP278697	476	188.5	11.4	590	1	AI151808	AI151808 u146c06.y
404	190	11.5	583	5	BP278792	BP278792	477	188.5	11.4	857	4	BI160643	BI160643 602865061
405	190	11.5	583	5	BP278933	BP278933	478	188.5	11.4	889	4	BI602413	BI602413 603251192
406	190	11.5	583	5	BP279202	BP279202	479	188	11.3	418	1	AL835535	AL835535 AL835535
407	190	11.5	583	5	BP279356	BP279356	480	188	11.3	515	4	BM753439	BM753439 K-EST0030
408	190	11.5	583	5	BP279519	BP279519	481	188	11.3	582	5	BP279321	BP279321 BP279321
409	190	11.5	583	5	BP279772	BP279772	482	188	11.3	582	5	BP353503	BP353503 BP353503
410	190	11.5	583	5	BP280081	BP280081	483	188	11.3	584	5	BP356262	BP356262 BP356262
411	190	11.5	583	5	BP280334	BP280334	484	187.5	11.3	579	5	BP339083	BP339083 BP339083
412	190	11.5	583	5	BP280604	BP280604	485	187.5	11.3	601	2	AW951906	AW951906 EST363976
413	190	11.5	583	5	BP280708	BP280708	486	187	11.3	557	6	CB140797	CB140797 K-EST0194
414	190	11.5	583	5	BP280810	BP280810	487	187	11.3	580	5	BP259795	BP259795 BP259795
415	190	11.5	583	5	BP280838	BP280838	488	187	11.3	583	5	BP277883	BP277883 BP277883
416	190	11.5	583	5	BP281053	BP281053	489	186.5	11.3	573	1	AA273296	AA273296 vco1e02.r
417	190	11.5	583	5	BP281058	BP281058	490	186	11.2	478	6	CD465065	CD465065 LeukoN1_1
418	190	11.5	583	5	BP281074	BP281074	491	186	11.2	495	6	CD465358	CD465358 LeukoN1_3
419	190	11.5	583	5	BP341512	BP341512	492	186	11.2	521	6	CD469959	CD469959 LeukoN4_2
420	190	11.5	583	5	BP352289	BP352289	493	186	11.2	526	6	CD464259	CD464259 LeukoN4_2
421	190	11.5	583	5	BP353855	BP353855	494	186	11.2	533	6	CD471150	CD471150 LeukoS5_4
422	190	11.5	583	5	BP354184	BP354184	495	186	11.2	548	6	CD469967	CD469967 LeukoS4_2
423	190	11.5	584	5	BP280286	BP280286	496	186	11.2	549	6	CD469106	CD469106 LeukoS2_1
424	190	11.5	585	5	BP253708	BP253708	497	186	11.2	549	6	CD471912	CD471912 LeukoS6_2
425	190	11.5	585	6	CB129134	CB129134 K-EST0178	498	186	11.2	554	6	CD469251	CD469251 LeukoS2_2
426	190	11.5	587	5	BP278759	BP278759	499	186	11.2	571	6	CD470950	CD470950 LeukoS5_3
427	190	11.5	587	5	BP278794	BP278794	500	186	11.2	576	6	CD471137	CD471137 LeukoS5_4
428	190	11.5	587	5	BP279977	BP279977	501	186	11.2	579	6	CD465192	CD465192 LeukoN1_2
429	190	11.5	587	5	BP280171	BP280171	502	186	11.2	582	5	BP365073	BP365073 BP365073
430	190	11.5	587	5	BP365344	BP365344	503	186	11.2	584	6	CD468526	CD468526 LeukoS3_3
431	190	11.5	588	5	BP236489	BP236489	504	186	11.2	596	6	CD471747	CD471747 LeukoS6_4
432	190	11.5	588	5	BP277748	BP277748	505	186	11.2	599	6	CD471683	CD471683 LeukoS6_4
433	190	11.5	588	5	BP278268	BP278268	506	186	11.2	602	6	CD470977	CD470977 LeukoS5_3
434	190	11.5	588	5	BP279065	BP279065	507	186	11.2	602	6	CD535917	CD535917 LeukoS5_5
435	190	11.5	588	5	BP365173	BP365173	508	186	11.2	607	5	BP280139	BP280139 BP280139
436	190	11.5	589	5	BP233222	BP233222	509	186	11.2	612	6	CD469627	CD469627 LeukoS2_7
437	190	11.5	589	6	CB130851	CB130851 K-EST0180	510	186	11.2	726	1	AV722410	AV722410 AV722410
438	190	11.5	592	4	BM848361	BM848361 K-EST0128	511	185.5	11.2	502	6	CA567008	CA567008 K0408F05-
439	190	11.5	593	4	BP277740	BP277740	512	185	11.2	488	6	CD536274	CD536274 LeukoN6_4
440	190	11.5	593	4	BM742647	BM742647 K-EST0015	513	185	11.2	515	6	CD464497	CD464497 LeukoN4_4
441	190	11.5	594	5	BP279022	BP279022	514	185	11.2	516	6	CD470165	CD470165 LeukoS4_1
442	190	11.5	597	5	BP280234	BP280234	515	185	11.2	548	4	BI960855	BI960855 MONO1_1_G
443	190	11.5	598	5	BP279140	BP279140	516	185	11.2	574	5	BP297283	BP297283 BP297283
444	190	11.5	598	5	BP280362	BP280362	517	185	11.2	592	5	BP279039	BP279039 BP279039
445	190	11.5	598	5	BP281033	BP281033	518	185	11.2	588	5	BP366031	BP366031 BP366031
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447	190	11.5	598	6	CB124471	CB124471 K-EST0173	520	185	11.2	941	4	BI602405	BI602405 603251183



521	184	11.1	329	7	W40206	W40206	zc8306.r1	594	175	10.6	582	5	BP365046	BP365046
522	184	11.1	544	4	BM762984	BM762984	K-EST0044	595	175	10.6	584	5	BP343491	BP343491
523	184	11.1	582	4	BP254097	BP254097		596	174	10.5	577	5	BP279183	BP279183
524	184	11.1	583	5	BP280763	BP280763		597	174	10.5	583	5	BP281087	BP281087
525	183	11.0	571	4	BM846524	BM846524	K-EST0125	598	174	10.5	582	5	BP299450	BP299450
526	183	11.0	581	5	BP234294	BP234294		599	174	10.5	843	4	B1868960	B1868960
527	183	11.0	582	5	BP235338	BP235338		600	174	10.5	905	4	BG251812	BG251812
528	183	11.0	584	5	BP277956	BP277956		601	173.5	10.5	611	1	A1787649	A1787649
529	183	11.0	584	5	BP354729	BP354729		602	173	10.4	588	5	BP280786	BP280786
530	183	11.0	587	5	BP365226	BP365226		603	173	10.4	697	4	BM019476	BM019476
531	183	11.0	875	4	B1193879	B1193879	6029482307	604	172.5	10.4	908	7	CF257407	CF257407
532	183	11.0	1181	4	BG704723	BG704723	603688307	605	172	10.4	580	5	BP355143	BP355143
533	182	11.0	321	7	C0261322	C0261322	4133483 B	606	172	10.4	581	5	BP208292	BP208292
534	182	11.0	511	4	BM848382	BM848382	K-EST0128	607	172	10.4	582	5	BP215537	BP215537
535	182	11.0	576	5	BP206244	BP206244		608	172	10.4	583	5	BP349577	BP349577
536	182	11.0	937	5	BP334408	BP334408		609	172	10.4	589	5	BP354144	BP354144
537	182	11.0	937	4	BG325414	BG325414	602424105	610	171.5	10.4	698	4	BG748079	BG748079
538	181.5	11.0	516	2	BM867486	BM867486		611	171	10.3	445	2	AW403376	AW403376
539	181	10.9	582	5	BP278478	BP278478		612	171	10.3	581	5	BP362018	BP362018
540	181	10.9	604	4	BM743657	BM743657	K-EST0016	613	171	10.3	869	5	BQ212256	BQ212256
541	181	10.9	679	6	CB135879	CB135879	K-EST0188	614	170.5	10.3	442	7	CF166420	CF166420
542	181	10.9	973	1	AL574433	AL574433		615	170.5	10.3	443	7	CF166401	CF166401
543	180	10.9	541	6	CD470152	CD470152	LeukoS4_1	616	170.5	10.3	448	2	B8859819	B8859819
544	180	10.9	930	5	BQ878706	BQ878706	AGENCOURT	617	170.5	10.3	465	2	B8859952	B8859952
545	179.5	10.8	708	4	B1157374	B1157374	602923863	618	170.5	10.3	571	4	BM764098	BM764098
546	179.5	10.8	732	4	BG615658	BG615658	602643016	619	170.5	10.3	676	6	BY752585	BY752585
547	179	10.8	534	6	CD464299	CD464299	LeukoN4_2	620	170	10.3	598	5	BP320978	BP320978
548	179	10.8	576	6	CD472209	CD472209	LeukoS6_1	621	170	10.3	1336	3	CR660524	CR660524
549	179	10.8	582	5	BP278062	BP278062		622	169.5	10.2	598	5	BP280260	BP280260
550	179	10.8	902	4	BM020134	BM020134	603648704	623	169.5	10.2	669	6	CB140905	CB140905
551	178.5	10.8	358	6	BY770042	BY770042		624	169	10.2	582	5	BP281083	BP281083
552	178	10.7	591	5	BP336010	BP336010		625	169	10.2	582	5	BP364971	BP364971
553	178	10.7	592	5	BP363850	BP363850		626	169	10.2	583	5	BP354393	BP354393
554	178	10.7	838	4	BG704722	BG704722	602688329	627	169	10.2	811	4	B1856520	B1856520
555	177.5	10.7	358	5	BY325378	BY325378		628	168.5	10.2	457	2	B8859479	B8859479
556	177.5	10.7	503	2	BM867301	BM867301		629	168.5	10.2	1243	5	BQ230605	BQ230605
557	177.5	10.7	1119	5	BQ675971	BQ675971	AGENCOURT	630	168	10.1	341	6	BY790716	BY790716
558	177	10.7	492	2	BM867185	BM867185		631	168	10.1	581	5	BP355480	BP355480
559	177	10.7	570	5	BP333735	BP333735		632	168	10.1	581	5	BP280217	BP280217
560	177	10.7	573	6	CB157265	CB157265	K-EST0216	633	167.5	10.1	341	6	BY790717	BY790717
561	177	10.7	580	5	BP299494	BP299494		634	167	10.1	582	5	BP315724	BP315724
562	177	10.7	581	5	BP305097	BP305097		635	167	10.1	582	5	BP354763	BP354763
563	177	10.7	581	5	BP324616	BP324616		636	166.5	10.0	457	2	BB862318	BB862318
564	177	10.7	581	5	BP353795	BP353795		637	166.5	10.0	463	6	CB120042	CB120042
565	177	10.7	581	5	BP354113	BP354113		638	166.5	10.0	464	1	AL048049	AL048049
566	177	10.7	581	5	BP363831	BP363831		639	166.5	10.0	480	6	CB139711	CB139711
567	177	10.7	581	5	BP365172	BP365172		640	166.5	10.0	482	4	BM752546	BM752546
568	177	10.7	582	5	BP279349	BP279349		641	166	10.0	582	5	BP236892	BP236892
569	177	10.7	582	5	BP279398	BP279398		642	166	10.0	669	6	CD638322	CD638322
570	177	10.7	582	5	BP279865	BP279865		643	166	10.0	770	6	CD559302	CD559302
571	177	10.7	582	5	BP279956	BP279956		644	165.5	10.0	464	2	BE127204	BE127204
572	177	10.7	582	5	BP299760	BP299760		645	165	10.0	550	5	BP279159	BP279159
573	177	10.7	582	5	BP359628	BP359628		646	165	10.0	582	5	BP339224	BP339224
574	177	10.7	582	5	BP366132	BP366132		647	165	10.0	583	5	BP255503	BP255503
575	177	10.7	583	5	BP279259	BP279259		648	165	10.0	748	2	BE546472	BE546472
576	177	10.7	583	5	BP279567	BP279567		649	164.5	9.9	452	4	BM742492	BM742492
577	177	10.7	583	5	BP365496	BP365496		650	164	9.9	448	4	BM797335	BM797335
578	177	10.7	583	5	BP379517	BP379517		651	164	9.9	583	5	BP366227	BP366227
579	177	10.7	584	5	BP263308	BP263308		652	164	9.9	737	7	CF121799	CF121799
580	177	10.7	592	5	BP279041	BP279041		653	163	9.8	548	4	BM818972	BM818972
581	177	10.7	596	5	BP365383	BP365383		654	162.5	9.8	433	5	BY252039	BY252039
582	177	10.7	603	5	BP279828	BP279828		655	162.5	9.8	446	4	B1960888	B1960888
583	177	10.7	603	5	BP280025	BP280025		656	162.5	9.8	476	6	CD465241	CD465241
584	177	10.7	607	5	BP279866	BP279866		657	162.5	9.8	915	5	BQ432026	BQ432026
585	176.5	10.7	499	2	BM855698	BM855698		658	162	9.8	477	4	BM825765	BM825765
586	176	10.6	581	5	BP322120	BP322120		659	161.5	9.7	450	7	CK613064	CK613064
587	176	10.6	583	5	BP333904	BP333904		660	161	9.7	582	5	BP323917	BP323917
588	176	10.6	592	5	BP281049	BP281049		661	160.5	9.7	693	4	B1557680	B1557680
589	176	10.6	696	2	BM274840	BM274840	601122795	662	160	9.7	887	4	BG528427	BG528427
590	176	10.6	804	2	B5618977	B5618977	601472779	663	159.5	9.6	332	6	CD584497	CD584497
591	175	10.6	486	4	BM847024	BM847024	K-EST0126	664	159.5	9.6	420	2	BE767810	BE767810
592	175	10.6	581	5	BP364418	BP364418		665	159.5	9.6	459	7	CF137888	CF137888
593	175	10.6	582	5	BP356350	BP356350		666	159.5	9.6	492	4	BM824519	BM824519

667	159.5	9.6	765	7	CN347077	170004177	740	145	8.8	868	5	BQ230041	AGENCOURT
668	158.5	9.6	483	5	BU661013	z168b03.z	741	144.5	8.7	432	6	CB128106	K-EST0177
669	158	9.5	549	1	AA282906	z164h05.r	742	144.5	8.7	500	1	AL544354	AL544354
670	158	9.5	998	2	BE616364	601279172	743	144.5	8.7	589	4	BI342110	369784 MA
671	157	9.5	570	5	BP369857	BP369857	744	144.5	8.7	673	6	CD772495	AGENCOURT
672	157	9.5	592	5	BP280439	BP280439	745	144.5	8.7	680	6	CD772495	AGENCOURT
673	157	9.5	676	6	CD528831	Leukoni_5	746	144	8.7	450	2	BE855266	ux28a10.y
674	156.5	9.4	628	5	BP278601	BP278601	747	144	8.7	467	2	BE478431	162683 BA
675	156.5	9.4	744	4	BG250382	602362532	748	144	8.7	467	4	BI132408	ARO30G05L
676	156.5	9.4	785	5	BX915863	BX915863	749	144	8.7	476	4	BM286008	526000 MA
677	156.5	9.4	931	7	CN321916	AGENCOURT	750	144	8.7	516	2	BE483741	170029 BA
678	156	9.4	583	5	BP278490	BP278490	c 751	144	8.7	520	2	AW488356	UI-M-BH3-
679	155.5	9.4	287	6	CB140504	K-EST0193	752	144	8.7	550	2	BE666586	150090 MA
680	155.5	9.4	449	6	CB120078	K-EST0167	753	144	8.7	585	5	BP289867	BP289867
681	155.5	9.4	459	6	CD469110	Leukos2_1	754	144	8.7	599	1	AV593707	AV593707
682	155	9.4	583	5	BP363547	BP363547	755	144	8.7	647	6	CB442528	693111 MA
683	155	9.4	815	9	BX188005	Danio rer	756	144	8.7	688	6	CD469382	Leukos2_3
684	154.5	9.3	582	5	BP361203	BP361203	757	144	8.7	796	2	BF031320	601559076
c 685	154.5	9.3	952	1	AL570563	AL570563	758	144	8.7	828	9	AY421184	Mus muscu
c 686	154	9.3	1003	5	BX380694	BX380694	759	144	8.7	895	6	CB205022	AGENCOURT
687	153.5	9.3	432	4	BM764097	K-EST0045	760	143.5	8.7	403	5	BY160556	BY160556
688	153.5	9.3	438	4	BM785480	K-EST0063	761	143.5	8.7	417	4	BM743706	K-EST0016
689	153.5	9.3	444	4	BM826025	K-EST0097	762	143.5	8.7	1090	5	BM908074	AGENCOURT
690	153.5	9.3	483	4	BM739115	K-EST0008	763	143	8.6	743	4	BI961594	MONOI_1 G
691	153.5	9.3	641	6	BY726835	BY726835	764	143	8.6	880	4	BI085422	602869908
692	153.5	9.3	879	5	BQ962151	AGENCOURT	765	143	8.6	2368	3	BC019712	Mus muscu
693	152.5	9.2	573	6	CD535920	Leukon5_5	766	142.5	8.6	451	2	BB858834	BB858834
694	152	9.2	3454	3	AK028441	Mus muscu	767	142.5	8.6	582	5	BP227819	BP227819
695	151.5	9.1	422	5	BU428717	UI-HF-BNO	768	142.5	8.6	606	6	CA347334	678437 NC
696	151.5	9.1	509	4	BM088473	501959 MA	769	142	8.6	227	1	AA029420	z696c11.r
697	151.5	9.1	717	7	CV221259	Le mx0_46	770	142	8.6	559	4	BI960863	MONOI_1 G
698	151	9.1	758	5	BQ227807	AGENCOURT	771	142	8.6	649	7	CN980729	48731_126
699	150.5	9.1	539	2	AW959677	EST371747	772	142	8.6	678	7	CN969354	16851_123
700	150	9.1	828	4	BM019684	603647966	773	141.5	8.5	378	7	W68991	T2873 MVAT4
701	149.5	9.0	418	6	CA567844	K0419D04-	774	141.5	8.5	427	4	BM847672	K-EST0127
702	149.5	9.0	467	6	CB149408	K-EST0205	775	141.5	8.5	879	3	CF251752	Homo sapi
703	149.5	9.0	482	1	AL553043	AL553043	776	141.5	8.5	3642	3	FSM801377	Homo sapi
704	149.5	9.0	598	6	CB724514	EST0318 R	c 777	140	8.4	428	5	BI013343	f440d02.y
705	149.5	9.0	806	7	CO566630	AGENCOURT	778	140	8.4	599	1	AI934454	wp58b10.x
706	149	9.0	608	7	CF371082	TGEST-yj6	779	140	8.4	603	5	BQ131025	fz47905.y
707	149	9.0	793	2	BE247176	601857845	780	140	8.4	604	2	AW958426	f3k37902.y
708	149	9.0	850	2	BE735557	601304365	781	140	8.4	617	7	CF906668	A050809-y
709	148.5	9.0	572	5	BP333480	BP333480	782	140	8.4	689	4	BG696649	602658956
710	148.5	9.0	719	6	CA342417	672284 NC	783	140	8.4	821	7	CK697330	f101-p00
711	148	8.9	574	5	BP278877	BP278877	784	140	8.4	876	6	CB321038	AGENCOURT
712	147.5	8.9	514	4	BG684702	602635990	785	140	8.4	905	7	CN510906	AGENCOURT
713	147.5	8.9	831	6	CA473822	AGENCOURT	786	139.5	8.4	387	6	CD471434	Leukos5_5
714	147.5	8.9	1110	7	CK028468	AGENCOURT	787	139	8.4	388	2	AW435659	74622 MAR
715	147	8.9	582	5	BP215565	BP215565	788	139	8.4	561	4	BI710853	1d92907.y
716	147	8.9	588	5	BP336450	BP336450	789	139	8.4	575	5	BP300359	BP300359
717	147	8.9	625	6	CD471271	Leukos5_1	790	139	8.4	583	5	BP304428	BP304428
718	147	8.9	702	7	CN347076	170004248	791	139	8.4	614	9	CG589077	OST240788
719	146.5	8.8	1073	4	BG822533	602725618	792	139	8.4	674	7	CK685212	ZF101-p00
720	146.5	8.8	1673	2	BE904427	601496388	793	138	8.3	694	4	BI771330	AGENCOURT
721	146	8.8	331	1	AA363579	EST373724	c 794	138	8.3	946	5	BQ720761	AGENCOURT
722	146	8.8	577	9	AY421183	Pan trogl	c 795	136.5	8.2	595	9	FR0036223	Fugu rubr
723	145	8.8	1122	7	CK028027	AGENCOURT	c 796	136	8.2	589	1	AI830544	wj51a03.x
724	145.5	8.8	444	2	BB860365	BB860365	c 797	136	8.2	808	6	CD512219	AGENCOURT
725	145.5	8.8	468	6	CA389865	CS103F03.	798	136	8.2	3085	3	AK034522	Mus muscu
726	145.5	8.8	582	5	BP205440	BP205440	799	135.5	8.2	718	5	BM951526	UI-M-BG0-
727	145.5	8.8	587	7	CV029518	8335 Full	800	135.5	8.2	2661	9	AY402614	Mus muscu
c 728	145.5	8.8	751	6	CD366440	UI-H-FT1-	801	135	8.1	466	5	BY153109	IPNb_B08
729	145.5	8.8	828	7	CK795924	AGENCOURT	802	134.5	8.1	442	7	CK608407	IPNb_B08
730	145.5	8.8	834	9	AY421182	Homo sapi	803	134.5	8.1	694	6	CA376384	654727 NC
731	145.5	8.8	1001	1	AL540999	AL540999	804	134.5	8.1	986	5	BX330379	BX330379
732	145	8.8	545	5	BX480271	DKEZp6860	805	134.5	8.1	3025	3	BC049247	Mus muscu
733	145	8.8	557	4	BI467634	BP194641	806	134	8.1	582	5	BP363410	BP363410
734	145	8.8	582	5	BP194641	BP194641	807	133.5	8.1	729	7	CN056501	Salamande
735	145	8.8	583	5	BP204751	BP204751	808	133	8.0	245	1	AA360733	EST70005
736	145	8.8	691	7	CO132920	EST00003	809	133	8.0	291	1	AA347120	EST53364
737	145	8.8	744	5	BU376182	603808158	c 810	133	8.0	669	5	BU631966	UI-H-PB1-
738	145	8.8	860	7	CV079185	AGENCOURT	811	132.5	8.0	878	6	CV0359001	AGENCOURT
739	145	8.8	866	7	CO390036	AGENCOURT	812	132	8.0	327	7	W40210	zc83b06.r1

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961	113	6.8	7102	9	AY418551	Homo sapi	1034	107	6.5	379	6	CB139630	K-EST0192
962	112.5	6.8	611	2	AW593307	hg12h10.x	1035	107	6.5	383	6	CD471716	Leuko86.4
963	112.5	6.8	748	7	CK138733	AGENCYCOURT	1036	107	6.5	561	2	BF527166	602039844
964	112.5	6.8	883	7	CN019296	AGENCYCOURT	1037	107	6.5	598	5	BU400752	603485038
965	112	6.8	372	4	BM743705	K-EST0016	1038	107	6.5	680	5	BU249879	604032339
966	112	6.8	629	7	CN412529	170005325	1039	107	6.5	681	2	BF347167	602020964
967	112	6.8	648	6	CB442867	693703 MA	1040	107	6.5	700	4	BG910156	602805533
968	112	6.8	669	9	DR49F8T	Danio rer	1041	107	6.5	716	7	CF536406	UI-M-G10-
969	112	6.8	721	4	BI219897	602936347	1042	107	6.5	745	7	CF723087	UI-M-GV0-
970	112	6.8	961	6	BY717654	BY717654	1043	107	6.5	763	5	BU410360	603158087
971	111.5	6.7	357	5	BY019919	BY019919	1044	107	6.5	785	4	BG911337	602807633
972	111.5	6.7	552	5	BQ472599	HB09A18T	1045	107	6.5	798	6	CD802962	UI-M-GV0-
973	111.5	6.7	570	2	BE233224	139315 MA	1046	107	6.5	855	7	CR448634	CR448634
974	111.5	6.7	652	5	BQ211047	UI-R-DY1-	1047	107	6.5	930	9	CNS06HXX	T3_end of
975	111.5	6.7	680	5	BQ191492	UI-R-DY0-	1048	107	6.5	941	5	BU409087	603158870
976	111.5	6.7	776	7	CO387930	AGENCYCOURT	1049	107	6.5	979	5	BU410188	602955232
977	111.5	6.7	783	5	BU479797	603841693	1050	107	6.5	1158	5	BU409151	603158151
978	111.5	6.7	850	9	CR198040	Forward s	1051	107	6.5	2248	3	AK081264	Mus muscu
979	111.5	6.7	911	2	BF339458	602039113	1052	106.5	6.4	362	5	BY173138	BY173138
980	111.5	6.7	977	4	BI857845	BF339458	1053	106.5	6.4	457	7	CN153458	940572 MA
981	111	6.7	360	6	CD471311	Leuko85.1	1054	106.5	6.4	555	6	CD180838	MS1-0027T
982	111	6.7	433	1	AL589309	DKF2P451H	1055	106.5	6.4	755	7	CN155571	942876 MA
983	111	6.7	585	4	BM812126	fx14f12.Y	1056	106.5	6.4	808	4	BG887918	EST513769
984	110.5	6.7	741	4	BG966850	602834350	1057	106.5	6.4	824	5	BU369144	603596992
985	110.5	6.7	857	9	BX966872	Forward s	1058	106.5	6.4	888	2	BF581527	602101046
986	110	6.6	630	6	CB044799	NISC_9C06	1059	106.5	6.4	1040	5	BQ714183	AGENCYCOURT
987	110	6.6	684	6	CA414871	UI-H-EZ0-	1060	106	6.4	378	2	AW486980	78517 MAR
988	110	6.6	781	9	AY418556	Mus muscu	1061	106	6.4	681	6	CA138598	SCFQRT202
989	110	6.6	794	7	CK458738	923144 MA	1062	106	6.4	848	5	BU410207	603159488
990	110	6.6	846	7	CK457667	921992 MA	1063	106	6.4	873	5	BU427310	603232069
991	109.5	6.6	640	4	BM637828	170006875	1064	106	6.4	962	2	BF300451	602032375
992	109.5	6.6	672	4	BM577341	170006871	1065	106	6.4	1739	2	BF683675	602133925
993	109.5	6.6	694	4	BM620184	170006874	1066	106	6.4	2736	9	AY402613	Pan trogl
994	109.5	6.6	697	2	BF528688	602043443	1067	105.5	6.4	371	6	CA599565	wawic.pk0
995	109.5	6.6	891	5	BU484122	603471770	1068	105.5	6.4	626	9	CG005573	ZUABW77TV
996	109.5	6.6	1362	4	BI524385	603052277	1069	105.5	6.4	698	1	AA941503	LD25669.5
997	109	6.6	491	6	CA353467	CA353467	1070	105.5	6.4	791	6	CB998003	AGENCYCOURT
998	109	6.6	589	4	BM769767	K-EST0053	1071	105.5	6.4	948	9	BX989560	Reverse s
999	109	6.6	748	5	BX882021	BX882021	1072	105	6.3	372	4	BM757210	K-EST0035
1000	109	6.6	759	5	BQ574012	UI-H-EZ0-	1073	105	6.3	499	5	BU534446	AGENCYCOURT
1001	109	6.6	783	9	BU479065	603843018	1074	105	6.3	756	6	CB327411	UI-R-FS0-
1002	109	6.6	789	9	CL688941	PRT014d F	1075	104.5	6.3	444	2	BF389806	UI-R-BS2-
1003	109	6.6	825	6	CA317002	UI-M-FW0-	1076	104.5	6.3	649	6	CD312012	Str-Pu691.
1004	109	6.6	877	6	CD253524	AGENCYCOURT	1077	104.5	6.3	690	9	CC745777	St-Pu691.
1005	109	6.6	913	5	BX929008	BX929008	1078	104.5	6.3	699	9	CC745777	ZMWB0012
1006	108.5	6.5	282	5	BU973380	HE24L19r	1079	104.5	6.3	714	2	BE454951	HVSMER009
1007	108.5	6.5	308	1	AA296020	EST10183	1080	104.5	6.3	749	8	BZ637147	OGCCJ87TC
1008	108.5	6.5	1116	1	AL571513	AL571513	1081	104.5	6.3	456	7	H93850	YV08A03.r1
1009	108	6.5	233	2	AW839650	RC6-LT007	1082	104.5	6.3	955	5	BU480294	603844970
1010	108	6.5	406	1	AA880234	vx39d06.r	1083	104.5	6.3	999	5	BX446538	603844970
1011	108	6.5	508	4	BI671638	fs50h08.Y	1084	104.5	6.3	1019	5	BU523320	AGENCYCOURT
1012	108	6.5	563	1	AL874048	AL874048	1085	104.5	6.3	1253	5	BQ884322	AGENCYCOURT
1013	108	6.5	574	6	CA346211	677050 NC	1086	104	6.3	456	7	H93850	YV08A03.r1
1014	108	6.5	654	4	BM697249	UI-E-DX0-	1087	104	6.3	503	5	BU480294	603844970
1015	108	6.5	659	7	CO872953	BoxGen.01	1088	104	6.3	663	7	CN368025	170005999
1016	108	6.5	701	6	CD354133	UI-M-GW0-	1089	104	6.3	664	1	AJ637165	AJ637165
1017	108	6.5	756	7	CO738793	SLDE04c21	1090	104	6.3	668	1	AJ637187	AJ637187
1018	108	6.5	775	9	AY418554	Homo sapi	1091	104	6.3	893	2	BF303297	602030211
1019	108	6.5	778	6	CA411964	UI-H-EZ0-	1092	104	6.3	896	5	BU160160	AGENCYCOURT
1020	108	6.5	824	9	CC551496	CH240_436	1093	104	6.3	952	3	CNS08HPM	Single re
1021	108	6.5	839	7	CV490818	AGENCYCOURT	1094	104	6.3	1070	5	BX359755	BX359755
1022	108	6.5	1029	1	AL539422	AL539422	1095	104	6.3	7102	9	AY418552	Pan trogl
1023	108	6.5	1042	2	BF527690	602040687	1096	103.5	6.2	259	2	B8570771	Pan trogl
1024	108	6.5	1161	4	BM467077	AGENCYCOURT	1097	103.5	6.2	353	5	BY337424	BB570771
1025	108	6.5	1278	3	CR597704	full-leng	1098	103.5	6.2	357	5	BY131735	BB570771
1026	108	6.5	1383	3	AK017865	Mus muscu	1099	103.5	6.2	357	5	BY1310928	BB570771
1027	108	6.5	1433	3	AK016123	Mus muscu	1100	103.5	6.2	522	5	BW588971	BB570771
1028	108	6.5	1630	3	CR605965	full-leng	1101	103.5	6.2	657	7	CK494148	BW588971
1029	107.5	6.5	639	1	AV734145	AV734145	1102	103.5	6.2	672	5	BQ263492	CK494148
1030	107.5	6.5	686	7	CF179894	814933 MA	1103	103.5	6.2	680	7	BE199523	fa23e07.
1031	107	6.5	353	5	BY135479	BY135479	1104	103.5	6.2	708	2	BE199523	fa23e07.

1105	103.5	6.2	710	1	AU002237	AU002237	AU002237	1178	101	6.1	872	5	BX336450
1106	103.5	6.2	713	7	CK863259	34489	In	1179	101	6.1	898	4	B1819191
1107	103.5	6.2	721	1	AU002317	AU002317		1180	101	6.1	947	7	CK272793
1108	103.5	6.2	731	7	CN314741	170004250		1181	101	6.1	952	3	CNS08VFR
1109	103.5	6.2	767	6	CD777760	TDsubS_RZ		1182	100.5	6.1	304	1	AA285261
1110	103.5	6.2	940	7	CF454398	AGENCOURT		1183	100.5	6.1	489	2	BE474876
1111	103.5	6.2	942	1	AL538775	AL538775		1184	100.5	6.1	499	5	BQ627677
1112	103.5	6.2	963	2	BE196206	HVSMHE009		1185	100.5	6.1	502	4	BG791104
1113	103.5	6.2	1931	9	CG755988	PO51-2-F0		1186	100.5	6.1	506	6	BG725909
1114	103	6.2	659	4	B1484574	RE67695.5		1187	100.5	6.1	506	6	CA937287
1115	103	6.2	738	7	CO423312	GGEZHT100		1188	100.5	6.1	508	2	BE022330
1116	103	6.2	932	2	BF346240	602018425		1189	100.5	6.1	509	2	BF065689
1117	102.5	6.2	495	6	CA343718	CA343718		1190	100.5	6.1	511	4	BG882222
1118	102.5	6.2	507	2	AV952258	AV952258		1191	100.5	6.1	520	2	AW309843
1119	102.5	6.2	558	4	BG637332	SD12566.5		1192	100.5	6.1	520	2	AW395001
1120	102.5	6.2	571	4	BG634902	BG634902		1193	100.5	6.1	523	4	BM252329
1121	102.5	6.2	578	5	BX666919	BX666919		1194	100.5	6.1	524	4	BG405102
1122	102.5	6.2	606	6	CA728823	wdilic_Pk0		1195	100.5	6.1	526	4	EG790894
1123	102.5	6.2	609	4	B1635691	B1635691		1196	100.5	6.1	526	5	B0081838
1124	102.5	6.2	610	1	A1258299	SD17118.5		1197	100.5	6.1	535	1	AL909801
1125	102.5	6.2	611	1	AA736027	AA736027		1198	100.5	6.1	535	2	BE210446
1126	102.5	6.2	619	4	B1629526	B1629526		1199	100.5	6.1	536	4	BM525281
1127	102.5	6.2	621	4	B1637617	B1637617		1200	100.5	6.1	537	2	BE022314
1128	102.5	6.2	625	1	A1403890	A1403890		1201	100.5	6.1	537	2	BE347125
1129	102.5	6.2	626	4	B1612186	B1612186		1202	100.5	6.1	540	4	BG790733
1130	102.5	6.2	629	1	A1259764	BM489811		1203	100.5	6.1	545	4	B1972116
1131	102.5	6.2	632	4	B1230753	B1230753		1204	100.5	6.1	547	4	B1701219
1132	102.5	6.2	633	1	B1585810	RH25484.5		1205	100.5	6.1	547	5	BQ080152
1133	102.5	6.2	634	1	A1387752	A1387752		1206	100.5	6.1	551	1	AL900434
1134	102.5	6.2	636	1	A1532736	SD04336.5		1207	100.5	6.1	552	4	BM527444
1135	102.5	6.2	639	4	BM489811	BM489811		1208	100.5	6.1	556	2	AW234664
1136	102.5	6.2	641	1	A1294933	LP08424.5		1209	100.5	6.1	556	5	BQ610888
1137	102.5	6.2	641	4	B1640558	B1640558		1210	100.5	6.1	557	2	BE329814
1138	102.5	6.2	646	4	B1632782	SD26650.5		1211	100.5	6.1	560	6	CA820060
1139	102.5	6.2	661	4	BG636508	SD14239.5		1212	100.5	6.1	564	4	BM524565
1140	102.5	6.2	662	7	CK662002	CK662002		1213	100.5	6.1	566	5	BQ610696
1141	102.5	6.2	670	7	CK659917	LP21896.5		1214	100.5	6.1	568	4	BM522788
1142	102.5	6.2	676	4	BG640688	BG640688		1215	100.5	6.1	578	5	B0084364
1143	102.5	6.2	682	1	AA695503	GM02930.5		1216	100.5	6.1	581	4	BM087557
1144	102.5	6.2	686	5	B0472335	B0472335		1217	100.5	6.1	586	7	CK494474
1145	102.5	6.2	688	4	BG641327	BQ472335		1218	100.5	6.1	593	2	AW704274
1146	102.5	6.2	688	4	BG641327	BG641327		1219	100.5	6.1	608	6	CA800135
1147	102.5	6.2	696	4	B1639642	B1639642		1220	100.5	6.1	614	5	B0760691
1148	102.5	6.2	701	4	B1641486	B1641486		1221	100.5	6.1	665	6	CD770921
1149	102.5	6.2	717	7	CK658252	CK658252		1222	100.5	6.1	679	7	CF8065326
1150	102.5	6.2	719	7	CK662192	LP22224.5		1223	100.5	6.1	681	7	CF806539
1151	102.5	6.2	1703	2	B3964515	BE964515		1224	100.5	6.1	687	7	CF806378
1152	102	6.2	356	5	B0969369	B0969369		1225	100.5	6.1	703	2	BE661120
1153	102	6.2	424	1	AJ689562	AJ689562		1226	100.5	6.1	704	9	CL923142
1154	102	6.2	646	9	AG075707	AG075707		1227	100.5	6.1	716	7	CF806583
1155	102	6.2	646	9	AG075708	AG075708		1228	100.5	6.1	738	6	CF069769
1156	102	6.2	707	6	CA274759	CA274759		1229	100.5	6.1	766	6	CA783649
1157	102	6.2	765	2	BF345919	BF345919		1230	100.5	6.1	845	7	CO571803
1158	102	6.2	799	4	BG367090	BG367090		1231	100.5	6.1	865	6	CD459095
1159	102	6.2	821	5	BM944051	BM944051		1232	100.5	6.1	902	6	BU409490
1160	102	6.2	882	5	BU249765	BU249765		1233	100.5	6.1	918	6	CA983981
1161	101.5	6.1	648	1	AL855810	AL855810		1234	100.5	6.1	921	2	BF133111
1162	101.5	6.1	744	4	B1830976	B1830976		1235	100.5	6.1	935	2	BF580970
1163	101.5	6.1	832	8	AL175656	AZ175656		1236	100.5	6.1	1031	9	CL445616
1164	101.5	6.1	954	3	CNS08UPL	BM029221		1237	100.5	6.1	1441	3	CR623874
1165	101.5	6.1	996	2	BF345477	BF345477		1238	100.5	6.1	9330	3	AK090118
1166	101.5	6.1	1105	4	BM806374	BM806374		1239	100	6.0	359	2	AW417692
1167	101	6.1	308	6	CD740276	CD740276		1240	100	6.0	376	4	BM742648
1168	101	6.1	345	1	A1873583	A1873583		1241	100	6.0	564	6	CA905778
1169	101	6.1	414	2	AW655801	AW655801		1242	100	6.0	572	6	CA859090
1170	101	6.1	466	1	AA454641	AA454641		1243	100	6.0	585	7	CF430580
1171	101	6.1	531	6	CA915507	CA915507		1244	100	6.0	618	1	A1973128
1172	101	6.1	660	6	CA883427	CA883427		1245	100	6.0	621	6	CB937331
1173	101	6.1	684	2	B3614952	BB614952		1246	100	6.0	631	5	BQ246369
1174	101	6.1	719	4	BC283856	BC283856		1247	100	6.0	643	6	CA859175
1175	101	6.1	751	6	CD351061	CD351061		1248	100	6.0	667	7	CF176921
1176	101	6.1	797	4	BG819983	BG819983		1249	100	6.0	675	6	CA905790
1177	101	6.1	863	2	B3964633	B3964633		1250	100	6.0	719	6	CA412730

c1251	100	6.0	733	1	AJ721352	AJ721352	1324	98	5.9	672	6	CD824112	BN25.051B
1252	100	6.0	754	4	BI155142	602903113	1325	98	5.9	678	6	CD824097	BN25.050P
c1253	100	6.0	885		XO08388	Single re	1326	98	5.9	737	6	CD823558	BN25.049C
1254	100	6.0	1200	3	CR703693	Tetraodon	1327	98	5.9	786	4	BG866550	602785516
1255	100	6.0	2453	3	AK033574	Mus muscu	c1328	98	5.9	794	6	CB326761	EST-R-020-
1256	99.5	6.0	563	6	CA998062	S234X.H10	1329	98	5.9	801	6	CD794302	US7665663
c1257	99.5	6.0	592	6	CB584777	AMGNNUC:U	1330	98	5.9	835	5	BW467001	BW467001
1258	99.5	6.0	598	4	BI578851	R872782.5	1331	98	5.9	837	1	AU119529	AU119529
c1259	99.5	6.0	598	6	CB582909	AMGNNUC:U	1332	98	5.9	886	5	BX458405	BX458405
c1260	99.5	6.0	616	4	BG576172	602597149	1333	98	5.9	889	7	CR582578	CR582578
c1261	99.5	6.0	652	1	AI950438	wq35d10.x	1334	98	5.9	921	3	CR622952	full-leng
c1262	99.5	6.0	713	2	BE979942	UI-M-BG2-	1335	98	5.9	999	4	BX964505	BX964505
c1263	99.5	6.0	722	6	CD349219	UI-M-PY0-	1336	98	5.9	1134	5	BX396679	BX396679
c1264	99.5	6.0	727	4	BJ781105	BJ778009	1337	98	5.9	1343	3	CR675256	Tetraodon
c1265	99.5	6.0	731	4	BJ811105	BJ811105	1338	98	5.9	1734	2	BF539725	602049936
c1266	99.5	6.0	872	3	CNS08H08	Single re	c1339	97.5	5.9	510	5	BW076358	BW076358
1267	99.5	6.0	941	3	CNS08H07	Single re	1340	97.5	5.9	513	5	BW211988	BW211988
1268	99.5	6.0	972	2	BF582640	602094031	1341	97.5	5.9	558	5	BQ264294	faa49f06.
1269	99.5	6.0	1116	2	BF527687	602040683	c1342	97.5	5.9	581	2	AW123236	UI-M-BH2.
1270	99.5	6.0	1148	3	CR690035	Tetraodon	1343	97.5	5.9	592	5	BQ309048	MRO-BT450
1271	99	6.0	447	1	AU281355	AU281355	1344	97.5	5.9	669	9	CR329616	Medicago
1272	99	6.0	449	6	CB743206	AMGNNUC:N	1345	97.5	5.9	706	7	CF865978	CF865978
1273	99	6.0	451	6	CA859348	EST633842	c1346	97.5	5.9	707	4	BM594363	170008674
c1274	99	6.0	507	2	BE655314	UI-M-BH0-	1347	97.5	5.9	713	5	BU408855	603158450
1275	99	6.0	532	1	AU265139	AU265139	1348	97.5	5.9	719	2	BE602747	HVSMER010
1276	99	6.0	533	4	BG367700	BG367700	1349	97.5	5.9	728	7	CF865730	tr1c0020x
1277	99	6.0	559	5	BM347955	BM347955	1350	97.5	5.9	737	7	CF867310	tr1c010xn
c1278	99	6.0	632	6	CD369984	UI-H-FT1-	1351	97.5	5.9	738	7	CF867311	tr1c010xn
1279	99	6.0	669	7	CO520360	3530_1_13	1352	97.5	5.9	742	5	BU427200	603234473
1280	99	6.0	686	6	CD535240	LeukN5.1	1353	97.5	5.9	751	7	CF867101	tr1c009x1
1281	99	6.0	706	7	CF435137	EST671482	1354	97.5	5.9	751	6	CO892908	BovGen.21
c1282	99	6.0	711	6	CD193256	MS1-0078G	1355	97.5	5.9	761	6	CB895920	tr1c00f0x
1283	99	6.0	836	7	CO738752	S1LE04c21	1356	97.5	5.9	783	6	CB895647	tr1c0020x
1284	99	6.0	922	5	BQ949185	AGENCOURT	1357	97.5	5.9	793	6	CB897342	tr1c010xn
1285	99	6.0	1002	3	CNS08YUL	Single re	1358	97.5	5.9	794	6	CB897341	tr1c010xn
1286	99	6.0	1018	4	BM552398	AGENCOURT	1359	97.5	5.9	807	6	CB897114	tr1c009x1
1287	99	6.0	1025	3	BC024540	Mus muscu	1360	97.5	5.9	835	1	AJ816579	AJ816579
1288	99	6.0	1233	9	AY417461	Mus muscu	1361	97.5	5.9	836	1	AJ816601	AJ816601
1289	99	6.0	2777	3	AK032047	Mus muscu	c1362	97.5	5.9	870	9	CL968328	OsIFCC040
1290	99	6.0	4634	3	AK032126	Mus muscu	1363	97.5	5.9	919	5	BQ960367	AGENCOURT
1291	98.5	5.9	419	1	AA448801	zx10G02.i	1364	97.5	5.9	956	6	CA077209	SCGAM104
1292	98.5	5.9	441	7	CN828071	170005329	1365	97.5	5.9	977	3	CNS08E4C	Single re
1293	98.5	5.9	514	5	BU764674	sa04h12.	1366	97.5	5.9	995	2	BE602834	HVSMER010
1294	98.5	5.9	548	7	CO876287	BovGen.04	1367	97	5.9	419	7	CF136553	UI-HF-BN0
1295	98.5	5.9	582	2	BF695021	602083052	1368	97	5.9	538	4	BJ047143	BJ047143
c1296	98.5	5.9	585	7	CF455030	CR455030	1369	97	5.9	577	7	CO149290	EST824343
c1297	98.5	5.9	588	1	AI850361	UI-M-BG1-	1370	97	5.9	601	2	AV999537	AV999537
c1298	98.5	5.9	597	6	CD084905	MC1-0013T	1371	97	5.9	631	4	BG365929	HVSMER000
c1299	98.5	5.9	624	2	BF586321	FW1_27.D1	c1372	97	5.9	648	6	BY705907	BY705907
c1300	98.5	5.9	634	4	BG052018	RH122_7.H	1373	97	5.9	655	6	CD816943	BN20.040D
1301	98.5	5.9	653	9	CG868310	ZMMBB036	1374	97	5.9	665	4	BJ234010	BJ234010
1302	98.5	5.9	654	1	AU205000	AU205000	1375	97	5.9	716	2	BE455072	HVSMER009
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AW917101 EST348405  
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ALIGNMENTS

AL550279 1091 bp mRNA linear EST 25-MAR-2004  
AL550279 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CSODI039YJ06 5-PRIME, mRNA sequence.  
AL550279  
AL550279.3 GI:45750655  
EST.  
Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1091)  
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 15, 2001 this sequence version replaced gi:31272096.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
5952.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CSODI039DE03QP1c&c=5952.r.  
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primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

## Alignment Scores:

Pred. No.: 5.17e-160 Length: 1091  
Score: 1657.00 Matches: 322  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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US-10-063-670-6 (1-322) x AL550279 (1-1091)

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Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
Db 479 CCAGAAATTAATCACCAAGATGCCATATTCACACTCAAACTGCAACACAAACACACA 538  
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Qy 321 GluVal 322  
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RESULT 2  
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LOCUS  
DEFINITION  
full-length cDNA clone CS0DI039YJ06 of Placentia Cot 25-normalized  
of Homo sapiens (human).  
ACCESSION  
CR598862  
VERSION  
CR598862.1 GI:50479669  
KEYWORDS  
HTC; CNSLT\_CDNA.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Euteria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 1781)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1781)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrsf@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen  
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Pred. No.: 1.07e-159 Length: 1781  
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Percent Similarity: 100.00% Conservativity: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
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Db 419 AGCCGACAGTTTGCAGCTATTGTTACAACTCACTGATCTTGACCTAACTCGTGCAATT 478
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 479 CCAGAAATTATCACCACCAAGATCCCATATTTCAACACTCAAACTGCAACCAACAACA 538
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 539 GAATTTATTTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC 598
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DEFINITION full-length cDNA clone CS0D1029YJ09 of Placentia Cot 25-normalized
of Homo sapiens (human).
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VERSION CR614245.1 GI:50495052
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 1786)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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Faraday Avenue
2 (bases 1 to 1786)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
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Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db 304 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCTCGTGGTCTCTTAGGATT 363
Qy 101 SerProAenProLysCysGlyValLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 364 AGCCCAACCCCAAGTGTGGGAAATGGGTGGTGTCTGATTGGAAGGTTCCAGTG 423
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrTrpThrAsnSerCysIle 140
Db 424 AGCGACAGTTTGACGCTATTGTTACAACTCATCTCTCTCTCTCTCTCTCTCTCTCT 483
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 484 CCAGAAATTATCACCACCAAGATCCCATATTTCAACACTCAAACTGCAACCAACAACA 543
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 544 GAATTTATTTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC 603
Qy 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 604 CCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 663
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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Db 664 TGTGTCAAGAGTTTATGAACTAGCACCATGCTACAGAACTGAACCATTTGTT 723
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 724 GAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCACCGCTCTG 783
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 784 CTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 843
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 844 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAATGATCGAAACC 903
Qy 281 LysValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 904 AAAGTAGTAAGGAGGAGGAGGCAATGATGACCAACCTTAATGAGGAATCAAGAAACT 963
Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 964 GATAAAAACCCAGAGAGTCCAGAGTCCAGAGTCCAGAGCAAAACTACCGTGCATGCTGGAAGCT 1023
Qy 321 GluVal 322
Db 1024 GAAGTT 1029
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## RESULT 4

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CR604450 1797 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSODI065YD17 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
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ACCESSION CR604450

VERSION CR604450.1 GI:50485257

KEYWORDS HTC; CNSLT\_CDNA.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1797)  
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
TITLE Full-length cDNA libraries and normalization.  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Paraday Avenue

REFERENCE 2 (bases 1 to 1797)

Genoscope.

AUTHORS Direct Submission

JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

FEATURES Location/Qualifiers

source

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1..1797
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI065YD17"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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## ORIGIN

Alignment Scores:

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Pred. No. : 1.08e-159 Length: 1797
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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RESULT 5

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DB: 3 Gaps: 0
US-10-063-670-6 (1-322) x CR604450 (1-1797)
Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 94 ATGCCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCCAGAGGCTCTG 153
Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 154 GTCACAGGCTCTTTGGCGTCAGAGAGCTTTCCATCCAGGTGTATGACAGAAATATGGGG 213
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnLysLeuAsnPheThrGluAlaLysGluAla 60
Db 214 ATCACCTTTGTGAGCAAAAAGGCGAACACGACAGCTGAATTTTCACAGAAAGCTAAGGAGCC 273
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 274 TGTAGGCTGCTGGGACTTAAGTTTGGCGCGCAAGGACCAAGTTGAAACACAGCCTTGAAGCT 333
Qy 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db 334 AGCTTTGAAAACCTTGCAGCTATGCTGGTTGGAGATGGATTCTGTGTCATCTCTAGATT 393
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 394 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTTGAAGGTTCCAGTG 453
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 454 AGCCGACAGTTTTCAGCCTATTGTTTACAACTCATCTGATACTTGGACTTAACCTCGTCATT 513
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 514 CCAGAAATATATACCAACCAAGATCCCATATTCAACTCAACTCAACTCAACTCAACTCA 573
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 574 GAATTTATTGTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 633
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuLeu 200
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Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 754 GAAAAATAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 813
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 814 CTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 873
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 874 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAATGATCGAAACC 933
Qy 281 LysValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 934 AAAGTAGTAAGGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 993
Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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Qy 321 GluVal 322
Db 1054 GAAGTT 1059
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CR612000 1820 bp mRNA linear HTC 21-JUL-2004  
LOCUS full-length cDNA clone CSODI069YN02 of Placenta Cot 25-normalized  
DEFINITION of Homo sapiens (human).  
ACCESSION CR612000  
VERSION CR612000.1 GI:50492807  
KEYWORDS HTC; CNSLT\_cDNA;  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1820)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1820)  
REFERENCE Genoscope.  
AUTHORS Direct Submission  
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSODI069YN02"  
/tissue type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"  
ORIGIN  
Alignment Scores:  
Pred. No.: 1..159 Length: 1820  
Score: 1657.00 Matches: 322  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
US-10-063-670-6 (1-322) x CR612000 (1-1820)  
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Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetCly 40  
Db 158 GTCCAAAGCTCTTTCGCGTCAGAGAGAGCTTCCATCCAGGTGTCATGCAGAAATATATGGGG 217  
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnLeuAenPheThrGluAlaLysGluAla 60  
Db 218 ATCACCCTTGTGACCAAAAGCGNACCAGCAGCTGAATTCACAGAAGCTTAAGAGGCC 277  
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
Db 278 TGTAGGCTGCTGGGACTAAGTTTGGCGCCGAAGACCAAGTTGAAACAGCCTTGAAGACT 337  
Qy 81 SerPheGluThrCysSerTyGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
Db 338 AGCTTTGAACCTTCAGCTATGCTGGTGGGTTCGAGATGGATTCGTTGCTCATCTCAGGATT 397  
Qy 101 SerProAnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
Db 398 AGCCCAAAACCCAAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTTGGAAAGTTCCAGTG 457

Qy 121 SerArgGlnPheAlaAlaTyrcysTyrcasnSerSerSerSerThrTrpThrThrAsnSerCysile 140  
Db 458 AGCCGACAGTTTGGAGCCTATTGTTTACAACATCATCTGATCTTGAATTAACCTGTCGTCATT 517  
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
Db 518 CCAGAAATTATCACCAACCAAGATCCCATATTCAACTCAACTCAACTGCACCAACAACA 577  
Qy 161 GluPheIleValSerAspSerThrTyrcSerValAlaSerProTyrcSerThrIleProAla 180  
Db 578 GAATTTATTGTCACTGACAGTACCTACTCGGTGGCATCCCTTACTCTTACAATACCTGCC 637  
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeu 200  
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Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
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Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
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Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrcVallys 260  
Db 818 CTAGTGTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 877  
Qy 261 ArgTyrcValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
Db 878 AGGTATGTGAAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 937  
Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
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Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
Db 998 GATAAAACCCAGAGAGTCCAGAGTCCAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1057  
Qy 321 GluVal 322  
Db 1058 GAAGTT 1063  
RESULT 6  
CR597409 1898 bp mRNA linear HTC 21-JUL-2004  
LOCUS full-length cDNA clone CSODI067YG15 of Placenta Cot 25-normalized  
DEFINITION of Homo sapiens (human).  
ACCESSION CR597409  
VERSION CR597409.1 GI:50478216  
KEYWORDS HTC; CNSLT\_cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1898)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1898)  
REFERENCE Genoscope.  
AUTHORS Direct Submission  
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a

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division of Invitrogen.
FEATURES
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ORIGIN
Alignment Scores:
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  Score:          1657.00         Matches:    322
  Percent Similarity: 100.00%     Conservative: 0
  Best Local Similarity: 100.00%  Mismatches: 0
  Query Match:     100.00%       Indels:    0
  DB:               3            Gaps:      0

US-10-063-670-6 (1-322) x CR597409 (1-1898)

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Db 190 ATGCCAGAGTCTTCAGCCTGGTGTCTCTCACTTCCATCTGGACCCAGGAGCTCTG 249
Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 250 GTCCAAAGCTCTTTCGTCGAGAAAGAGCTTTCATCCAGGTGTCATCAGAAATATGGG 309
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 310 ATCACCCTTGTGAGCAAAAAGGCGAACACGAGCTGAATTCACAGAAGCTAAGGAGGCC 369
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 370 TGTAGGCTGCTGGAGCTAAGTTTCGCCGCGAAGCAAGTGAACAGCCTTGAAGAGCT 429
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db 430 AGCTTTGAAACTTCACACTATGGCTGGTGGAGATGGATTCGTGTCATCTCTAGATT 489
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 490 AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTCTCTGATTTCGAAAGTTCACAGTG 549
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 550 AGCCGACAGTTTGCAGCCTATTGTTACAACTCACTCTGATCTGGACTTAACCTCGTCATT 609
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 610 CCAGAAATTATCACACCAAGATCCCATATTCACACTCMAACTGCAACACAACAACA 669
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 670 GAATTTATTGTCAGTGACGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 729
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 730 CCTACTACTACTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTCATT 789
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 790 TGTGTCACAGAGTTTATGGAACCTAGCACCATGTCACAGAACTGAACCACTTTGTT 849
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 850 GAAAAATAAGCAGCATTCAGAAATGAAGCTCTCGGTGGTGGAGGTGTCACACGGCTCTG 909
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 910 CTAGTGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 969
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Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla 320
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Qy 321 GluVal 322
Db 1150 GAAGTT 1155

RESULT 7
CR614790
LOCUS
DEFINITION
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  full-length cDNA clone CS0D1018YG12 of Placenta Cot 25-normalized
  of Homo sapiens (human) .
ACCESSION
  CR614790
VERSION
  CR614790.1 GI:50495597
KEYWORDS
  HTC; CNSLT_cDNA.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1. (bases 1 to 1911)
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  Full-length cDNA libraries and normalization
  Unpublished
  Contact : Feng Liang Email : fliang@lifetech.com URL :
  http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
  Faraday Avenue
  Genoscope.
REFERENCE
  2. (bases 1 to 1911)
  Direct Submission
  Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
  BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
  - Web : www.genoscope.cns.fr)
COMMENT
  1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
  end enriched, double-strand cDNA was digested with Not I and cloned
  into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
  was normalized. Library was constructed by Life Technologies, a
  division of Invitrogen.
FEATURES
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    1. .1911
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ORIGIN
Alignment Scores:
  Pred. No.:      1.18e-159      Length:      1911
  Score:          1657.00         Matches:    322
  Percent Similarity: 100.00%     Conservative: 0
  Best Local Similarity: 100.00%  Mismatches: 0
  Query Match:     100.00%       Indels:    0
  DB:               3            Gaps:      0

US-10-063-670-6 (1-322) x CR614790 (1-1911)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
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Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 231 GTCCAAAGGCTCTTTCGCTGCGAGAGAGCTTTCATCCAGGTGTCATGAGAAATATGGG 290
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Qy 41 IleThrLeuValSerLysGlyAlaAsnGlnGlnIleuAenPheThrGluAlaLysGluAla 60
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Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 351 TGTAGCTGTGGGACTAAGTTTGGCGCGCAAGACCAAGTTGAAACAGCCTTGAAGCT 410
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db 411 AGCTTTGAACCTTGCAGCTATGCTGGGTGGAGATGATTCGTGGTTCATCTCAGGATT 470
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 471 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGTGGTGCCTGATTGGAAAGTTCCAGTG 530
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 531 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTTAACTCGTGCAAT 590
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
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Qy 161 GluPheIleValSerAspSerThrTyrSerValIleSerProTyrSerThrIleProAla 180
Db 651 GAATTTATTGTGACGTACAGTACTTCTCGGTGGCATCCCTTACTCTACAACTACCTGCC 710
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Db 891 CTAGTGCTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 950
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValAlaGlyCysLeuAla 320
Db 1071 GATAAAACCCAGAGAGTCCAAAGAGTCCAAAGCAAACTACCGTCGATGCTCGAAGCT 1130
Qy 321 GluVal 322
Db 1131 GAAGTT 1136

RESULT 8
CR595979
LOCUS full-length cDNA clone CS0D1059YA12 of Placentia Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR595979
VERSION CR595979.1 GI:50476786
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

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REFERENCE
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1925)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
Location/Qualifiers
1..1925
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1059YA12"
/tissue_type="Placentia Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores:
Pred. No.: 1,2e-159 Length: 1925
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-10-063-670-6 (1-322) x CR595979 (1-1925)
Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 190 ATGCCAGGTGCTTCAGCTGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 249
Qy 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetCly 40
Db 250 GTCCAAAGGCTCTTTCGCTGCAGAGAGCTTTCATCCAGGTGTCATCGAAGTTATGGGG 309
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 310 ATCAACCTTGTGACAAAGGCGAACAGCAGCTGAATTCACAGAACTTAAGAGGCC 369
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 370 TGTAGGCTGTGGGACTAAGTTTGGCGCGCAAGACCAAGTTGAAACAGCCTTGAAGCT 429
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db 430 AGCTTTGAAACTTGCAGCTATGCTGGGTGGAGATGATTCGTGGTTCATCTCAGGATT 489
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 490 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGTGGGTGCTCTGATTGGAGGTTCCAGTG 549
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 550 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGAAGCTTAACTCGGCAAT 609
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 610 CCAGAAATTATCACCAACCAAGATCCCATATTCACACTCAAACTCAAACTCAAAACAACA 669
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 670 GAATTTATTGTGACGTACAGTACCTACTCTCGGTGGCATCCCTTACTCTACAACTACCTGCC 729

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Qy      321 GluVal 322
Db      1182 GAAGTT 1187

RESULT 10
AL550621
LOCUS      1045 bp      mRNA      linear      EST 25-MAR-2004
DEFINITION Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI058YN14 5-PRIME, mRNA sequence.
ACCESSION AL550621
VERSION    AL550621.3 GI:45750987
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 1045)
            Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
            Full-length cDNA libraries and normalization
            Unpublished (2001)
            On Feb 15, 2001 this sequence version replaced gi:31272438.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Crenieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            5952.x
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CSODI058DGO7QPl&c=5952.x.
            Location/Qualifiers
            1..1045
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CSODI058YN14"
            /tissue_type="PLACENTA COT 25-NORMALIZED"
            /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
            /note="1st strand cDNA was primed with a NotI-oligo(dT)
            primer. Five prime end enriched, double-strand cDNA was
            digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized."

FEATURES
            source
            1..1045
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CSODI058YN14"
            /tissue_type="PLACENTA COT 25-NORMALIZED"
            /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
            /note="1st strand cDNA was primed with a NotI-oligo(dT)
            primer. Five prime end enriched, double-strand cDNA was
            digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized."

ORIGIN
Alignment Scores:
Pred. No.:      6.33e-145      Length:      1045
Score:          1510.50      Matches:      296
Percent Similarity: 95.53%      Conservative: 3
Best Local Similarity: 94.57%      Mismatches: 11
Query Match:    91.16%      Indels:      3
DB:             1      Gaps:      1

US-10-063-670-6 (1-322) x AL550621 (1-1045)

Qy      1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20
Db      94 ATGCCAGGCTCTCAGCGTGGTGTGCTTCTACTTCATCTGCAGCAGGCTCTG 153

Qy      21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      154 GTCCAGGCTCTTTCGCGTCAGAGAGAGCTTCCATCCAGGTGTATGAGAAATATGGG 213

Qy      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      214 ATCACCTTGTGAGCAAAAGCGCAACAGCAGCTGAATTTACAGAGAGCTTAAGAGGCC 273

Qy      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      274 TGTAGGCTGCTGGGACTAAGTTTGGCCGGAAGGACCAAGTTGAACAGCCTTGAAGACT 333

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Qy      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      334 AGCTTTGAAACTTGCAGCTATGCTGGTGGAGATGGATTCTGGTTCATCTCTAGGATT 393

Qy      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      394 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTCTCTGATTGGAGAGTTCCAGTG 453

Qy      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      454 AGCCGACAGTTTGCAGCCTATTGTTACAACATCATCTCATCTGACTTAACCTCGTGCAAT 513

Qy      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      514 CCAGAAATTTATCCACCACCAAGATCCCATATTTCAACACTCAAACTGCAACCAACAACA 573

Qy      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      574 AATTTATTGTTCAGTGACGTACCTACTCGGTGCATCCCTTACTCTACAAATACCTGCC 633

Qy      181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      634 CCTACTACTACTCTCTCTCTCTCCAGCTTCCACTTCTATTCCACGAGAGAAAAAATTGATT 693

Qy      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      694 TGTGTCACAGAAAGTTTATTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCACTTTGTT 753

Qy      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      754 GAAATTAAGACAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCACACGGCTCTG 813

Qy      241 LeuValLeuAlaLeuLeuPhePheGlyValAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      814 CTAGTGGTCTCTCTCTCTCTCTTTGGTGGTGGTGGTCTTGGATTTCGTATGTCAAA 873

Qy      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      874 AGGTATGTGAAGGCTTCCCTTTTACAAAMAARAATCAGCGAAGAGAAATGTCGADACC 933

Qy      281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      934 MAAGTAGTAAGGAGGAGAGAGGCAATGATWASACCCCYAATGAGGGATCAAGAAACT 993

Qy      301 AspLysAsnProGluGluSerLysSerProSerLysThr 313
Db      994 GWTAAACCCCG-----AAGAGTCCAGAGTCMAGC 1023

RESULT 11
AL552299
LOCUS      965 bp      mRNA      linear      EST 30-MAR-2004
DEFINITION AL552299 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI069YN02 5-PRIME, mRNA sequence.
ACCESSION AL552299
VERSION    AL552299.3 GI:45857087
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 965)
            Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
            Full-length cDNA libraries and normalization
            Unpublished (2001)
            On Feb 15, 2001 this sequence version replaced gi:31274114.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Crenieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and EcoR V
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

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was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r

For more information about this cluster, see

<http://www.genoscope.cns.fr/cdna?s=CS0D1069DG01QP1&c=5952.r>.

## FEATURES

source

Location/Qualifiers

1..965

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0D1069YN02"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Alignment Scores:  
Pred. No.: 7.89e-142 Length: 965  
Score: 1480.00 Matches: 288  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 89.32% Indels: 0  
DB: 1 Gaps: 0

US-10-063-670-6 (1-322) x AL552299 (1-965)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20  
Db 94 ATGCCAGGTGCTTTCAGCGTGGTGTCTCTCACTTCCATCTGCACGAGGCTCCTG 153  
Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
Db 154 GTCCAAAGGCTCTTTCGCTGCAGAGAGCTTTCATCCAGGTGTCATCAGAAATATATGGG 213  
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
Db 214 ATCACTCTGTGAGCAAAAGGCGAACACGAGCTGAATTCACAGAAGCTAGGAGGCC 273  
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
Db 274 TGTAGGTGCTGGGCAAGTTCGCGCGCAAGCAAGCTGAACAGGCTTGAAGCT 333  
Qy 81 SerPheGluThrCysSerTyrrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
Db 334 AGCTTTGAAACTTCAGCTATGGCTGGGTGGAGATGGAATTCGGGTCACTCTAGGATT 393  
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
Db 394 AGCCCAACCCCAAGTGGGAAAATGGGTGGGTGCTGCTGATTTGGAAGGTTCCAGTG 453  
Qy 121 SerArgGlnPheAlaAlaTyrrCysTyrrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
Db 454 AGCCGACAGTTTGCAGCCTATTGTTTACAACTCATCTGATCTGCACTTAACCTCGCAT 513  
Qy 141 ProGluIleIleThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
Db 514 CCAGAAATATATCCACCAAGATGCCATATATCAACACTCAACTGCAACCAACAACA 573  
Qy 161 GluPheIleValSerAspSerThrTyrrSerValAlaSerProTyrrSerThrIleProAla 180  
Db 574 GAATTTATGTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAACTCTGCC 633  
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeu 200  
Db 634 CCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCACGAGAAAAAATTGATT 693  
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
Db 694 TGTGTACAGAAAGTTTATGGAACATAGCACCATGTCTACAGAAATGAACCAATTGTT 753

Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240  
Db 754 GAAATATAAGCAGCATTTCAAGATGAAGCTGCTGGTGGTGGAGGTGCCACGGCTCTG 813  
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrrValLys 260  
Db 814 CTAGTGTCTTGTCTCTCTCTTCTTGTGTGTGCAGCTGGTCTTGATTTTGTCTATGCAAA 873  
Qy 261 AtgTyrrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
Db 874 AGTATGTGAAGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAATGATCGAAACC 933  
Qy 281 LysValValLysGluLysAla 288  
Db 934 AAAGTAGTAAGGAGGAGGAGGCC 957

## RESULT 12

AL546669

LOCUS

DEFINITION AL546669 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0D1029YJ09 5-PRIME, mRNA sequence.

ACCESSION AL546669

VERSION AL546669.3 GI:45747132

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1090)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31268502.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

5952.r

For more information about this cluster, see

<http://www.genoscope.cns.fr/cdna?s=CS0D1029CE05QP1&c=5952.r>.

Location/Qualifiers

1..1090

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0D1029YJ09"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

Alignment Scores:

Pred. No.: 2.17e-141 Length: 1090

Score: 1476.50 Matches: 302

Percent Similarity: 96.24% Conservative: 5

Best Local Similarity: 94.67% Mismatches: 11

Query Match: 89.11% Indels: 5

DB: 1 Gaps: 1

US-10-063-670-6 (1-322) x AL546669 (1-1090)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20

Db 64 ATGCCAGGTGCTTTCAGCTGGTGGTGTCTCTCACTTCCATCTGACCAAGGCTCCTG 123



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QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 124 GTCCAAAGGCTCTTTTCGGTGCAGAGAGCTTCCATCCAGGGTGCATGCAGAAATATATGGG 183
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 184 ATCCACCTTGTGAGCAAAAAGGCAACAGCAGCTGAATTTACAGAGAGCTAAGAGGCC 243
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 244 TGTAGGCTGCTGGGACTAAGTTTGGCGCGCAGGACCAAGTTGAAACAGCCTTGAAGCT 303
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db 304 AGCTTTGAACACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTCACTCTAGGATT 363
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 364 AGCCCAAAACCCCAAGTGTGGGAAANAATGGGGTGGGTCTCTGATTTGGAAGTTCCAGTG 423
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 424 AGCCGACAGTTTGCAGCCTATTGTTTACAACATCATCTGATCTGGACTTAACCTCGTCATT 483
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 484 CCAGAAATATTATCACCAACAAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 543
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 544 GAATTTATTTGTCAGTGACAGTACCTACTCGTGGGATCCCTTACTCTACAAATACCTGCC 603
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle 200
Db 604 CCTACTACTACTCTCTCTGCTCCAGCTCCACTTCTATTCCAGGAGAAAAAATTGATT 663
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 664 TGTGTGCAGAGAAGTTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCAATTGTT 723
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 724 GAAATAAAGCAGCATTTCAAGNATGAAGCTGCTGGGTTTGGAGGTGTCCTCCAGCGCTCG 783
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 784 CTAGTGCTTGCTCTCTCTCTTCTGCTGCAGCTGCTTGGATTTTGTATGTCAA 843
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 844 AGGTATGTGAAGGCCCTTCCCTTTTCAAAACAAGAAATCAGAGAAGGAAATGATCGAAACC 903
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 904 ACAGTAGTAAAGGAGGR--GAGGGCAATGATAGCAM--CCTAATGCGATC--AAAGAACT 959
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGlu 319
Db 960 GATAAAAA--CCAGAGAGTCCAGA---GTCCAGCAAACTTTCGTCGCGATGCTCGGAG 1012
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RESULT 13
AL551020 1043 bp mRNA linear EST 25-MAR-2004
LOCUS
DEFINITION
AL551020 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1066YL13 5-PRIME, mRNA sequence.
ACCESSION
AL551020
VERSION
AL551020.3 GI:45751381
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1043)
```

AUTHORS  
TITLE  
JOURNAL  
COMMENT

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 15, 2001 this sequence version replaced gi:31272837.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE  
Email: seqre@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
5952.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0D1066CF07QPI&c=5952.r.

FEATURES  
source

Location/Qualifiers  
1..1043  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0D1066YL13"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:  
Pred. No.: 158-137 Length: 1043  
Score: 1439.00 Matches: 300  
Percent Similarity: 94.98% Conservative: 3  
Best Local Similarity: 94.04% Mismatches: 14  
Query Match: 86.84% Indels: 7  
DB: 1 Gaps: 2  
US-10-063-670-6 (1-322) x AL551020 (1-1043)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20  
Db 31 ATGCCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCACAGGCTCCTG 90  
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
Db 91 GTCCAAGGCTCTTTCGTGCAGAAAGAGCTTTCATCCAGGTGTCATGCAGAAATATATGGG 150  
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
Db 151 ATCACCTTGTGACCAAAAAGGCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 210  
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
Db 211 TGTAGGCTGCTGGGACTTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 270  
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100  
Db 271 AGCTTTGAACACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTCACTCTAGGATT 330  
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
Db 331 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGGAAAGTTCCAGTG 390  
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
Db 391 AGCCGACAGTTTGCAGCCTATTGTTTACAACATCATCTGATCTGGACTTAACCTCGTCATT 450  
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Db 451 CCAGAAATATTATCACCAACAAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 510  
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

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511 GAATTTATTGTGACGTACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 570
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181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuLeu 200
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571 CCTACTACTACTCTCTGCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT 630
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201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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631 TGTGTACAGAAGTTTTTATGGAACTAGCACCAGTGTCTACAGAACTGAACTATTGTT 690
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221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
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691 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 750
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241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLysLysGlyPheCysTyrValLys 260
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751 CTAGTGTCTGCTCTCTCTCTTTGGTGTGCACTGTCTGTGATTTTGTATGTCAAA 810
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261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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811 AGGTATGTGAAGC-TTCCCTTTTACAAACAGNATCAGCAGAGGAAATGATCGAAACC 869
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281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
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870 AAGTA-GTAAAGGDCGAGAGGC-AATGATAGCAA-CCTAATGAGGA-TCAAAGMAAAT 925
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301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGlu 319
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926 GATAAAACC---AGAAGAGTCAAGAGTCCAGCAAACTACGKG---CGATGCTRGCA 976
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RESULT 14
CR599107 1823 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0D1030YC09 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human) .
ACCESSION CR599107
VERSION CR599107.1 GI:50479914
KEYWORDS HTC; CNSLT cDNA
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1823)
AUTHORS Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1823)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
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/clone="CS0D1030YC09"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Alignment Scores:
Pred. No.: 9.45e-128 Length: 1823

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Score: 1347.50 Matches: 273
Percent Similarity: 84.10% Conservative: 2
Best Local Similarity: 83.49% Mismatches: 16
Query Match: 81.32% Indels: 36
DB: 3 Gaps: 3

US-10-063-670-6 (1-322) x CR599107 (1-1823)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleThrThrThrArgLeuLeu 20
Db 187 ATGGCCAGGTGCTTCAGCTGGTGTGCTTCTCATTCTCCATCTGGACCCAGAGGCTCTG 246
Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 247 GTCCAGGCTCTTTGGTGCAGAAAGGTAGTCTTTTATTAGCTCTGTGTTCTTTCAGCA 306
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 307 ATAGAGATG-----AAGCCTTCTAATCAT----- 330
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 331 -----TTT 333
Qy 81 Ser-PheGluThrCys-----SerTyrGlyTyrValGlyAspGlyPheValVa 96
Db 334 TCTGTTCAACTAGTGTGTTATCTTTTACAGCTATGCTGGTTGGAGATGGAATTCGTGTT 393
Qy 96 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTr 116
Db 394 CATCTCTAGGATTAGGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTC 453
Qy 116 pLysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpTh 136
Db 454 GAAGGTTTCAGTGAGCCGACAGTTTTCAGCCCTATTGTTCAACTCATCTGATATTGGAC 513
Qy 136 rAsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAl 156
Db 514 TAACTCGTGCAATTCAGAAATTTATACCACCAAGATCCCATATTCAACACTCAAACTGC 573
Qy 156 aThrGlnThrThrGluPheIleValSerAspSerThrThrSerValAlaSerProTyrSe 176
Db 574 AACACAAACAAACAGAAATTTATTGTCAGTGACAGTACTACTCGTGGCATCCCTTACTC 633
Qy 176 rThrIleProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgAr 196
Db 634 TACAATACCTGCCCCCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTTCACGGAG 693
Qy 196 glyLysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThrGluTh 216
Db 694 AAAAAAATTGATTTGTGTACAGAAAGTTTTTATGGAAACTTAGCACCATGTCTACAGAAAC 753
Qy 216 rGluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyVa 236
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Qy 236 lProThrAlaLeuLeuValLeuAlaLeuLeuPhePheGlyValAlaAlaGlyLysGlyPh 256
Db 814 CCCACGGCTCTGCTAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGATT 873
Qy 256 eCysTyrValLysArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGly 276
Db 874 TTGCTATGTCAAAGGATATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAGGA 933
Qy 276 uMetIleGluThrLysValValLysGluLysAlaAsnAspSerAsnProAsnGluGl 296
Db 934 AATGATCGAAACCAAAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTAATAGGA 993
Qy 296 uSerLysLysThrAspLysAsnProGluGluSerLysSerProSerLysThrThrValAr 316
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Qy 316 gCysLeuGluAlaGluVal 322

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Db 1054 ATGCTGGAGCTGAAGTT 1072

RESULT 15
AL553858
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DEFINITION AL553858 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
ACCESSION AL553858
VERSION AL553858.3 GI:45858623
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 946)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31275672.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5952.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna/s=CS0D1077CEB09QPl&c=5952.r.
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 1,07e-125 Length: 946
Score: 1323.50 Matches: 272
Percent Similarity: 98.55% Conservative: 0
Best Local Similarity: 98.55% Mismatches: 4
Query Match: 79.87% Indels: 4
DB: 1 Gaps: 0

US-10-063-670-6 (1-322) x AL553858 (1-946)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20
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Db 94 ATGCCAGGTGCTTCAGCTGGTGTCTTCTCCTCTCCTCTCCATCGACACGAGGCTCTG 153
|||||
Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
|||||
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|||||
Qy 41 IleThrLeuValSerIleValLeuAlaAsnGlnLeuAsnPheThrGluAlaLysGluAla 60
|||||
Db 214 ATCACCTTGTGACAAAAGGCGAACCAGCAGCTGAATTTACAGAGCTTAAGGAGGCC 273..
|||||
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
|||||
Db 274 TGTAGGCTGCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 333
|||||
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
|||||
Db 334 AGCTTTGAAAATTGCACTATGGCTGGTGGAGATGGATTTCGGTGGTCATCTTAGGATT 393
|||||
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
|||||
Db 394 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGTGTCTTGATTTGGAAGTTCCAGTG 453
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Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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Db 454 AGCCGACAGTTTGCAGGCTATTGTTACAACTCATCTGATCTTGGACTTAACCTCGTGCATT 513
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Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
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Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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Db 574 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC 633
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Db 634 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT 693
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Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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Db 694 TGTGTCTACAGAAGTTTATTTGGAAACTAGCACCATGTCTACAGAACTGAACCACTTTGTT 753
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Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
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Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
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Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGlu 276
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Db 872 AGGTATGTGAAGGCTT--CCYTTTACAAACAR-AATCAGCAGAGAGGAA 916
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Search completed: October 8, 2005, 22:44:56  
Job time : 4259.4 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 8, 2005, 22:45:22 ; Search time 860.456 Seconds  
(without alignments)  
2606.386 Million cell updates/sec

Perfect score: 1657  
Sequence: 1 MARCFSLVLLTSTWTRLL.....NPEESKSPKTTVRCLEAEV 322

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

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-THR\_MIN=0 -ALIGN=0 -MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0  
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Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

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1	1657	100.0	2029	15	US-10-079-111-2	Sequence 2, Appli
2	1657	100.0	2029	22	US-10-820-474A-198	Sequence 198, App
5	1657	100.0	2372	9	US-09-905-291A-200	Sequence 200, App
94	1657	100.0	2372	15	US-10-223-085-31	Sequence 31, Appl
95	1657	100.0	2372	15	US-10-223-084-31	Sequence 31, Appl
96	1657	100.0	2372	15	US-10-223-088-31	Sequence 31, Appl
97	1657	100.0	2372	15	US-10-223-090-31	Sequence 31, Appl
99	1657	100.0	2372	15	US-10-223-087-31	Sequence 31, Appl
103	1657	100.0	2372	15	US-10-223-083-31	Sequence 31, Appl
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136	1657	100.0	2372	16	US-10-299-976-200	Sequence 200, App
211	1657	100.0	2372	16	US-10-063-742-5	Sequence 5, Appli
214	1657	100.0	2372	16	US-10-299-937-200	Sequence 200, App
224	1657	100.0	2372	16	US-10-223-081-31	Sequence 31, Appl
230	1657	100.0	2372	17	US-10-223-082-31	Sequence 31, Appl
231	1657	100.0	2372	17	US-10-298-993-200	Sequence 200, App
232	1657	100.0	2372	17	US-10-305-654-31	Sequence 31, Appl
233	1657	100.0	2372	17	US-10-448-923-200	Sequence 200, App
234	1657	100.0	2372	17	US-10-449-656-200	Sequence 200, App
235	1657	100.0	2372	17	US-10-448-713-200	Sequence 200, App
236	1657	100.0	2372	17	US-10-425-447-200	Sequence 200, App
238	1657	100.0	2372	18	US-10-081-056-31	Sequence 31, Appl
239	1657	100.0	2372	19	US-10-215-371-200	Sequence 200, App
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242	1657	100.0	2372	21	US-10-963-467-200	Sequence 200, App
243	1657	100.0	2372	21	US-10-978-255-200	Sequence 200, App
244	1657	100.0	2372	22	US-10-797-366-200	Sequence 200, App
245	1657	100.0	2372	22	US-10-970-823-200	Sequence 200, App
246	1657	100.0	2436	22	US-10-756-149-3836	Sequence 3836, Ap
247	1657	100.0	2667	20	US-10-723-860-7823	Sequence 7823, Ap
248	1654	99.8	2313	15	US-10-276-774-999	Sequence 999, App
249	1651	99.6	2313	15	US-10-291-634-12	Sequence 1, Appli
250	1651	99.6	2369	17	US-10-264-237-1260	Sequence 1260, Ap
251	1638	98.9	2313	20	US-10-723-860-3908	Sequence 3908, Ap
252	1638	98.9	2313	22	US-10-287-436A-215	Sequence 215, App
253	1511.5	91.2	1127	17	US-10-138-588-1	Sequence 1, Appli
254	1103	66.6	1896	10	US-09-866-050A-595	Sequence 595, App
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256	673	40.6	411	10	US-09-918-995-8107	Sequence 8107, Ap
257	627.5	37.9	531	21	US-10-696-639-2768	Sequence 2768, Ap
258	595.5	35.9	559	15	US-10-079-111-3	Sequence 3, Appli
259	440	26.6	486	10	US-09-918-995-10116	Sequence 10116, A
260	386	23.3	279	15	US-10-079-111-4	Sequence 4, Appli
261	354	21.4	492	15	US-10-291-634-12	Sequence 12, Appl
262	349	21.1	466	15	US-10-291-634-13	Sequence 13, Appl
263	306	18.5	469	9	US-09-864-761-2325	Sequence 2325, Ap
264	286.5	17.3	498	15	US-10-291-634-15	Sequence 15, Appl
265	281.5	17.0	457	9	US-09-864-761-15431	Sequence 15431, A
266	231	14.1	1089	22	US-10-024-607-25	Sequence 25, Appl
267	231	13.9	2747	9	US-09-917-800A-1588	Sequence 1588, Ap
268	231	13.9	2747	22	US-10-024-607-7	Sequence 7, Appli
269	223	13.5	1972	22	US-10-024-607-24	Sequence 24, Appl
270	222	13.4	1992	15	US-10-101-510-436	Sequence 436, App
271	215	13.0	1354	11	US-09-864-761-19060	Sequence 19060, A
272	213	12.9	1794	15	US-09-836-544-31	Sequence 31, Appl
273	213	12.9	1794	15	US-10-007-926A-376	Sequence 376, App
274	213	12.9	1794	21	US-10-482-029-254	Sequence 254, App
275	213	12.9	1794	21	US-10-852-335A-36	Sequence 36, Appl
276	213	12.9	4335	19	US-10-356-157-443	Sequence 443, App
277	213	12.9	4335	21	US-10-741-601-56	Sequence 56, Appl
278	212	12.8	1033	22	US-10-741-600-220	Sequence 220, App
279	212	12.8	1981	15	US-10-505-769-1	Sequence 1, Appli
280	212	12.8	1981	15	US-10-084-817-180	Sequence 180, App
281	212	12.8	4365	16	US-10-247-671-72	Sequence 72, Appl
			5165	10	US-09-814-353-20099	Sequence 20099, A

282	210	12.7	1297	18	US-10-641-643-876	Sequence 876, App	355	145.5	8.8	7840	18	US-10-634-574-15	Sequence 15, Appl
283	210	12.7	1297	22	US-10-024-607-23	Sequence 23, Appl	356	145	8.8	351	14	US-10-060-036-880	Sequence 880, App
284	209.5	12.6	5452	19	US-10-741-601-57	Sequence 57, Appl	357	145	8.8	466	17	US-10-242-535A-58386	Sequence 58386, A
285	209.5	12.6	5452	21	US-10-741-600-219	Sequence 219, App	358	145	8.8	466	18	US-10-085-783A-58386	Sequence 58386, A
286	205.5	12.4	3091	22	US-10-783-271-86	Sequence 86, Appl	359	145	8.8	1414	9	US-09-799-118-1	Sequence 1, Appl
287	205.5	12.4	3091	22	US-10-287-436A-196	Sequence 196, App	360	143.5	8.7	336	10	US-09-918-995-17767	Sequence 17767, A
288	205.5	12.4	3091	22	US-10-287-436A-807	Sequence 807, App	361	143.5	8.7	431	18	US-10-424-599-106015	Sequence 106015,
289	205.5	12.4	4633	19	US-10-741-601-61	Sequence 61, Appl	362	142.5	8.6	8444	17	US-10-028-248A-1	Sequence 1, Appl
290	205.5	12.4	4633	21	US-10-741-600-224	Sequence 224, App	363	142.5	8.6	8444	17	US-10-107-782-1	Sequence 1, Appl
291	205	12.4	4723	19	US-10-741-601-53	Sequence 53, App	364	141.5	8.5	3625	22	US-10-667-723-17	Sequence 17, Appl
292	205	12.4	4723	21	US-10-741-600-217	Sequence 217, App	365	141.5	8.5	8495	17	US-10-028-248A-3	Sequence 3, Appl
293	204.5	12.3	3083	21	US-10-690-880-18	Sequence 18, Appl	366	141.5	8.5	8495	17	US-10-107-782-3	Sequence 3, Appl
294	203	12.3	3091	21	US-10-741-600-226	Sequence 226, App	367	138.5	8.4	1411	9	US-09-765-231A-44	Sequence 44, Appl
295	203	12.3	5468	19	US-10-741-601-60	Sequence 60, Appl	368	137	8.3	3260	17	US-10-028-248A-210	Sequence 210, App
296	203	12.3	5468	21	US-10-741-600-225	Sequence 225, App	369	137	8.3	3260	17	US-10-107-782-210	Sequence 210, App
297	203	12.3	5674	19	US-10-741-601-54	Sequence 54, Appl	370	137	8.3	4576	9	US-09-842-930A-24	Sequence 24, Appl
298	203	12.3	5674	21	US-10-741-600-218	Sequence 218, App	371	137	8.3	4576	21	US-10-990-844-24	Sequence 24, Appl
299	203	12.3	5739	19	US-10-741-601-55	Sequence 55, Appl	372	137	8.3	4642	15	US-10-133-172-3	Sequence 3, Appl
300	203	12.3	5739	21	US-10-741-600-221	Sequence 221, App	373	137	8.3	4962	15	US-10-133-172-19	Sequence 19, Appl
301	199.5	12.0	1737	21	US-10-505-680-474	Sequence 474, App	374	136	8.2	4706	9	US-09-842-930A-1	Sequence 1, Appl
302	199.5	12.0	1737	22	US-10-024-607-22	Sequence 22, Appl	375	136	8.2	4706	15	US-10-133-172-1	Sequence 1, Appl
303	199.5	12.0	1824	21	US-10-486-226-1	Sequence 1, Appl	376	136	8.2	4706	15	US-10-990-844-1	Sequence 1, Appl
304	199.5	12.0	2100	15	US-10-012-969C-1	Sequence 1, Appl	377	135.5	8.2	3153	21	US-09-759-130B-343	Sequence 343, App
305	199.5	12.0	2100	22	US-10-505-769-3	Sequence 3, Appl	378	135.5	8.2	3153	14	US-10-189-123-73	Sequence 73, Appl
306	199.5	12.0	2308	11	US-09-836-544-33	Sequence 33, Appl	379	135.5	8.2	3153	16	US-10-188-495-73	Sequence 73, Appl
307	199.5	12.0	2316	10	US-09-983-000A-15	GENERAL INFORMATI	380	135.5	8.2	3153	19	US-10-741-790-343	Sequence 343, App
308	199.5	12.0	2316	21	US-10-652-981-15	Sequence 15, Appl	381	132.5	8.0	2160	17	US-10-104-047-1824	Sequence 1824, Ap
309	198.5	12.0	4674	9	US-09-974-298-22	Sequence 22, Appl	382	131.5	7.9	2652	14	US-10-195-970-4	Sequence 4, Appl
310	199.5	12.0	4674	10	US-09-971-429B-51	Sequence 51, Appl	383	131.5	7.9	2652	17	US-10-453-420-4	Sequence 4, Appl
311	199.5	12.0	4674	15	US-10-084-817-181	Sequence 181, App	384	131	7.9	2013	10	US-09-759-130B-330	Sequence 330, App
312	199.5	12.0	4675	22	US-10-765-700-97	Sequence 97, App	385	131	7.9	2013	14	US-10-189-123-60	Sequence 60, Appl
313	198	11.9	5053	19	US-10-741-601-52	Sequence 52, Appl	386	131	7.9	2013	16	US-10-188-495-60	Sequence 60, Appl
314	198	11.9	5053	21	US-10-741-600-216	Sequence 216, App	387	131	7.9	2013	19	US-10-741-790-330	Sequence 330, App
315	197	11.9	2097	22	US-10-505-769-5	Sequence 5, Appl	388	131	7.9	2730	10	US-09-759-130B-329	Sequence 329, App
316	197	11.9	2263	21	US-10-956-157-4279	Sequence 4279, Ap	389	131	7.9	2730	14	US-10-189-123-59	Sequence 59, Appl
317	197	11.9	2265	21	US-10-696-639-33	Sequence 33, Appl	390	131	7.9	2730	16	US-10-188-495-59	Sequence 59, Appl
318	197	11.9	2387	19	US-10-648-593-41	Sequence 41, Appl	391	131	7.9	2730	19	US-10-741-790-329	Sequence 329, App
319	197	11.9	2387	22	US-10-783-271-67	Sequence 67, Appl	392	131	7.9	3438	18	US-10-312-352-60	Sequence 60, Appl
320	197	11.9	2905	13	US-10-044-090-495	Sequence 495, App	401	131	7.9	3476	14	US-10-237-535-51	Sequence 51, Appl
321	197	11.9	3474	9	US-09-981-353-9	Sequence 9, Appl	410	131	7.9	3476	14	US-10-239-196-51	Sequence 51, Appl
322	197	11.9	4874	19	US-10-741-601-59	Sequence 59, Appl	501	131	7.9	3476	21	US-10-936-626-11	Sequence 11, Appl
323	197	11.9	4874	21	US-10-741-600-223	Sequence 223, App	502	131	7.9	3476	21	US-10-938-061-11	Sequence 11, Appl
324	196	11.8	1735	21	US-10-956-157-4281	Sequence 4281, Ap	503	130.5	7.9	2652	14	US-10-195-970-5	Sequence 5, Appl
325	191.5	11.6	339	21	US-10-487-620-5	Sequence 5, Appl	504	130.5	7.9	2652	17	US-10-453-420-5	Sequence 5, Appl
326	191	11.5	1760	21	US-10-956-157-4280	Sequence 4280, Ap	505	130.5	7.9	3681	17	US-10-264-237-1320	Sequence 1320, Ap
327	190	11.5	336	21	US-10-487-620-1	Sequence 1, Appl	506	130.5	7.9	7137	21	US-10-956-157-582	Sequence 582, App
328	188	11.3	336	21	US-10-487-620-7	Sequence 7, Appl	507	130.5	7.9	7137	22	US-10-287-436A-235	Sequence 235, App
329	186	11.2	336	21	US-10-487-620-9	Sequence 9, Appl	508	130	7.8	8038	20	US-10-497-991-1	Sequence 1, Appl
330	184	11.1	336	21	US-10-487-620-11	Sequence 11, Appl	509	130	7.8	8038	20	US-10-723-860-5739	Sequence 5739, Ap
331	182	11.0	336	21	US-10-487-620-3	Sequence 3, Appl	510	127.5	7.7	488	10	US-10-098-841-328	Sequence 328, App
332	180.5	10.9	2764	22	US-10-450-763-17058	Sequence 17058, A	511	127.5	7.7	1365	13	US-10-098-841-328	Sequence 328, App
333	179	10.8	2273	22	US-10-450-763-17062	Sequence 17062, A	512	127.5	7.7	1925	20	US-10-723-860-6530	Sequence 6530, Ap
334	170	10.3	106	9	US-09-864-761-31946	Sequence 31946, A	515	127.5	7.7	1985	9	US-09-905-291A-212	Sequence 212, App
335	166.5	10.0	309	10	US-09-918-995-36412	Sequence 36412, A	1045	127.5	7.7	1985	16	US-10-174-587-27	Sequence 27, Appl
336	165	10.0	820	15	US-10-079-111-5	Sequence 5, Appl	1080	127.5	7.7	1985	16	US-10-299-937-212	Sequence 212, App
337	164.5	9.9	444	21	US-10-696-639-1827	Sequence 1827, Ap	1082	127.5	7.7	1985	16	US-10-299-937-212	Sequence 212, App
338	158	9.5	549	15	US-10-101-510-85	Sequence 85, Appl	1092	127.5	7.7	1985	17	US-10-298-993-212	Sequence 212, App
339	158	9.5	549	21	US-10-505-680-476	Sequence 476, App	1097	127.5	7.7	1985	17	US-10-448-923-212	Sequence 212, App
340	153.5	9.3	270	10	US-09-927-463-7	Sequence 7, Appl	1098	127.5	7.7	1985	17	US-10-449-658-212	Sequence 212, App
341	153.5	9.3	270	20	US-10-837-671-7	Sequence 7, Appl	1099	127.5	7.7	1985	17	US-10-448-713-212	Sequence 212, App
342	151	9.1	2863	17	US-10-104-047-610	Sequence 610, App	1101	127.5	7.7	1985	17	US-10-425-447-212	Sequence 212, App
343	148.5	9.0	425	10	US-09-918-995-35733	Sequence 35733, A	1109	127.5	7.7	1985	19	US-10-215-371-212	Sequence 212, App
344	148.5	9.0	836	13	US-10-027-632-148987	Sequence 148987, A	1110	127.5	7.7	1985	19	US-10-771-187-212	Sequence 212, App
345	148.5	9.0	836	17	US-10-027-632-148987	Sequence 148987, A	1111	127.5	7.7	1985	21	US-10-963-467-212	Sequence 212, App
346	145.5	8.8	1144	13	US-10-044-090-446	Sequence 446, App	1112	127.5	7.7	1985	21	US-10-978-255-212	Sequence 212, App
347	145.5	8.8	1144	16	US-10-247-671-124	Sequence 124, App	1113	127.5	7.7	1985	22	US-10-797-366-212	Sequence 212, App
348	145.5	8.8	1422	17	US-10-295-027-291	Sequence 291, App	1117	127.5	7.7	1985	22	US-10-970-823-212	Sequence 212, App
349	145.5	8.8	1430	17	US-10-295-027-1020	Sequence 1020, Ap	1118	127.5	7.7	2558	10	US-09-983-000A-13	GENERAL INFORMATI
350	145.5	8.8	1440	20	US-10-723-860-4325	Sequence 4325, Ap	1119	127.5	7.7	2558	21	US-10-652-981-13	Sequence 13, Appl
351	145.5	8.8	1440	21	US-10-728-698-280	Sequence 280, App	1120	127.5	7.7	2558	21	US-10-936-626-12	Sequence 12, Appl
352	145.5	8.8	1440	21	US-10-728-698-794	Sequence 794, App	1121	127.5	7.7	2558	21	US-10-938-061-12	Sequence 12, Appl
353	145.5	8.8	1461	20	US-10-723-860-8161	Sequence 8161, Ap	1122	127.5	7.7	2558	21	US-10-852-335A-1	Sequence 1, Appl
354	145.5	8.8	1728	13	US-10-044-090-445	Sequence 445, App	1123	127.5	7.7	2878	17	US-10-453-420-7	Sequence 7, Appl

1124	127.5	7.7	2878	17	US-10-295-027-259	Sequence 259, App	1197	111	6.7	1720	10	US-09-148-545-53	Sequence 53, Appl
1125	127	7.7	2465	9	US-09-917-800A-500	Sequence 500, App	1198	111	6.7	1720	22	US-10-979-111-53	Sequence 53, Appl
1126	126.5	7.6	2753	10	US-09-774-639-12	Sequence 12, Appl	1199	110.5	6.7	434	18	US-10-424-599-41662	Sequence 41662, A
1127	126.5	7.6	2753	10	US-09-969-730-13	Sequence 13, Appl	1200	110	6.6	1308	10	US-09-948-820-14	Sequence 14, Appl
1128	126.5	7.6	2753	17	US-10-621-363-13	Sequence 13, Appl	1201	110	6.6	1308	20	US-10-613-076-14	Sequence 14, Appl
1129	126	7.6	201	21	US-10-741-600-7000	Sequence 7000, App	1202	110	6.6	2343	19	US-10-437-963-46994	Sequence 46994, A
1130	125	7.5	201	19	US-10-741-601-1565	Sequence 1565, App	1203	109.5	6.6	1466	19	US-10-437-963-51867	Sequence 51867, A
1131	125	7.5	201	19	US-10-741-601-1575	Sequence 1575, App	1204	109.5	6.6	6310	9	US-09-795-651-45	Sequence 45, Appl
1132	125	7.5	201	19	US-10-741-601-1591	Sequence 1591, App	1205	109	6.6	6310	15	US-10-241-220-26	Sequence 26, Appl
1133	125	7.5	201	19	US-10-741-601-1608	Sequence 1608, App	1206	109	6.6	6310	17	US-10-295-027-261	Sequence 261, App
1134	125	7.5	201	19	US-10-741-601-1617	Sequence 1617, App	1207	109	6.6	6310	20	US-10-872-972-26	Sequence 26, Appl
1135	125	7.5	201	19	US-10-741-601-1632	Sequence 1632, App	1208	109	6.6	6310	20	US-10-872-991-26	Sequence 26, Appl
1136	125	7.5	201	19	US-10-741-601-1648	Sequence 1648, App	1209	109	6.6	6310	22	US-10-698-190-17	Sequence 17, Appl
1137	125	7.5	201	19	US-10-741-601-1663	Sequence 1663, App	1210	108	6.5	1492	18	US-10-120-907A-27	Sequence 27, Appl
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1139	125	7.5	201	21	US-10-741-600-6888	Sequence 6888, App	1212	108	6.5	1640	9	US-09-764-853-249	Sequence 249, App
1140	125	7.5	201	21	US-10-741-600-6888	Sequence 6888, App	1213	108	6.5	1640	14	US-10-091-438-33	Sequence 33, Appl
1141	125	7.5	201	21	US-10-741-600-6904	Sequence 6904, App	1214	108	6.5	1641	9	US-09-764-853-420	Sequence 420, App
1142	125	7.5	201	21	US-10-741-600-6920	Sequence 6920, App	1215	108	6.5	1641	14	US-10-091-438-94	Sequence 94, Appl
1143	125	7.5	201	21	US-10-741-600-6927	Sequence 6927, App	1216	108	6.5	1790	15	US-10-311-455-2348	Sequence 2348, App
1144	125	7.5	201	21	US-10-741-600-6943	Sequence 6943, App	1217	108	6.5	1957	18	US-10-120-907A-2	Sequence 2, Appl
1145	125	7.5	201	21	US-10-741-600-6961	Sequence 6961, App	1218	108	6.5	1957	18	US-10-120-907A-6	Sequence 6, Appl
1146	125	7.5	201	21	US-10-741-600-6971	Sequence 6971, App	1219	108	6.5	1957	18	US-10-120-907A-8	Sequence 8, Appl
1147	125	7.5	201	21	US-10-741-600-6986	Sequence 6986, App	1220	108	6.5	1957	18	US-10-120-907A-10	Sequence 10, Appl
1148	125	7.5	1414	11	US-09-968-007A-208	Sequence 208, App	1221	108	6.5	1957	18	US-10-120-907A-12	Sequence 12, Appl
1149	125	7.5	1414	17	US-10-133-937-18	Sequence 18, Appl	1222	108	6.5	1957	18	US-10-120-907A-14	Sequence 14, Appl
1150	125	7.5	1414	17	US-10-295-027-293	Sequence 293, App	1223	108	6.5	1957	18	US-10-120-907A-16	Sequence 16, Appl
1151	125	7.5	1414	17	US-10-159-563-18	Sequence 18, Appl	1224	108	6.5	1957	18	US-10-120-907A-18	Sequence 18, Appl
1152	125	7.5	1414	19	US-10-755-889-117	Sequence 117, App	1225	108	6.5	1957	18	US-10-120-907A-20	Sequence 20, Appl
1153	125	7.5	1414	21	US-10-278-698-79	Sequence 79, Appl	1226	108	6.5	1957	18	US-10-120-907A-22	Sequence 22, Appl
1154	125	7.5	1414	21	US-10-278-698-593	Sequence 593, App	1227	108	6.5	1957	18	US-10-120-907A-26	Sequence 26, Appl
1155	125	7.5	1414	21	US-10-843-641A-6678	Sequence 6678, App	1228	108	6.5	1957	18	US-10-120-907A-6	Sequence 6, Appl
1156	124	7.5	474	10	US-09-918-995-32777	Sequence 32777, A	1229	108	6.5	2166	18	US-10-120-907A-4	Sequence 4, Appl
c1157	121.5	7.3	2694	14	US-10-050-704-40	Sequence 40, Appl	1230	108	6.5	2166	18	US-10-120-907A-61	Sequence 61, Appl
c1158	121.5	7.3	2694	19	US-10-798-512-40	Sequence 40, Appl	1231	108	6.5	2166	18	US-10-120-907A-63	Sequence 63, Appl
1159	121	7.3	1587	21	US-10-314-942-19	Sequence 19, Appl	1232	108	6.5	2538	20	US-10-723-860-6874	Sequence 6874, App
1160	118.5	7.2	1783	18	US-10-112-344-153	Sequence 153, App	1233	107.5	6.5	6279	24	US-11-097-143-8399	Sequence 42389, A
1161	118.5	7.2	1185	9	US-09-880-107-3311	Sequence 3311, App	c1234	107	6.5	1851	17	US-10-972-079-42389	Sequence 3, Appl
1162	118.5	7.2	1185	10	US-09-873-367C-1039	Sequence 1039, App	1235	107	6.5	2011	22	US-10-667-723-3	Sequence 58, Appl
1163	118.5	7.2	1185	16	US-10-269-909-12	Sequence 12, Appl	1236	107	6.5	3858	19	US-10-741-601-58	Sequence 222, App
1164	118.5	7.2	1185	17	US-10-159-563-100	Sequence 100, App	1237	107	6.5	3858	21	US-09-801-368-103	Sequence 103, App
1165	118.5	7.2	1185	22	US-10-843-641A-1039	Sequence 1039, App	1238	107	6.5	4614	17	US-10-369-493-25085	Sequence 25085, A
1166	118.5	7.2	1185	22	US-10-631-467-315	Sequence 315, App	1239	107	6.5	4614	17	US-10-698-190-23	Sequence 23, Appl
1167	118.5	7.2	1214	17	US-10-062-674-1454	Sequence 1454, App	1240	107	6.5	5259	22	US-11-097-143-36209	Sequence 36209, A
1168	118.5	7.2	12319	16	US-10-240-965-240	Sequence 240, App	1241	107	6.5	5388	24	US-11-097-143-36209	Sequence 16, Appl
c1169	118	7.1	1627	19	US-10-437-963-14608	Sequence 14608, A	1242	107	6.5	5864	21	US-10-324-035-16	Sequence 36208, A
1170	118	7.1	7375	22	US-10-631-467-1178	Sequence 1178, App	1243	107	6.5	7782	24	US-11-097-143-36208	Sequence 23078, A
1171	115.5	7.0	410	10	US-09-918-995-16642	Sequence 16642, A	c1244	107	6.5	1174	20	US-10-363-345A-29077	Sequence 23077, A
1172	115.5	7.0	7291	21	US-10-741-600-348	Sequence 348, App	1245	106.5	6.4	1174	20	US-10-363-345A-29078	Sequence 23078, A
1173	115.5	7.0	7358	21	US-10-741-600-350	Sequence 350, App	1246	106.5	6.4	1174	21	US-10-363-483A-29078	Sequence 23077, A
1174	115.5	7.0	12553	21	US-10-741-600-344	Sequence 344, App	c1247	106.5	6.4	1174	21	US-10-363-483A-29078	Sequence 23078, A
1175	115.5	7.0	12620	21	US-10-741-600-345	Sequence 345, App	1248	106.5	6.4	1174	21	US-10-305-720-230	Sequence 230, App
1176	114.5	6.9	5191	18	US-10-152-119A-1928	Sequence 1928, App	1249	106.5	6.4	1482	17	US-10-305-720-230	Sequence 1560, App
1177	114.5	6.9	5191	22	US-10-698-190-21	Sequence 21, Appl	1250	106	6.4	201	19	US-10-741-601-1560	Sequence 1580, App
1178	114	6.9	8924	24	US-11-097-143-8398	Sequence 8398, App	1251	106	6.4	201	19	US-10-741-601-1570	Sequence 1580, App
1179	113	6.8	2087	20	US-10-270-253-1	Sequence 1, Appl	1252	106	6.4	201	19	US-10-741-601-1580	Sequence 1597, App
1180	113	6.8	4330	21	US-10-741-600-346	Sequence 346, App	1253	106	6.4	201	19	US-10-741-601-1597	Sequence 1614, App
1181	113	6.8	7182	14	US-10-116-802-207	Sequence 207, App	1254	106	6.4	201	19	US-10-741-601-1614	Sequence 1622, App
1182	113	6.8	8224	15	US-10-177-293-89	Sequence 89, Appl	1255	106	6.4	201	19	US-10-741-601-1622	Sequence 1643, App
1183	113	6.8	8224	18	US-10-240-425-1534	Sequence 1534, App	1256	106	6.4	201	19	US-10-741-601-1643	Sequence 1653, App
1184	113	6.8	8224	21	US-10-482-029-193	Sequence 193, App	1257	106	6.4	201	19	US-10-741-601-1653	Sequence 1667, App
1185	113	6.8	8224	21	US-10-852-335A-90	Sequence 90, Appl	1258	106	6.4	201	21	US-10-741-600-6873	Sequence 6873, App
1186	113	6.8	9592	21	US-10-741-600-349	Sequence 349, App	1259	106	6.4	201	21	US-10-741-600-6883	Sequence 6883, App
1187	113	6.8	9647	14	US-10-198-846-11006	Sequence 11006, A	1260	106	6.4	201	21	US-10-741-600-6893	Sequence 6893, App
1188	113	6.8	9659	21	US-10-741-600-347	Sequence 347, App	1261	106	6.4	201	21	US-10-741-600-6910	Sequence 6910, App
c1189	113	6.8	12644	14	US-10-161-803-45	Sequence 45, Appl	1262	106	6.4	201	21	US-10-741-600-6924	Sequence 6924, App
1190	112.5	6.8	972	9	US-09-764-853-156	Sequence 156, App	1263	106	6.4	201	21	US-10-741-600-6932	Sequence 6932, App
1191	112	6.8	340	17	US-10-242-535A-49165	Sequence 49165, A	1264	106	6.4	201	21	US-10-741-600-6956	Sequence 6956, App
1192	112	6.8	340	18	US-10-085-783A-49165	Sequence 49165, A	1265	106	6.4	201	21	US-10-741-600-6966	Sequence 6966, App
1193	112	6.8	10550	19	US-10-741-601-5630	Sequence 5630, App	1266	106	6.4	201	21	US-10-741-600-6976	Sequence 6976, App
1194	112	6.8	10550	21	US-10-741-600-17620	Sequence 17620, A	1267	106	6.4	201	21	US-10-741-600-6998	Sequence 6998, App
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1282	103	6.2	1962	10	US-09-148-545-111	Sequence 111, App	c1355	97.5	5.9	2242716	22	US-10-915-740A-1068	Sequence 1068, Ap
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1293	102	6.2	1323	18	US-10-425-114-13953	Sequence 13953, A	c1366	97.5	5.9	1347	21	US-10-363-483A-28466	Sequence 28466, A
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1295	101.5	6.1	1276	20	US-10-363-345A-27853	Sequence 27853, A	c1368	97.5	5.9	2751	17	US-10-094-749-624	Sequence 624, App
1296	101.5	6.1	1276	20	US-10-363-345A-27854	Sequence 27854, A	c1369	97.5	5.9	1230025	17	US-10-289-762-1	Sequence 1, Appli
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1304	101.5	6.1	6112	20	US-10-480-846-34	Sequence 34, Appli	c1377	95.5	5.8	1131	9	US-09-801-368-205	Sequence 205, App
1305	101	6.1	871	18	US-10-425-114-4960	Sequence 4960, Ap	c1378	95.5	5.8	1798	21	US-10-868-381-95	Sequence 95, Appli
1306	101	6.1	2313	17	US-10-243-552-681	Sequence 681, App	c1379	95.5	5.8	2404	19	US-10-437-963-16578	Sequence 16578, A
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1309	101	6.1	33302	21	US-10-741-600-17866	Sequence 17866, A	c1382	95.5	5.8	4435	19	US-10-766-711-1	Sequence 1, Appli
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1311	100.5	6.1	1209	18	US-10-257-174-23	Sequence 23, Appli	c1384	95.5	5.8	12781	18	US-10-221-714A-107	Sequence 107, App
1312	100.5	6.1	1241	19	US-10-729-807-33	Sequence 33, Appli	c1385	95.5	5.8	12781	18	US-10-240-589C-37	Sequence 37, Appli
1313	100.5	6.1	1475	17	US-10-343-953-1	Sequence 1, Appli	c1386	95.5	5.8	65140	19	US-10-203-295-1	Sequence 1, Appli
1314	100.5	6.1	1612	19	US-10-437-963-92511	Sequence 92511, A	c1387	95.5	5.8	125401	19	US-10-203-295-35	Sequence 35, Appli
1315	100.5	6.1	1825	19	US-10-437-963-93701	Sequence 93701, A	c1388	95	5.7	1380	21	US-10-847-918-10	Sequence 10, Appli
1316	100.5	6.1	2865	18	US-10-424-599-24135	Sequence 24135, A	c1389	95	5.7	1440	17	US-10-295-027-301	Sequence 301, App
1317	100.5	6.1	4140	24	US-11-097-143-33611	Sequence 33611, A	c1390	95	5.7	1440	21	US-10-391-939A-3	Sequence 3, Appli
1318	100.5	6.1	7596	16	US-10-004-113-57	Sequence 57, Appli	c1391	95	5.7	1455	17	US-10-282-122A-17996	Sequence 17996, A
1319	100.5	6.1	8064	16	US-10-004-113-56	Sequence 56, Appli	c1392	95	5.7	2211	24	US-11-097-143-16301	Sequence 16301, A
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1322	100	6.0	645	20	US-10-363-345A-696	Sequence 696, App	c1395	95	5.7	2450	19	US-10-437-963-2523	Sequence 2523, Ap
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1326	100	6.0	9487	19	US-10-788-792-43	Sequence 43, Appli	c1399	94.5	5.7	632	19	US-10-437-963-40393	Sequence 40393, A
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1331	99	6.0	4287	24	US-11-097-143-37922	Sequence 37922, A	c1404	94.5	5.7	1032	20	US-10-363-345A-22310	Sequence 22310, A
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1337	98.5	5.9	684973	21	US-09-263-959-1	Sequence 1, Appli	c1410	94.5	5.7	1608	14	US-10-218-743-22	Sequence 22, Appli
1338	98	5.9	6353	24	US-11-097-143-8000	Sequence 8000, Ap	c1411	94.5	5.7	1665	14	US-10-218-743-17	Sequence 17, Appli
1339	98	5.9	8429	24	US-11-097-143-7999	Sequence 7999, Ap	c1412	94.5	5.7	1665	14	US-10-218-743-19	Sequence 19, Appli
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1342	97.5	5.9	585	21	US-10-363-483A-38453	Sequence 38453, A	c1415	94.5	5.7	1752	14	US-10-218-743-16	Sequence 16, Appli



1416	94.5	5.7	2901	9	US-09-801-368-371	Sequence 371, App	1489	93	5.6	5931	24	US-11-097-143-35048	Sequence 35048, A
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1419	94	5.7	819	18	US-10-425-114-4720	Sequence 4720, Ap	1492	92.5	5.6	647	20	US-10-363-345A-740	Sequence 740, App
1420	94	5.7	819	18	US-10-425-114-4725	Sequence 4725, Ap	c1493	92.5	5.6	647	21	US-10-363-483A-739	Sequence 739, App
1421	94	5.7	1019	19	US-10-437-963-1250	Sequence 1250, Ap	1494	92.5	5.6	647	21	US-10-363-483A-740	Sequence 740, App
1422	94	5.7	1199	20	US-10-363-345A-33551	Sequence 33551, A	1495	92.5	5.6	757	20	US-10-425-115-13921	Sequence 13921, A
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1424	94	5.7	1199	21	US-10-363-483A-33551	Sequence 33551, A	c1497	92.5	5.6	907	19	US-10-767-795-843	Sequence 843, App
1425	94	5.7	1199	21	US-10-363-483A-33552	Sequence 33552, A	1498	92.5	5.6	918	20	US-10-425-115-36844	Sequence 36844, A
1426	94	5.7	1482	19	US-10-437-963-36908	Sequence 36908, A	1499	92.5	5.6	1099	15	US-10-188-012-28	Sequence 28, Appl
1427	94	5.7	1494	19	US-10-767-701-11834	Sequence 11834, A	1500	92.5	5.6	1099	21	US-10-663-497-28	Sequence 28, Appl
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1429	94	5.7	1946	14	US-11-097-143-15890	Sequence 15890, A							
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1431	94	5.7	3946	24	US-11-097-143-15889	Sequence 15889, A							
1432	94	5.7	4404	19	US-10-437-963-92371	Sequence 92371, A							
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1436	93.5	5.6	739	20	US-10-363-345A-38980	Sequence 38980, A							
1437	93.5	5.6	739	21	US-10-363-483A-38979	Sequence 38979, A							
1438	93.5	5.6	739	21	US-10-363-483A-38980	Sequence 38980, A							
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1442	93.5	5.6	1080	15	US-10-188-012-20	Sequence 20, Appl							
1443	93.5	5.6	1080	21	US-10-663-497-18	Sequence 18, Appl							
1444	93.5	5.6	1080	21	US-10-663-497-20	Sequence 20, Appl							
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1448	93.5	5.6	1185	21	US-10-363-483A-38981	Sequence 38981, A							
1449	93.5	5.6	1185	21	US-10-363-483A-38982	Sequence 38982, A							
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1451	93.5	5.6	1190	20	US-10-363-345A-31168	Sequence 31168, A							
1452	93.5	5.6	1190	21	US-10-363-483A-31167	Sequence 31167, A							
1453	93.5	5.6	1190	21	US-10-363-483A-31168	Sequence 31168, A							
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1458	93.5	5.6	7568	22	US-10-450-763-16627	Sequence 16627, A							
1459	93.5	5.6	9161	17	US-10-133-937-37	Sequence 37, Appl							
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1463	93.5	5.6	9220	20	US-10-357-930-25254	Sequence 25254, A							
1464	93.5	5.6	9416	19	US-10-755-889-614	Sequence 614, App							
1465	93.5	5.6	9416	21	US-10-489-740-114	Sequence 114, App							
1466	93.5	5.6	11917	22	US-10-765-700-32	Sequence 32, Appl							
1467	93.5	5.6	11950	16	US-10-252-157-218	Sequence 218, App							
1468	93.5	5.6	34570	11	US-09-997-722-157	Sequence 157, App							
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1482	93	5.6	2050	17	US-10-413-899-15	Sequence 15, Appl							
1483	93	5.6	2111	18	US-10-424-599-105989	Sequence 105989, A							
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253	86.5	5.2	2334	4	US-09-476-242-7	Sequence 6, Appl	C 326	85	5.1	1797	3	US-09-669-974-4	Sequence 4, Appl
254	86.5	5.2	2352	4	US-09-476-242-26	Sequence 26, Appl	C 327	85	5.1	1797	4	US-09-797-862-4	Sequence 4, Appl
255	86.5	5.2	2358	4	US-09-475-515-50	Sequence 50, Appl	C 328	85	5.1	6013	4	US-09-774-528-109	Sequence 109, App
256	86.5	5.2	2358	4	US-09-476-242-25	Sequence 25, Appl	C 329	85	5.1	7194	4	US-09-601-326-76	Sequence 76, Appl
257	86.5	5.2	2466	4	US-09-475-515-49	Sequence 49, Appl	C 330	85	5.1	7661	4	US-09-902-540-912	Sequence 912, App
258	86.5	5.2	2517	4	US-09-476-242-16	Sequence 16, Appl	C 331	85	5.1	12588	2	US-08-387-942C-1	Sequence 1, Appl
259	86.5	5.2	2517	4	US-09-476-242-17	Sequence 17, Appl	C 332	85	5.1	12685	3	US-09-479-467A-3	Sequence 3, Appl
260	86.5	5.2	2523	4	US-09-476-242-15	Sequence 15, Appl	C 333	85	5.1	15378	3	US-08-785-420-1	Sequence 1, Appl
261	86.5	5.2	2529	4	US-09-476-242-14	Sequence 14, Appl	C 334	85	5.1	15420	4	US-09-601-326-54	Sequence 54, Appl
262	86.5	5.2	2541	4	US-09-476-242-9	Sequence 9, Appl	C 335	85	5.1	15420	4	US-09-902-540-1207	Sequence 1207, Ap
263	86.5	5.2	2541	4	US-09-476-242-10	Sequence 10, Appl	C 336	85	5.1	28804	2	US-08-582-874-1	Sequence 1, Appl
264	86.5	5.2	2541	4	US-09-476-242-11	Sequence 11, Appl	C 337	85	5.1	28804	3	US-09-096-942-2	Sequence 2, Appl
265	86.5	5.2	2547	4	US-09-475-515-48	Sequence 48, Appl	C 338	85	5.1	28804	3	US-09-096-867-2	Sequence 2, Appl
266	86.5	5.2	2640	4	US-09-962-357-1	Sequence 1, Appl	C 339	85	5.1	43507	4	US-09-949-016-13297	Sequence 13297, A
267	86.5	5.2	3136	4	US-09-949-016-2550	Sequence 2550, Ap	C 340	85	5.1	49225	4	US-09-902-540-1269	Sequence 1269, Ap
268	86.5	5.2	3136	4	US-09-949-016-2659	Sequence 2659, Ap	C 341	85	5.1	50453	4	US-09-949-016-16642	Sequence 16642, A
269	86.5	5.2	4608	4	US-09-475-515-76	Sequence 76, Appl	C 342	85	5.1	51242	4	US-09-949-016-12486	Sequence 12486, A
270	86.5	5.2	4689	4	US-09-475-515-74	Sequence 74, Appl	C 343	84.5	5.1	601	4	US-09-949-016-61087	Sequence 61087, A
271	86.5	5.2	7541	4	US-09-637-048C-4	Sequence 4, Appl	C 344	84.5	5.1	1016	4	US-09-220-132-17	Sequence 17, Appl
272	86.5	5.2	7541	4	US-10-435-835-4	Sequence 4, Appl	C 345	84.5	5.1	1017	4	US-09-949-016-4435	Sequence 4435, Ap
273	86.5	5.2	9700	4	US-09-698-295-9	Sequence 9, Appl	C 346	84.5	5.1	2158	4	US-09-949-016-3018	Sequence 3018, Ap
274	86.5	5.2	9865	4	US-09-698-295-2	Sequence 2, Appl	C 347	84.5	5.1	2158	4	US-09-949-016-3026	Sequence 3026, Ap
275	86.5	5.2	13068	4	US-09-902-540-1123	Sequence 1123, Ap	C 348	84.5	5.1	3033	3	US-08-836-325-1	Sequence 1, Appl
276	86.5	5.2	17859	4	US-09-949-016-12334	Sequence 12334, A	C 349	84.5	5.1	3033	4	US-09-457-571-1	Sequence 1, Appl
277	86.5	5.2	57859	4	US-09-949-016-14657	Sequence 14657, A	C 350	84.5	5.1	3243	4	US-09-543-681A-1875	Sequence 1875, Ap
278	86.5	5.2	57859	4	US-09-949-016-14658	Sequence 14658, A	C 351	84.5	5.1	3486	4	US-09-614-221A-292	Sequence 292, App
279	86	5.2	564	4	US-09-583-110-2585	Sequence 2585, Ap	C 352	84.5	5.1	5697	3	US-08-814-052-11	Sequence 11, Appl
280	86	5.2	813	4	US-09-248-796A-372	Sequence 372, App	C 353	84.5	5.1	5697	3	US-08-812-829-11	Sequence 11, Appl
281	86	5.2	813	4	US-09-949-016-2247	Sequence 2247, Ap	C 354	84.5	5.1	6002	4	US-09-949-016-13696	Sequence 13696, A
282	86	5.2	1150	4	US-09-771-317-96	Sequence 96, Appl	C 355	84.5	5.1	6452	3	US-08-836-325-9	Sequence 9, Appl
283	86	5.2	1150	4	US-10-059-579A-96	Sequence 96, Appl	C 356	84.5	5.1	6452	4	US-09-457-571-9	Sequence 9, Appl
284	86	5.2	1797	3	US-09-377-155-12	Sequence 12, Appl	C 357	84.5	5.1	10521	4	US-09-949-016-13516	Sequence 13516, A
285	86	5.2	1797	3	US-09-669-974-12	Sequence 12, Appl	C 358	84.5	5.1	51723	4	US-09-949-016-12152	Sequence 12152, A
286	86	5.2	1797	4	US-09-797-862-12	Sequence 12, Appl	C 359	84.5	5.1	51723	4	US-09-949-016-16991	Sequence 16991, A
287	86	5.2	3385	3	US-08-666-221B-9	Sequence 9, Appl	C 360	84.5	5.1	276237	4	US-09-949-016-17504	Sequence 17504, A
288	86	5.2	5774	4	US-09-949-016-13989	Sequence 13989, A	C 361	84.5	5.1	421491	4	US-09-949-016-12805	Sequence 12805, A
289	86	5.2	16720	4	US-09-902-540-1168	Sequence 1168, Ap	C 362	84.5	5.1	421494	4	US-09-949-016-14060	Sequence 14060, A
290	86	5.2	33529	3	US-09-144-085-3	Sequence 3, Appl	C 363	84	5.1	993	4	US-09-252-991A-10494	Sequence 10494, A
291	86	5.2	34094	4	US-09-292-034-1	Sequence 1, Appl	C 364	84	5.1	1125	2	US-08-997-080-153	Sequence 153, App
292	86	5.2	53500	4	US-09-266-965-76	Sequence 76, Appl	C 365	84	5.1	1125	2	US-08-997-362-153	Sequence 153, App
293	86	5.2	142783	4	US-09-949-016-15127	Sequence 15127, A	C 366	84	5.1	1125	3	US-08-095-855-153	Sequence 153, App
294	86	5.2	176006	4	US-09-949-016-16804	Sequence 16804, A	C 367	84	5.1	1125	3	US-09-324-542-153	Sequence 153, App
295	86	5.2	253375	4	US-09-949-016-12849	Sequence 12849, A	C 368	84	5.1	1125	3	US-09-205-426-153	Sequence 153, App
296	86	5.2	254405	4	US-09-949-016-14381	Sequence 14381, A	C 369	84	5.1	2007	3	US-09-052-089A-7	Sequence 7, Appl
297	85.5	5.2	985	3	US-09-160-246-9	Sequence 9, Appl	C 370	84	5.1	2007	4	US-09-949-016-793	Sequence 793, App
298	85.5	5.2	985	3	US-09-160-246-13	Sequence 13, Appl	C 371	84	5.1	2403	1	US-09-471-013-30	Sequence 30, Appl
299	85.5	5.2	1173	4	US-09-826-509-426	Sequence 426, App	C 372	84	5.1	2403	2	US-08-471-044-30	Sequence 30, Appl
300	85.5	5.2	1320	3	US-09-221-654-1	Sequence 1, Appl	C 373	84	5.1	2403	2	US-08-463-483A-30	Sequence 30, Appl
301	85.5	5.2	1320	3	US-08-989-358A-1	Sequence 1, Appl	C 374	84	5.1	2403	2	US-08-471-046A-30	Sequence 30, Appl
302	85.5	5.2	1359	4	US-09-010-147B-21	Sequence 21, Appl	C 375	84	5.1	2403	2	US-08-470-566B-30	Sequence 30, Appl
303	85.5	5.2	1401	4	US-09-253-991A-10908	Sequence 10908, A	C 376	84	5.1	2403	2	US-08-838-219B-7	Sequence 7, Appl
304	85.5	5.2	1440	4	US-09-253-991A-11041	Sequence 11041, A	C 377	84	5.1	2403	2	US-08-469-334-30	Sequence 30, Appl
305	85.5	5.2	1593	3	US-08-993-359-23	Sequence 23, Appl	C 378	84	5.1	2403	3	US-09-300-529-30	Sequence 30, Appl
306	85.5	5.2	1593	4	US-09-482-558A-23	Sequence 23, Appl	C 379	84	5.1	2403	3	US-09-233-336A-7	Sequence 7, Appl
307	85.5	5.2	1690	2	US-08-461-812-3	Sequence 3, Appl	C 380	84	5.1	2403	3	US-09-233-752A-7	Sequence 7, Appl
308	85.5	5.2	1690	4	US-09-371-705-3	Sequence 3, Appl	C 381	84	5.1	2403	3	US-09-402-036-7	Sequence 7, Appl
309	85.5	5.2	2346	4	US-09-949-016-1088	Sequence 1088, Ap	C 382	84	5.1	2471	4	US-09-904-226-7	Sequence 7, Appl
310	85.5	5.2	2635	4	US-09-016-434-1258	Sequence 1258, Ap	C 383	84	5.1	2471	4	US-08-806-536A-16	Sequence 16, Appl
311	85.5	5.2	4227	4	US-09-902-540-8919	Sequence 8919, Ap	C 384	84	5.1	2635	4	US-09-620-312D-1070	Sequence 1070, Ap
312	85.5	5.2	5043	4	US-09-902-540-574	Sequence 574, App	C 385	84	5.1	3250	1	US-07-718-575-9	Sequence 9, Appl
313	85.5	5.2	6060	4	US-08-956-171E-534	Sequence 534, App	C 386	84	5.1	3250	1	US-08-481-206-9	Sequence 9, Appl
314	85.5	5.2	6060	4	US-08-781-986A-534	Sequence 534, App	C 387	84	5.1	3250	2	US-08-486-269A-9	Sequence 9, Appl
315	85.5	5.2	9367	4	US-09-902-540-951	Sequence 951, App	C 388	84	5.1	4386	3	US-09-300-008B-1	Sequence 1, Appl
316	85.5	5.2	16011	4	US-09-600-319-3	Sequence 3, Appl	C 389	84	5.1	5163	3	US-08-700-651-1	Sequence 1, Appl
317	85.5	5.2	30350	4	US-10-118-328-3	Sequence 3, Appl	C 390	84	5.1	5163	3	US-08-928-361B-4	Sequence 4, Appl
318	85	5.1	804	4	US-09-902-540-5636	Sequence 5636, Ap	C 391	84	5.1	5163	3	US-09-588-995A-4	Sequence 4, Appl
319	85	5.1	957	4	US-09-902-540-2935	Sequence 2935, Ap	C 392	84	5.1	5318	3	US-08-700-651-2	Sequence 2, Appl
320	85	5.1	1176	2	US-08-387-942C-17	Sequence 17, Appl	C 393	84	5.1	5318	3	US-08-928-361B-3	Sequence 3, Appl
321	85	5.1	1251	4	US-09-614-912-81	Sequence 81, Appl	C 394	84	5.1	5318	3	US-09-588-995A-3	Sequence 3, Appl
322	85	5.1	1371	4	US-09-350-756-3	Sequence 3, Appl	C 395	84	5.1	5511	3	US-08-928-361B-2	Sequence 2, Appl
323	85	5.1	1636	4	US-09-614-912-69	Sequence 69, Appl	C 396	84	5.1	5511	4	US-09-588-995A-2	Sequence 2, Appl

406	84	5.1	5679	3	US-08-814-052-9	Sequence 9, Appli	479	83	5.0	6885	4	US-09-854-856-49	Sequence 49, Appli
407	84	5.1	5679	3	US-08-812-829-9	Sequence 9, Appli	480	83	5.0	6969	4	US-09-854-856-33	Sequence 33, Appli
408	84	5.1	7334	3	US-08-928-361B-1	Sequence 1, Appli	481	83	5.0	7065	4	US-09-854-856-17	Sequence 17, Appli
409	84	5.1	7334	4	US-09-588-995A-1	Sequence 1, Appli	482	83	5.0	7149	4	US-09-854-856-1	Sequence 1, Appli
410	84	5.1	13926	3	US-08-961-527-5	Sequence 5, Appli	c 483	83	5.0	32207	2	US-08-770-379-20	Sequence 20, Appli
411	84	5.1	20870	4	US-09-949-016-16017	Sequence 16017, A	c 484	83	5.0	32207	3	US-08-757-669A-20	Sequence 20, Appli
412	84	5.1	21511	4	US-09-902-540-1201	Sequence 1201, Ap	c 485	83	5.0	32207	3	US-09-230-371A-20	Sequence 20, Appli
413	84	5.1	99960	4	US-09-762-311-2	Sequence 2, Appli	c 486	83	5.0	40897	4	US-09-949-016-13910	Sequence 13910, A
c 414	83.5	5.0	429	4	US-09-252-991A-11731	Sequence 11731, A	c 487	83	5.0	40897	4	US-09-949-016-13911	Sequence 13911, A
c 415	83.5	5.0	840	4	US-09-902-340-56	Sequence 36, Appli	c 488	83	5.0	40897	4	US-09-949-016-13912	Sequence 13912, A
416	83.5	5.0	939	4	US-09-248-796A-6040	Sequence 6040, Ap	c 489	83	5.0	40897	4	US-09-949-016-13913	Sequence 13913, A
417	83.5	5.0	1107	2	US-08-991-300-1	Sequence 1, Appli	c 490	83	5.0	40897	4	Sequence 14409, A	Sequence 14409, A
418	83.5	5.0	1344	4	US-09-252-991A-11510	Sequence 11510, A	c 491	83	5.0	40897	4	Sequence 14410, A	Sequence 14410, A
c 419	83.5	5.0	1459	3	US-09-377-557-13	Sequence 13, Appli	c 492	83	5.0	40897	4	Sequence 14411, A	Sequence 14411, A
c 420	83.5	5.0	1620	4	US-09-252-991A-499	Sequence 499, App	c 493	83	5.0	40897	4	Sequence 14412, A	Sequence 14412, A
c 421	83.5	5.0	1995	4	US-09-252-991A-11521	Sequence 11521, A	c 494	83	5.0	72704	4	US-09-902-540-1273	Sequence 1273, Ap
422	83.5	5.0	2136	4	US-09-252-991A-11628	Sequence 11628, A	c 495	83	5.0	194889	4	US-09-949-016-15654	Sequence 15654, A
423	83.5	5.0	2353	4	US-09-369-247-12	Sequence 12, Appli	c 496	83	5.0	767677	4	US-09-949-016-12147	Sequence 12147, A
424	83.5	5.0	2945	4	US-09-714-767A-3	Sequence 3, Appli	c 497	83	5.0	767677	4	US-09-949-016-17361	Sequence 17361, A
425	83.5	5.0	2951	1	US-08-413-118-104	Sequence 104, App	c 498	83	5.0	1830121	4	US-09-557-884-1	Sequence 1, Appli
426	83.5	5.0	2951	3	US-08-473-446-104	Sequence 104, App	c 499	83	5.0	1830121	4	US-09-643-990A-1	Sequence 1, Appli
427	83.5	5.0	3000	1	US-08-220-151-1	Sequence 1, Appli	500	82.5	5.0	660	3	US-09-134-001C-2814	Sequence 2814, Ap
428	83.5	5.0	3000	1	US-08-413-118-1	Sequence 1, Appli	501	82.5	5.0	669	3	US-09-221-017B-288	Sequence 288, App
429	83.5	5.0	3000	3	US-08-473-446-1	Sequence 1, Appli	502	82.5	5.0	1119	3	US-07-757-022B-63	Sequence 63, Appli
c 430	83.5	5.0	3177	4	US-09-252-991A-521	Sequence 521, App	503	82.5	5.0	1269	3	US-07-757-022B-67	Sequence 67, Appli
c 431	83.5	5.0	3211	2	US-08-574-959A-8	Sequence 8, Appli	504	82.5	5.0	1269	3	US-07-757-022B-65	Sequence 65, Appli
c 432	83.5	5.0	3211	2	US-09-357-014-8	Sequence 8, Appli	505	82.5	5.0	1392	3	US-07-757-022B-53	Sequence 53, Appli
c 433	83.5	5.0	3901	2	US-08-574-959A-6	Sequence 6, Appli	c 506	82.5	5.0	1647	4	US-09-540-236-469	Sequence 469, App
c 434	83.5	5.0	3901	3	US-09-357-014-6	Sequence 6, Appli	507	82.5	5.0	1776	4	US-09-270-767-1058	Sequence 1058, Ap
c 435	83.5	5.0	7478	4	US-09-618-425-10	Sequence 10, Appli	508	82.5	5.0	1776	4	US-09-270-767-16340	Sequence 16340, A
436	83.5	5.0	7498	2	US-08-816-693A-1	Sequence 1, Appli	c 509	82.5	5.0	1842	4	US-09-016-434-12336	Sequence 12336, Ap
437	83.5	5.0	7498	3	US-08-895-291-1	Sequence 1, Appli	510	82.5	5.0	2298	4	US-09-252-991A-13540	Sequence 13540, A
438	83.5	5.0	7498	3	US-09-456-672-1	Sequence 1, Appli	511	82.5	5.0	2373	4	US-09-949-016-1146	Sequence 1146, Ap
c 439	83.5	5.0	13926	3	US-08-961-527-5	Sequence 5, Appli	512	82.5	5.0	2373	4	US-09-949-016-2298	Sequence 2298, Ap
440	83.5	5.0	26659	4	US-09-902-540-1237	Sequence 1237, Ap	513	82.5	5.0	2373	4	US-09-949-016-2299	Sequence 2299, Ap
441	83.5	5.0	65848	4	US-09-949-016-13285	Sequence 13285, A	c 514	82.5	5.0	2412	4	US-09-252-991A-13908	Sequence 13908, A
442	83	5.0	601	4	US-09-949-016-66454	Sequence 66454, A	515	82.5	5.0	6022	4	US-08-956-171B-92	Sequence 92, Appli
443	83	5.0	615	4	US-09-248-796A-7881	Sequence 7881, Ap	516	82.5	5.0	6022	4	US-08-781-986A-92	Sequence 92, Appli
444	83	5.0	630	4	US-09-270-767-1924	Sequence 1924, Ap	517	82.5	5.0	6373	4	US-09-949-016-12830	Sequence 12830, A
445	83	5.0	630	4	US-09-270-767-17206	Sequence 17206, A	518	82.5	5.0	6373	4	US-09-949-016-12888	Sequence 12888, A
446	83	5.0	966	4	US-09-252-991A-11896	Sequence 11896, A	519	82.5	5.0	6374	4	US-09-949-016-12888	Sequence 12888, A
447	83	5.0	1056	4	US-09-248-796A-9572	Sequence 9572, Ap	520	82.5	5.0	6374	4	US-09-949-016-14041	Sequence 14041, A
448	83	5.0	1084	4	US-09-949-016-2175	Sequence 2175, Ap	521	82.5	5.0	9461	3	US-09-221-017B-513	Sequence 513, App
449	83	5.0	1084	4	US-09-949-016-2176	Sequence 2176, Ap	522	82.5	5.0	23847	4	US-09-902-540-1177	Sequence 1177, Ap
c 450	83	5.0	1225	4	US-09-976-594-416	Sequence 416, App	c 523	82.5	5.0	24333	4	US-09-639-207-9	Sequence 9, Appli
c 451	83	5.0	1350	3	US-09-149-476-248	Sequence 248, App	524	82.5	5.0	49377	1	US-08-764-233A-1	Sequence 1, Appli
c 452	83	5.0	1779	3	US-09-377-155-16	Sequence 16, Appli	c 525	82.5	5.0	58909	4	US-09-596-002-30	Sequence 30, Appli
c 453	83	5.0	1779	3	US-09-669-974-16	Sequence 16, Appli	c 526	82.5	5.0	194937	4	US-09-949-016-17032	Sequence 17032, A
c 454	83	5.0	1779	4	US-09-797-862-16	Sequence 16, Appli	c 527	82.5	5.0	194937	4	US-09-949-016-17033	Sequence 17033, A
455	83	5.0	2241	2	US-08-838-219B-20	Sequence 20, Appli	528	82	4.9	423	1	US-08-470-179-160	Sequence 160, App
456	83	5.0	2241	3	US-09-233-336A-20	Sequence 20, Appli	c 529	82	4.9	855	4	US-09-252-991A-10673	Sequence 10673, A
457	83	5.0	2241	3	US-09-233-336A-20	Sequence 20, Appli	530	82	4.9	875	4	US-09-443-067-27	Sequence 27, Appli
458	83	5.0	2241	3	US-09-402-036-20	Sequence 20, Appli	531	82	4.9	1208	4	US-09-602-787A-409	Sequence 409, App
459	83	5.0	2241	3	US-09-904-226-20	Sequence 20, Appli	532	82	4.9	1280	4	US-09-602-787A-407	Sequence 407, App
460	83	5.0	2370	2	US-08-838-219B-19	Sequence 19, Appli	533	82	4.9	1371	4	US-09-252-991A-9440	Sequence 9440, Ap
461	83	5.0	2370	3	US-09-233-336A-19	Sequence 19, Appli	c 534	82	4.9	1383	4	US-09-489-039A-3928	Sequence 3928, Ap
462	83	5.0	2370	3	US-09-233-336A-19	Sequence 19, Appli	535	82	4.9	1521	2	US-09-004-502-2	Sequence 2, Appli
463	83	5.0	2370	3	US-09-402-036-19	Sequence 19, Appli	536	82	4.9	1521	2	US-09-360-125-2	Sequence 2, Appli
464	83	5.0	2370	3	US-09-904-226-19	Sequence 19, Appli	537	82	4.9	1527	4	US-09-248-796A-4088	Sequence 4088, Ap
465	83	5.0	2905	4	US-09-949-016-410	Sequence 410, App	538	82	4.9	1575	4	US-09-248-796A-4898	Sequence 4898, Ap
466	83	5.0	2906	4	US-09-949-016-5249	Sequence 5249, Ap	539	82	4.9	1590	4	US-09-248-796A-6083	Sequence 6083, Ap
467	83	5.0	3252	4	US-09-614-221A-303	Sequence 303, App	540	82	4.9	1617	4	US-09-248-796A-6739	Sequence 6739, Ap
468	83	5.0	3489	2	US-08-728-323A-1	Sequence 1, Appli	541	82	4.9	1662	1	US-08-651-572-1	Sequence 1, Appli
469	83	5.0	3489	3	US-09-238-568-1	Sequence 1, Appli	542	82	4.9	1662	3	US-09-066-544-1	Sequence 1, Appli
470	83	5.0	3489	4	US-09-410-399-1	Sequence 1, Appli	543	82	4.9	1662	3	US-08-951-086-1	Sequence 1, Appli
471	83	5.0	3489	4	US-09-894-273-1	Sequence 1, Appli	544	82	4.9	1662	3	US-09-430-669-1	Sequence 1, Appli
c 472	83	5.0	3924	1	US-08-395-246C-1	Sequence 1, Appli	545	82	4.9	1867	4	US-09-949-016-4889	Sequence 4889, Ap
c 473	83	5.0	4063	4	US-09-902-540-595	Sequence 595, App	546	82	4.9	1867	4	US-09-949-016-4890	Sequence 4890, Ap
474	83	5.0	4545	3	US-09-221-017B-1011	Sequence 1011, Ap	c 547	82	4.9	2016	4	US-09-949-016-5734	Sequence 5734, Ap
475	83	5.0	6474	4	US-09-854-856-51	Sequence 51, Appli	c 548	82	4.9	2065	2	US-08-968-751-1	Sequence 1, Appli
476	83	5.0	6558	4	US-09-854-856-35	Sequence 35, Appli	549	82	4.9	3081	4	US-09-248-796A-2025	Sequence 2025, Ap
477	83	5.0	6654	4	US-09-854-856-19	Sequence 19, Appli	550	82	4.9	4014	4	US-09-949-016-4648	Sequence 4648, Ap
478	83	5.0	6738	4	US-09-854-856-3	Sequence 3, Appli	551	82	4.9	4014	4	US-09-949-016-4649	Sequence 4649, Ap

C 552	82	4.9	5449	4	US-09-949-016-2138	Sequence 2138, Ap	625	81	4.9	7680	4	US-09-953-318-3	Sequence 3, Appli
553	82	4.9	15163	4	US-09-949-016-13246	Sequence 13246, A	626	81	4.9	7718	4	US-09-976-594-244	Sequence 2144, App
554	82	4.9	40586	4	US-09-949-016-16965	Sequence 16965, A	C 627	81	4.9	14367	4	US-09-902-540-1113	Sequence 1113, App
C 555	82	4.9	44821	4	US-09-949-016-13764	Sequence 13764, A	628	81	4.9	18853	4	US-09-820-005-3	Sequence 3, Appli
556	81.5	4.9	767	4	US-09-270-767-2226	Sequence 2226, Ap	629	81	4.9	18853	4	US-10-109-856-3	Sequence 3, Appli
557	81.5	4.9	767	4	US-09-270-767-17508	Sequence 17508, A	630	81	4.9	80161	3	US-09-036-987A-1	Sequence 1, Appli
C 558	81.5	4.9	879	5	PCT-US96-03916-16	Sequence 16, Appl	631	81	4.9	80161	3	US-09-370-700-1	Sequence 1, Appli
559	81.5	4.9	1069	4	US-09-949-016-2654	Sequence 2654, Ap	632	81	4.9	80161	4	US-09-603-207-1	Sequence 1, Appli
560	81.5	4.9	1069	4	US-09-949-016-2655	Sequence 2655, Ap	C 633	81	4.9	110848	4	US-09-596-002-39	Sequence 39, Appl
561	81.5	4.9	1421	3	US-09-188-930-70	Sequence 70, Appl	634	81	4.9	110585	4	US-09-949-016-13427	Sequence 13427, A
562	81.5	4.9	1421	4	US-09-312-283C-18	Sequence 18, Appl	635	81	4.9	119211	4	US-09-596-002-40	Sequence 40, Appl
563	81.5	4.9	1569	4	US-09-248-796A-70	Sequence 70, Appl	636	81	4.9	271134	4	US-09-949-016-12705	Sequence 12705, A
564	81.5	4.9	1677	4	US-09-252-931A-9544	Sequence 9544, Ap	C 637	81	4.9	305491	4	US-09-949-016-17550	Sequence 17550, A
565	81.5	4.9	1758	2	US-08-630-822A-69	Sequence 69, Appl	638	80.5	4.9	771	4	US-09-902-540-5814	Sequence 5814, Ap
566	81.5	4.9	1758	2	US-09-005-069-69	Sequence 69, Appl	639	80.5	4.9	837	3	US-08-339-214-23	Sequence 23, Appl
567	81.5	4.9	1758	3	US-09-171-156A-29	Sequence 29, Appl	640	80.5	4.9	927	3	US-08-339-214-36	Sequence 36, Appl
568	81.5	4.9	1758	4	US-09-004-730A-29	Sequence 29, Appl	641	80.5	4.9	927	3	US-08-339-214-103	Sequence 103, App
569	81.5	4.9	1758	4	US-08-981-799A-29	Sequence 29, Appl	642	80.5	4.9	940	3	US-09-479-524-2	Sequence 2, Appli
570	81.5	4.9	1788	4	US-09-614-912-65	Sequence 65, Appl	C 643	80.5	4.9	940	3	US-09-479-524-8	Sequence 8, Appli
571	81.5	4.9	1795	4	US-09-197-970B-6	Sequence 6, Appli	C 644	80.5	4.9	1071	4	US-09-902-540-4828	Sequence 4828, Ap
572	81.5	4.9	2309	3	US-09-091-725-9	Sequence 9, Appli	645	80.5	4.9	1099	4	US-09-949-016-1829	Sequence 1829, Ap
C 573	81.5	4.9	2586	4	US-10-101-464A-883	Sequence 883, App	C 646	80.5	4.9	1119	4	US-09-252-991A-9448	Sequence 9448, Ap
574	81.5	4.9	2886	4	US-09-248-796A-5312	Sequence 5312, Ap	647	80.5	4.9	1140	3	US-09-462-270-1	Sequence 1, Appli
575	81.5	4.9	2943	1	US-08-042-747A-7	Sequence 7, Appli	648	80.5	4.9	1227	3	US-09-074-912-3	Sequence 3, Appli
576	81.5	4.9	4338	1	US-08-015-986A-1	Sequence 1, Appli	649	80.5	4.9	1227	3	US-09-280-136-3	Sequence 3, Appli
C 577	81.5	4.9	4338	2	US-08-446-363-1	Sequence 1, Appli	650	80.5	4.9	1239	4	US-09-252-991A-9383	Sequence 9383, Ap
578	81.5	4.9	4760	3	US-09-221-017B-875	Sequence 875, App	C 651	80.5	4.9	1293	4	US-09-902-540-5999	Sequence 5999, Ap
579	81.5	4.9	6301	4	US-09-902-540-842	Sequence 842, App	C 652	80.5	4.9	1356	4	US-09-328-352-4027	Sequence 4027, Ap
580	81.5	4.9	8697	3	US-08-961-527-123	Sequence 123, App	653	80.5	4.9	1417	4	US-09-949-016-4521	Sequence 4521, Ap
581	81.5	4.9	13473	5	PCT-US96-03916-1	Sequence 1, Appli	654	80.5	4.9	1421	3	US-09-188-930-254	Sequence 254, App
582	81.5	4.9	18912	5	PCT-US96-03916-59	Sequence 59, Appl	655	80.5	4.9	1421	4	US-09-312-283C-254	Sequence 254, App
583	81.5	4.9	20250	4	US-09-902-540-1213	Sequence 1213, Ap	656	80.5	4.9	1476	4	US-09-976-594-147	Sequence 147, App
584	81.5	4.9	23598	3	US-09-341-587-6	Sequence 6, Appli	C 657	80.5	4.9	1505	4	US-09-620-312D-544	Sequence 544, App
585	81.5	4.9	33748	4	US-09-949-016-14283	Sequence 14283, A	658	80.5	4.9	1537	4	US-09-902-540-222	Sequence 222, App
586	81	4.9	621	1	US-08-028-463-7	Sequence 7, Appli	659	80.5	4.9	1707	3	US-08-339-214-31	Sequence 31, Appl
587	81	4.9	621	1	US-08-461-836-7	Sequence 7, Appli	C 660	80.5	4.9	1716	3	US-09-040-681A-3	Sequence 3, Appli
C 588	81	4.9	801	4	US-09-489-039A-1028	Sequence 1028, Ap	C 661	80.5	4.9	1716	3	US-09-457-897-3	Sequence 3, Appli
589	81	4.9	1023	4	US-09-492-709A-102	Sequence 102, App	662	80.5	4.9	1783	4	US-09-949-016-1954	Sequence 1954, Ap
590	81	4.9	1291	2	US-08-887-365-35	Sequence 35, Appl	672	80.5	4.9	1875	3	US-09-877-730-23	Sequence 23, Appl
591	81	4.9	1389	4	US-09-602-787A-77	Sequence 77, Appl	673	80.5	4.9	2139	3	US-09-877-730-21	Sequence 21, Appl
592	81	4.9	1425	4	US-09-578-063-2	Sequence 2, Appli	674	80.5	4.9	2382	3	US-09-877-730-27	Sequence 27, Appl
593	81	4.9	1555	3	US-08-669-408B-9	Sequence 9, Appli	C 675	80.5	4.9	2458	3	US-09-071-101-5	Sequence 5, Appli
594	81	4.9	1596	4	US-09-248-796A-1457	Sequence 1457, Ap	C 676	80.5	4.9	2458	3	US-09-369-618-6	Sequence 6, Appli
595	81	4.9	1656	4	US-09-578-063-1	Sequence 1, Appli	C 677	80.5	4.9	2458	3	US-09-369-618-6	Sequence 6, Appli
596	81	4.9	1850	4	US-09-848-726-1	Sequence 1, Appli	678	80.5	4.9	2976	3	US-09-877-730-11	Sequence 11, Appl
597	81	4.9	1875	3	US-09-039-609-1	Sequence 1, Appli	679	80.5	4.9	3190	4	US-09-949-016-5181	Sequence 5181, Ap
598	81	4.9	2001	4	US-09-248-796A-4560	Sequence 4560, Ap	680	80.5	4.9	3210	3	US-09-877-730-1	Sequence 1, Appli
C 599	81	4.9	2040	3	US-08-604-789B-1	Sequence 1, Appli	681	80.5	4.9	3219	3	US-09-877-730-17	Sequence 17, Appl
C 600	81	4.9	2040	3	US-08-604-789B-12	Sequence 12, Appl	682	80.5	4.9	3453	3	US-09-877-730-7	Sequence 7, Appli
C 601	81	4.9	2040	3	US-09-312-721A-1	Sequence 1, Appli	683	80.5	4.9	3604	4	US-09-799-451-287	Sequence 287, App
C 602	81	4.9	2040	3	US-09-312-721A-12	Sequence 12, Appl	684	80.5	4.9	3622	4	US-09-949-016-2172	Sequence 2172, Ap
C 603	81	4.9	2040	4	US-09-733-300-1	Sequence 1, Appli	685	80.5	4.9	3627	2	US-08-232-087A-1	Sequence 1, Appli
C 604	81	4.9	2040	4	US-09-733-300-12	Sequence 12, Appl	686	80.5	4.9	3630	4	US-09-023-655-1028	Sequence 1028, Ap
C 605	81	4.9	2071	4	US-09-949-016-1517	Sequence 1517, Ap	687	80.5	4.9	3630	4	US-09-949-016-177	Sequence 177, App
606	81	4.9	2313	1	US-08-232-538-5	Sequence 5, Appli	688	80.5	4.9	3874	3	US-09-877-730-31	Sequence 31, Appl
607	81	4.9	2313	1	US-09-427-353-1	Sequence 1, Appli	689	80.5	4.9	5220	4	US-09-677-046A-1	Sequence 1, Appli
608	81	4.9	2465	5	PCT-US92-08090-1	Sequence 1, Appli	C 690	80.5	4.9	5682	4	US-10-164-595-1	Sequence 1, Appli
609	81	4.9	2523	3	US-09-051-363-1	Sequence 1, Appli	691	80.5	4.9	6114	4	US-09-914-272A-4	Sequence 4, Appli
C 610	81	4.9	2553	4	US-09-949-016-488	Sequence 488, App	692	80.5	4.9	6114	4	US-10-638-333-4	Sequence 4, Appli
611	81	4.9	2582	4	US-09-270-767-12851	Sequence 12851, A	693	80.5	4.9	6359	4	US-09-475-252-1	Sequence 1, Appli
612	81	4.9	2651	2	US-08-786-164-5	Sequence 5, Appli	694	80.5	4.9	7000	4	US-09-902-540-833	Sequence 833, App
613	81	4.9	2651	4	US-09-953-318-19	Sequence 19, Appl	C 695	80.5	4.9	7948	4	US-09-949-016-14929	Sequence 14929, A
614	81	4.9	2652	4	US-09-248-796A-4828	Sequence 4828, Ap	C 696	80.5	4.9	7960	4	US-09-949-016-14930	Sequence 14930, A
615	81	4.9	2674	4	US-10-066-130-19	Sequence 19, Appl	697	80.5	4.9	9542	3	US-08-968-685A-9	Sequence 9, Appli
616	81	4.9	2771	4	US-10-066-130-18	Sequence 18, Appl	C 698	80.5	4.9	12180	4	US-09-949-016-12527	Sequence 12527, A
C 617	81	4.9	2911	4	US-09-799-451-888	Sequence 888, App	C 699	80.5	4.9	12180	4	US-09-949-016-14323	Sequence 14323, A
618	81	4.9	3498	4	US-09-520-781-3	Sequence 3, Appli	700	80.5	4.9	16924	4	US-09-949-016-13720	Sequence 13720, A
619	81	4.9	4200	1	US-07-841-654B-1	Sequence 1, Appli	C 701	80.5	4.9	21164	4	US-09-949-016-16457	Sequence 16457, A
620	81	4.9	4200	1	US-07-946-234A-1	Sequence 1, Appli	C 702	80.5	4.9	21164	4	US-09-949-016-16331	Sequence 16331, A
621	81	4.9	4200	1	US-08-123-161A-1	Sequence 1, Appli	C 703	80	4.9	40408	4	US-08-225-477B-7	Sequence 7, Appli
622	81	4.9	4200	1	US-08-483-278-1	Sequence 1, Appli	704	80	4.8	156	5	PCT-US95-04153-7	Sequence 7, Appli
623	81	4.9	4200	5	PCT-US93-01560-1	Sequence 1, Appli	705	80	4.8	156	5	PCT-US95-04153-7	Sequence 7, Appli
624	81	4.9	5860	4	US-10-066-130-17	Sequence 17, Appl	706	80	4.8	288	4	US-09-252-991A-11933	Sequence 11933, A
									4.8	597	4	US-09-902-540-8148	Sequence 8148, Ap

707	80	4.8	615	4	US-09-902-540-6862	Sequence 6862, Ap	780	79.5	4.8	3048	1	US-08-332-643-41	Sequence 41, Appl
C 708	80	4.8	618	4	US-09-902-540-58	Sequence 58, Appl	781	79.5	4.8	3048	1	US-08-332-638-47	Sequence 47, Appl
C 709	80	4.8	744	4	US-09-252-991A-15538	Sequence 15538, A	782	79.5	4.8	3452	4	US-09-023-655-1219	Sequence 1219, Ap
C 710	80	4.8	756	4	US-09-248-796A-9113	Sequence 9113, Ap	783	79.5	4.8	3677	4	US-09-949-016-1969	Sequence 1969, Ap
C 711	80	4.8	774	4	US-09-902-540-7907	Sequence 7907, Ap	784	79.5	4.8	3683	3	US-09-844-634-3	Sequence 3, Appli
C 712	80	4.8	807	4	US-09-252-991A-15427	Sequence 15427, A	785	79.5	4.8	3683	3	US-09-968-455-1	Sequence 1, Appli
C 713	80	4.8	975	3	US-09-365-150-4	Sequence 4, Appli	786	79.5	4.8	3683	4	US-09-949-016-148	Sequence 148, App
C 714	80	4.8	1119	4	US-09-248-796A-5793	Sequence 5793, Ap	787	79.5	4.8	3976	4	US-09-799-451-131	Sequence 131, App
C 715	80	4.8	1216	4	US-09-270-767-10155	Sequence 10155, A	788	79.5	4.8	4171	4	US-09-667-422-3	Sequence 3, Appli
C 716	80	4.8	1270	4	US-09-270-767-12871	Sequence 12871, A	789	79.5	4.8	5491	4	US-09-667-422-3	Sequence 3, Appli
C 717	80	4.8	1275	4	US-09-252-991A-15254	Sequence 15254, A	790	79.5	4.8	5597	4	US-09-262-537-5	Sequence 5, Appli
C 718	80	4.8	1315	4	US-09-902-540-215	Sequence 215, App	791	79.5	4.8	5598	4	US-09-262-537-33	Sequence 33, Appli
C 719	80	4.8	1359	4	US-09-252-991A-15302	Sequence 15302, A	792	79.5	4.8	5617	4	US-09-262-537-3	Sequence 83, Appli
C 720	80	4.8	1419	4	US-09-902-540-4922	Sequence 4922, Ap	793	79.5	4.8	28473	3	US-08-961-527-83	Sequence 83, Appl
C 721	80	4.8	1645	4	US-09-949-016-4275	Sequence 4275, A	794	79.5	4.8	31300	4	US-09-949-016-16967	Sequence 16967, A
C 722	80	4.8	2093	1	US-08-287-001A-1	Sequence 1, Appli	795	79.5	4.8	38239	4	US-09-949-016-12348	Sequence 12348, A
C 723	80	4.8	2093	5	FCT-US95-09941-1	Sequence 1, Appli	796	79.5	4.8	38252	4	US-09-949-016-13570	Sequence 13570, A
C 724	80	4.8	2472	4	US-09-248-796A-2596	Sequence 2596, Ap	797	79.5	4.8	38252	4	US-09-949-016-13570	Sequence 13570, A
C 725	80	4.8	2538	4	US-09-248-796A-3859	Sequence 3859, Ap	798	79.5	4.8	121427	4	US-09-949-016-11950	Sequence 11950, A
C 726	80	4.8	2839	5	FCT-US94-07297-38	Sequence 38, Appl	799	79.5	4.8	121433	4	US-09-949-016-13230	Sequence 13230, A
C 727	80	4.8	2893	4	US-09-902-540-9663	Sequence 9663, Ap	800	79.5	4.8	157866	4	US-09-949-016-12982	Sequence 12982, A
C 728	80	4.8	4359	4	US-08-943-144-3	Sequence 3, Appli	801	79.5	4.8	157866	4	US-09-949-016-12983	Sequence 12983, A
C 729	80	4.8	5720	3	US-09-442-100-1	Sequence 1, Appli	802	79.5	4.8	1230025	4	US-09-198-452A-1	Sequence 1, Appli
C 730	80	4.8	5720	4	US-08-939-106-1	Sequence 1, Appli	803	79.5	4.8	1230230	4	US-09-438-185A-1	Sequence 1, Appli
C 731	80	4.8	5720	4	US-09-442-102-1	Sequence 1, Appli	804	79.5	4.8	1664976	4	US-08-916-421B-1	Sequence 1, Appli
C 732	80	4.8	6269	4	US-09-902-540-836	Sequence 836, App	805	79.5	4.8	1664976	4	US-08-916-421B-1	Sequence 1, Appli
C 733	80	4.8	7994	4	US-09-902-540-797	Sequence 797, App	806	79.5	4.8	1664976	4	US-09-692-570-1	Sequence 1, Appli
C 734	80	4.8	14555	4	US-09-902-540-1096	Sequence 1096, Ap	807	79.5	4.8	1664976	4	US-09-692-570-1	Sequence 1, Appli
C 735	80	4.8	16283	4	US-09-902-540-1126	Sequence 1126, Ap	808	79.5	4.8	465	4	US-09-377-502-58	Sequence 58, Appl
C 736	80	4.8	28785	4	US-09-902-540-1242	Sequence 1242, Ap	809	79.5	4.8	615	4	US-09-134-000C-149	Sequence 149, App
C 737	80	4.8	36519	3	US-08-923-137-2	Sequence 2, Appli	810	79.5	4.8	714	4	US-09-252-991A-8966	Sequence 8966, Ap
C 738	80	4.8	36800	4	US-08-311-731A-139	Sequence 139, App	811	79.5	4.8	837	4	US-09-252-991A-9123	Sequence 9123, Ap
C 739	80	4.8	42325	4	US-08-311-731A-131	Sequence 131, App	812	79.5	4.8	900	4	US-09-248-796A-2142	Sequence 2142, Ap
C 740	80	4.8	247781	4	US-09-949-016-14193	Sequence 14193, A	822	79.5	4.8	975	4	US-09-498-520A-1	Sequence 1, Appli
C 741	80	4.8	284206	4	US-09-949-016-12731	Sequence 12731, A	823	79.5	4.8	975	4	US-09-583-110-1252	Sequence 1252, Ap
C 742	80	4.8	264304	4	US-09-949-016-13249	Sequence 13249, A	824	79.5	4.8	975	4	US-09-968-129-1	Sequence 1, Appli
C 743	80	4.8	536165	4	US-09-214-808-1	Sequence 1, Appli	825	79.5	4.8	996	4	US-09-107-433-2480	Sequence 2480, Ap
C 744	79.5	4.8	462	4	US-09-252-991A-1309	Sequence 1309, Ap	826	79.5	4.8	1005	4	US-09-107-532A-2682	Sequence 2682, Ap
C 745	79.5	4.8	462	4	US-09-270-767-8870	Sequence 8870, Ap	827	79.5	4.8	1063	4	US-09-949-016-5303	Sequence 5303, Ap
C 746	79.5	4.8	462	4	US-09-270-767-24152	Sequence 24152, A	828	79.5	4.8	1383	4	US-09-813-453B-40	Sequence 40, Appl
C 747	79.5	4.8	601	4	US-09-949-016-22247	Sequence 22247, A	829	79.5	4.8	1446	4	US-09-543-681A-554	Sequence 554, App
C 748	79.5	4.8	601	4	US-09-949-016-51354	Sequence 51354, A	830	79.5	4.8	1510	1	US-08-361-920-26	Sequence 26, Appl
C 749	79.5	4.8	612	4	US-09-270-767-3415	Sequence 3415, A	831	79.5	4.8	1510	1	US-08-479-939-26	Sequence 26, Appl
C 750	79.5	4.8	612	4	US-09-270-767-18697	Sequence 18697, A	832	79.5	4.8	1510	1	US-08-483-432-26	Sequence 26, Appl
C 751	79.5	4.8	768	4	US-09-248-796A-7148	Sequence 7148, Ap	833	79.5	4.8	1675	4	US-09-774-528-343	Sequence 343, App
C 752	79.5	4.8	909	4	US-09-252-991A-2103	Sequence 2103, Ap	834	79.5	4.8	1686	4	US-09-252-991A-7673	Sequence 7673, Ap
C 753	79.5	4.8	959	4	US-09-902-540-102	Sequence 102, App	835	79.5	4.8	1722	4	US-09-902-540-9668	Sequence 9668, Ap
C 754	79.5	4.8	975	4	US-09-489-039A-1422	Sequence 1422, Ap	836	79.5	4.8	1762	4	US-09-489-847-50	Sequence 50, Appl
C 755	79.5	4.8	1002	4	US-09-252-991A-2014	Sequence 2014, Ap	837	79.5	4.8	1917	4	US-09-248-796A-4636	Sequence 4636, Ap
C 756	79.5	4.8	1125	4	US-09-248-796A-3180	Sequence 3180, Ap	847	79.5	4.8	2091	3	US-08-899-437-22	Sequence 22, Appl
C 757	79.5	4.8	1194	4	US-09-248-796A-7496	Sequence 7496, Ap	848	79.5	4.8	2091	3	US-09-126-121-22	Sequence 22, Appl
C 758	79.5	4.8	1505	1	US-07-915-246-1	Sequence 1, Appli	849	79.5	4.8	2196	4	US-10-069-540A-1	Sequence 1, Appli
C 759	79.5	4.8	1641	1	US-08-385-229-1	Sequence 1, Appli	850	79.5	4.8	2313	3	US-08-738-168B-14	Sequence 14, Appl
C 760	79.5	4.8	1641	2	US-08-650-000-1	Sequence 1, Appli	851	79.5	4.8	2352	1	US-08-232-538-17	Sequence 17, Appl
C 761	79.5	4.8	1641	4	US-08-406-824A-1	Sequence 1, Appli	852	79.5	4.8	2352	2	US-08-786-164-17	Sequence 17, Appl
C 762	79.5	4.8	1641	4	US-09-758-124-1	Sequence 1, Appli	853	79.5	4.8	2379	4	US-09-252-991A-9205	Sequence 9205, Ap
C 763	79.5	4.8	1641	6	5395760-1	Patent No. 5395760	854	79.5	4.8	2481	4	US-09-270-767-14710	Sequence 14710, A
C 764	79.5	4.8	1641	6	5395760-1	Patent No. 5395760	855	79.5	4.8	2502	3	US-08-899-437-5	Sequence 5, Appli
C 765	79.5	4.8	1680	4	US-09-543-681A-3069	Sequence 3069, Ap	856	79.5	4.8	2502	3	US-09-126-121-5	Sequence 5, Appli
C 766	79.5	4.8	1803	4	US-08-809-767-13926	Sequence 13926, A	857	79.5	4.8	2689	4	US-09-902-540-2831	Sequence 2831, Ap
C 767	79.5	4.8	1965	2	US-08-809-763-5	Sequence 5, Appli	858	79.5	4.8	3767	4	US-09-823-038A-44	Sequence 44, Appl
C 768	79.5	4.8	1965	3	US-08-956-253-5	Sequence 5, Appli	859	79.5	4.8	3813	4	US-09-902-540-7085	Sequence 7085, Ap
C 769	79.5	4.8	2070	4	US-09-252-991A-16098	Sequence 16098, A	860	79.5	4.8	3813	4	US-09-902-540-634	Sequence 634, App
C 770	79.5	4.8	2212	4	US-09-270-767-14682	Sequence 14682, A	861	79.5	4.8	3919	1	US-08-301-722A-1	Sequence 1, Appli
C 771	79.5	4.8	2224	3	US-08-477-347-2	Sequence 2, Appli	862	79.5	4.8	3926	4	US-09-949-016-1224	Sequence 1224, Ap
C 772	79.5	4.8	2224	3	US-08-476-862-1	Sequence 1, Appli	863	79.5	4.8	3946	4	US-09-949-016-146	Sequence 146, App
C 773	79.5	4.8	2224	4	US-09-800-909-1	Sequence 1, Appli	864	79.5	4.8	3960	4	US-09-902-540-8918	Sequence 8918, Ap
C 774	79.5	4.8	2224	4	US-09-800-908-2	Sequence 2, Appli	865	79.5	4.8	4226	4	US-09-620-312D-480	Sequence 480, App
C 775	79.5	4.8	2388	4	US-09-270-767-12079	Sequence 12079, A	866	79.5	4.8	5183	1	US-08-459-568-3	Sequence 3, Appli
C 776	79.5	4.8	2454	4	US-09-614-221A-393	Sequence 393, App	867	79.5	4.8	5183	2	US-08-399-411-3	Sequence 3, Appli
C 777	79.5	4.8	2905	4	US-09-902-540-473	Sequence 473, App	868	79.5	4.8	5516	4	US-09-949-016-868	Sequence 868, App
C 778	79.5	4.8	3003	1	US-08-434-730-15	Sequence 15, Appl	869	79.5	4.8	5868	3	US-08-516-859A-3	Sequence 3, Appli
C 779	79.5	4.8	3048	1	US-08-188-228-47	Sequence 47, Appl	870	79.5	4.8	5868	3	US-09-586-472-3	Sequence 3, Appli



C 871	79	4.8	5868	3	US-09-528-706-3	Sequence 3, Appli	C 944	78	4.7	1630	4	US-09-949-016-3674	Sequence 3674, Ap
C 872	79	4.8	6002	3	US-09-345-882-4	Sequence 4, Appli	945	78	4.7	1632	1	US-08-324-243-34	Sequence 34, Appl
C 873	79	4.8	6008	4	US-09-949-016-5058	Sequence 5058, Ap	946	78	4.7	1632	1	US-08-532-390-34	Sequence 34, Appl
C 874	79	4.8	6173	4	US-09-949-016-5511	Sequence 5511, Ap	947	78	4.7	1632	3	US-08-717-294-34	Sequence 34, Appl
C 875	79	4.8	6173	4	US-09-949-016-5512	Sequence 5512, Ap	948	78	4.7	1632	5	PCT-US95-11511-34	Sequence 34, Appl
C 876	79	4.8	9367	4	US-09-902-540-951	Sequence 951, App	949	78	4.7	1677	3	US-09-545-814-13	Sequence 13, Appl
C 877	79	4.8	9578	4	US-09-949-016-17106	Sequence 17106, A	950	78	4.7	1677	3	US-09-545-814-13	Sequence 13, Appl
C 878	79	4.8	11907	3	US-08-061-376-4	Sequence 4, Appli	951	78	4.7	1749	3	US-09-545-814-13	Sequence 13, Appl
C 879	79	4.8	14464	4	US-09-902-540-1135	Sequence 1135, Ap	952	78	4.7	1749	3	US-09-545-814-13	Sequence 13, Appl
C 880	79	4.8	14555	4	US-09-902-540-1096	Sequence 1096, Ap	953	78	4.7	1758	4	US-09-545-814-13	Sequence 13, Appl
C 881	79	4.8	19702	3	US-08-961-527-7	Sequence 7, Appli	954	78	4.7	1809	4	US-09-902-540-9019	Sequence 9019, Ap
C 882	79	4.8	23257	4	US-09-949-016-12894	Sequence 12894, A	955	78	4.7	1892	3	US-09-252-991A-13958	Sequence 13958, A
C 883	79	4.8	23260	4	US-09-949-016-14300	Sequence 14300, A	956	78	4.7	1892	3	US-09-232-160-8	Sequence 8, Appli
C 884	79	4.8	36519	3	US-08-923-137-2	Sequence 2, Appli	957	78	4.7	1919	3	US-09-545-814-33	Sequence 31, Appl
C 885	79	4.8	42672	4	US-09-949-016-17253	Sequence 17253, A	958	78	4.7	1919	3	US-09-545-814-33	Sequence 31, Appl
C 886	79	4.8	42672	4	US-09-949-016-17254	Sequence 17254, A	959	78	4.7	2157	4	US-09-252-991A-15294	Sequence 15294, A
C 887	79	4.8	49225	4	US-09-902-540-1269	Sequence 1269, Ap	960	78	4.7	2280	4	US-09-248-796A-5157	Sequence 5157, Ap
C 888	79	4.8	78125	4	US-09-949-016-16006	Sequence 16006, A	961	78	4.7	2361	4	US-09-252-991A-15546	Sequence 15546, Ap
C 889	79	4.8	154746	4	US-09-827-688-8	Sequence 8, Appli	962	78	4.7	2421	4	US-09-565-501A-103	Sequence 103, App
C 890	79	4.8	246240	2	US-08-724-394A-20	Sequence 20, Appl	963	78	4.7	2421	4	US-09-639-206A-103	Sequence 103, App
C 891	79	4.8	246240	2	US-08-724-394A-21	Sequence 21, Appl	964	78	4.7	2421	4	US-09-874-923-103	Sequence 103, App
C 892	79	4.8	246240	2	US-08-724-394A-22	Sequence 22, Appl	965	78	4.7	2481	1	US-08-324-243-35	Sequence 35, Appl
C 893	78.5	4.7	532	4	US-09-270-767-1305	Sequence 1305, Ap	966	78	4.7	2481	3	US-08-532-390-35	Sequence 35, Appl
C 894	78.5	4.7	532	4	US-09-270-767-1305	Sequence 1305, Ap	967	78	4.7	2481	3	US-08-717-294-35	Sequence 35, Appl
C 895	78.5	4.7	966	4	US-09-248-766A-9577	Sequence 9577, Ap	968	78	4.7	2481	5	PCT-US95-11511-35	Sequence 35, Appl
C 896	78.5	4.7	1043	4	US-09-489-039A-2212	Sequence 2212, Ap	969	78	4.7	2571	4	US-09-532-950-4	Sequence 4, Appli
C 897	78.5	4.7	1440	4	US-09-270-767-12289	Sequence 12289, A	970	78	4.7	2571	4	US-09-532-950-4	Sequence 4, Appli
C 898	78.5	4.7	1482	4	US-09-252-991A-9689	Sequence 9689, Ap	971	78	4.7	2610	3	US-09-545-814-1	Sequence 1, Appli
C 899	78.5	4.7	1596	4	US-09-270-767-1002	Sequence 1002, Ap	972	78	4.7	2610	3	US-09-545-814-3	Sequence 3, Appli
C 900	78.5	4.7	1596	4	US-09-270-767-16284	Sequence 16284, A	973	78	4.7	2610	3	US-08-446-794A-3	Sequence 3, Appli
C 901	78.5	4.7	1614	4	US-09-252-991A-9607	Sequence 9607, Ap	974	78	4.7	2610	3	US-09-902-540-587	Sequence 587, App
C 902	78.5	4.7	1623	4	US-09-252-991A-9650	Sequence 9650, Ap	975	78	4.7	2610	3	US-09-602-777A-359	Sequence 359, App
C 903	78.5	4.7	1692	4	US-09-252-991A-978	Sequence 978, App	976	78	4.7	2610	3	US-09-949-016-2026	Sequence 2026, Ap
C 904	78.5	4.7	1764	4	US-09-857-669-5	Sequence 5, Appli	977	78	4.7	4152	3	US-08-826-134-5	Sequence 5, Appli
C 905	78.5	4.7	1770	4	US-09-902-540-7164	Sequence 7164, Ap	978	78	4.7	4792	3	US-09-221-017B-107	Sequence 107, App
C 906	78.5	4.7	1779	4	US-09-302-626B-5	Sequence 5, Appli	979	78	4.7	5280	4	US-09-949-016-5586	Sequence 5586, Ap
C 907	78.5	4.7	1788	1	US-08-225-989-1	Sequence 1, Appli	980	78	4.7	5293	3	US-08-826-134-1	Sequence 1, Appli
C 908	78.5	4.7	1788	1	US-08-570-923-1	Sequence 1, Appli	981	78	4.7	5293	3	US-08-826-134-1	Sequence 1, Appli
C 909	78.5	4.7	1788	1	US-08-580-014-1	Sequence 1, Appli	982	78	4.7	5516	4	US-09-949-016-13954	Sequence 13954, A
C 910	78.5	4.7	1788	3	US-09-079-785-1	Sequence 1, Appli	983	78	4.7	5541	1	US-08-920-812-20	Sequence 20, Appl
C 911	78.5	4.7	1788	4	US-09-921-667-5	Sequence 5, Appli	984	78	4.7	5541	1	US-08-920-827-20	Sequence 20, Appl
C 912	78.5	4.7	1788	4	US-09-628-126-1	Sequence 1, Appli	985	78	4.7	5541	1	US-08-921-177-20	Sequence 20, Appl
C 913	78.5	4.7	1800	3	US-09-377-155-14	Sequence 14, Appl	986	78	4.7	5541	2	US-08-362-577C-20	Sequence 20, Appl
C 914	78.5	4.7	1800	3	US-09-669-974-14	Sequence 14, Appl	987	78	4.7	5541	2	US-08-920-828-20	Sequence 20, Appl
C 915	78.5	4.7	1800	4	US-09-797-862-14	Sequence 14, Appl	988	78	4.7	5631	4	US-09-949-016-15416	Sequence 15416, A
C 916	78.5	4.7	2341	4	US-09-520-781-9	Sequence 9, Appli	989	78	4.7	5751	4	US-09-023-655-1415	Sequence 1415, Ap
C 917	78.5	4.7	2450	4	US-09-620-312D-336	Sequence 336, App	990	78	4.7	6008	4	US-09-949-016-5058	Sequence 5058, Ap
C 918	78.5	4.7	2467	4	US-09-799-451-628	Sequence 628, App	991	78	4.7	6312	1	US-08-531-601-3	Sequence 3, Appli
C 919	78.5	4.7	2950	4	US-09-710-279-3349	Sequence 3349, Ap	992	78	4.7	6312	2	US-08-859-032-3	Sequence 3, Appli
C 920	78.5	4.7	3233	4	US-09-949-016-2531	Sequence 2531, Ap	993	78	4.7	7198	3	US-08-994-035C-4	Sequence 4, Appli
C 921	78.5	4.7	3352	4	US-10-101-464A-868	Sequence 868, App	994	78	4.7	7198	3	US-09-395-861-4	Sequence 4, Appli
C 922	78.5	4.7	3424	3	US-09-336-643A-9	Sequence 9, Appli	995	78	4.7	7376	4	US-09-949-016-4052	Sequence 4052, Ap
C 923	78.5	4.7	3760	4	US-09-710-279-4029	Sequence 4029, Ap	996	78	4.7	10085	4	US-09-902-540-964	Sequence 964, App
C 924	78.5	4.7	3941	4	US-09-902-540-660	Sequence 660, App	997	78	4.7	10085	4	US-09-902-540-1203	Sequence 1203, Ap
C 925	78.5	4.7	6891	4	US-09-902-540-886	Sequence 886, App	998	78	4.7	23738	4	US-08-752-760A-1	Sequence 1, Appli
C 926	78.5	4.7	6922	4	US-09-949-016-16700	Sequence 16700, A	999	78	4.7	35081	2	US-09-453-702B-206	Sequence 206, App
C 927	78.5	4.7	30922	4	US-09-949-016-16700	Sequence 16700, A	1000	78	4.7	43360	3	US-09-453-702B-261	Sequence 261, App
C 928	78.5	4.7	30922	4	US-09-949-016-16700	Sequence 16700, A	1001	78	4.7	45325	3	US-09-428-517-1	Sequence 1, Appli
C 929	78.5	4.7	70770	4	US-09-949-016-16938	Sequence 16938, A	1002	78	4.7	50937	3	US-09-949-016-1771	Sequence 11771, A
C 930	78.5	4.7	81819	4	US-09-949-016-16661	Sequence 16661, A	1003	78	4.7	57139	4	US-09-949-016-16233	Sequence 16233, A
C 931	78	4.7	81819	4	US-09-949-016-16662	Sequence 16662, A	1004	78	4.7	57139	4	US-09-949-016-16233	Sequence 16233, A
C 932	78	4.7	510	4	US-09-252-991A-9469	Sequence 9469, Ap	1005	78	4.7	84761	4	US-09-949-016-13914	Sequence 13914, A
C 933	78	4.7	772	4	US-09-367-572-3	Sequence 3, Appli	1006	78	4.7	84761	4	US-09-949-016-13914	Sequence 13914, A
C 934	78	4.7	1140	4	US-09-489-039A-4643	Sequence 4643, Ap	1007	78	4.7	84875	4	US-09-949-016-17334	Sequence 17334, A
C 935	78	4.7	1197	4	US-09-248-796A-875	Sequence 875, App	1008	78	4.7	84875	4	US-09-949-016-17336	Sequence 17336, A
C 936	78	4.7	1245	4	US-09-489-039A-5399	Sequence 5399, Ap	1009	78	4.7	84875	4	US-09-949-016-17337	Sequence 17337, A
C 937	78	4.7	1340	4	US-09-949-016-1700	Sequence 1700, Ap	1010	78	4.7	85152	4	US-09-949-016-12665	Sequence 12665, A
C 938	78	4.7	1419	3	US-09-625-188-5	Sequence 5, Appli	1011	78	4.7	85152	4	US-09-949-016-12666	Sequence 12666, A
C 939	78	4.7	1478	3	US-09-545-814-28	Sequence 28, Appl	1012	78	4.7	85152	4	US-09-949-016-12667	Sequence 12667, A
C 940	78	4.7	1485	4	US-09-248-796A-2443	Sequence 2443, Ap	1013	78	4.7	85152	4	US-09-949-016-12668	Sequence 12668, A
C 941	78	4.7	1549	2	US-08-865-537A-1	Sequence 1, Appli	1014	78	4.7	152481	4	US-09-949-016-12521	Sequence 12521, A
C 942	78	4.7	1596	2	US-08-531-601-2	Sequence 2, Appli	1015	78	4.7	152798	4	US-09-949-016-12775	Sequence 12775, A
C 943	78	4.7	1596	2	US-08-859-032-2	Sequence 2, Appli	1016	78	4.7	152822	4	US-09-949-016-17518	Sequence 17518, A
								78	4.7	152822	4	US-09-949-016-17519	Sequence 17519, A



1163	76.5	4.6	975	4	US-09-252-991A-7594	Sequence 7594, Ap	c1236	76.5	4.6	9775	3	US-09-647-540A-5	Sequence 5, Appli
1164	76.5	4.6	1029	4	US-09-252-991A-3332	Sequence 3332, Ap	1237	76.5	4.6	9775	3	US-09-647-540A-7	Sequence 7, Appli
c1165	76.5	4.6	1047	4	US-09-252-991A-3235	Sequence 3235, Ap	c1238	76.5	4.6	9775	4	US-10-119-600A-1	Sequence 1, Appli
1166	76.5	4.6	1065	4	US-09-340-798A-31	Sequence 31, Appl	c1239	76.5	4.6	9775	4	US-10-119-600-3	Sequence 3, Appli
1167	76.5	4.6	1122	4	US-09-902-540-7103	Sequence 7103, Ap	c1240	76.5	4.6	9775	4	US-10-119-600-5	Sequence 5, Appli
1168	76.5	4.6	1129	4	US-09-270-767-12501	Sequence 12501, A	1241	76.5	4.6	9775	4	US-10-119-600-7	Sequence 7, Appli
1169	76.5	4.6	1341	4	US-09-252-991A-15277	Sequence 15277, A	c1242	76.5	4.6	9775	4	US-10-119-651-1	Sequence 1, Appli
c1170	76.5	4.6	1340	4	US-09-513-999C-14928	Sequence 14928, A	c1243	76.5	4.6	9775	4	US-10-119-651-3	Sequence 3, Appli
1171	76.5	4.6	1356	4	US-09-248-796A-2116	Sequence 2116, Ap	c1244	76.5	4.6	9775	4	US-10-119-651-5	Sequence 5, Appli
c1172	76.5	4.6	1386	4	US-09-270-767-15263	Sequence 15263, A	1245	76.5	4.6	9775	4	US-10-119-651-7	Sequence 7, Appli
1173	76.5	4.6	1398	4	US-09-252-991A-15327	Sequence 15327, A	c1246	76.5	4.6	10106	4	US-09-949-016-17187	Sequence 7, Appli
1174	76.5	4.6	1551	4	US-09-252-991A-8277	Sequence 8277, Ap	c1247	76.5	4.6	10318	4	US-09-902-540-973	Sequence 973, App
c1175	76.5	4.6	1578	4	US-09-107-532A-2089	Sequence 2089, Ap	1248	76.5	4.6	11003	4	US-09-949-016-13166	Sequence 13166, A
1176	76.5	4.6	1608	4	US-09-252-991A-8157	Sequence 8157, Ap	c1249	76.5	4.6	12498	4	US-09-949-016-16639	Sequence 16639, A
1177	76.5	4.6	1620	3	US-08-814-052-12	Sequence 12, Appl	c1250	76.5	4.6	15363	3	US-08-961-527-139	Sequence 139, App
1178	76.5	4.6	1620	3	US-08-814-052-13	Sequence 13, Appl	c1251	76.5	4.6	16387	4	US-09-902-540-1156	Sequence 1156, Ap
1179	76.5	4.6	1697	4	US-09-799-451-509	Sequence 509, App	1252	76.5	4.6	17605	4	US-09-949-016-13599	Sequence 13599, A
c1180	76.5	4.6	1725	4	US-09-943-075A-7	Sequence 7, Appli	1253	76.5	4.6	18475	3	US-08-961-527-38	Sequence 38, Appl
1181	76.5	4.6	1734	4	US-09-252-991A-7986	Sequence 7986, Ap	1254	76.5	4.6	25231	4	US-09-949-016-12041	Sequence 12041, A
c1182	76.5	4.6	1770	3	US-09-377-155-18	Sequence 18, Appl	1255	76.5	4.6	27933	4	US-09-949-016-12369	Sequence 12369, A
c1183	76.5	4.6	1770	3	US-09-669-974-18	Sequence 18, Appl	c1256	76.5	4.6	32379	4	US-09-949-016-15217	Sequence 15217, A
1184	76.5	4.6	1770	4	US-09-797-862-18	Sequence 18, Appl	c1257	76.5	4.6	32379	4	US-09-949-016-15218	Sequence 15218, A
c1185	76.5	4.6	1771	4	US-09-949-016-4307	Sequence 4307, Ap	c1258	76.5	4.6	32379	4	US-09-949-016-15219	Sequence 15219, A
c1186	76.5	4.6	1927	4	US-09-949-016-3372	Sequence 3372, Ap	c1259	76.5	4.6	32379	4	US-09-949-016-15220	Sequence 15220, A
1187	76.5	4.6	1941	4	US-09-603-208A-55	Sequence 55, Appl	c1260	76.5	4.6	32379	4	US-09-949-016-15221	Sequence 15221, A
c1188	76.5	4.6	2001	1	US-08-674-168-24	Sequence 24, Appl	c1261	76.5	4.6	32379	4	US-09-949-016-15222	Sequence 15222, A
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c1190	76.5	4.6	2001	3	US-08-852-730-23	Sequence 23, Appl	c1263	76.5	4.6	32379	4	US-09-949-016-15224	Sequence 15224, A
c1191	76.5	4.6	2213	3	US-09-383-586-27	Sequence 27, Appl	c1264	76.5	4.6	32379	4	US-09-949-016-15225	Sequence 15225, A
c1192	76.5	4.6	2213	4	US-09-823-038A-27	Sequence 27, Appl	c1265	76.5	4.6	32379	4	US-09-949-016-15226	Sequence 15226, A
1193	76.5	4.6	2219	3	US-08-510-646B-17	Sequence 17, Appl	c1266	76.5	4.6	36620	4	US-09-952-060-31	Sequence 31, Appl
c1194	76.5	4.6	2406	4	US-09-902-540-8703	Sequence 8703, Ap	c1267	76.5	4.6	37474	4	US-09-952-060-36	Sequence 36, Appl
c1195	76.5	4.6	2496	1	US-08-073-384C-2	Sequence 2, Appli	c1268	76.5	4.6	38519	4	US-09-952-060-29	Sequence 29, Appl
1196	76.5	4.6	2496	1	US-08-254-359A-2	Sequence 2, Appli	c1269	76.5	4.6	61158	4	US-09-949-016-15041	Sequence 15041, A
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c1199	76.5	4.6	2496	2	US-08-471-066B-2	Sequence 2, Appli	c1272	76.5	4.6	64377	4	US-09-949-016-15214	Sequence 15214, A
1200	76.5	4.6	2496	2	US-08-484-953-2	Sequence 2, Appli	c1273	76.5	4.6	64377	4	US-09-949-016-15215	Sequence 15215, A
c1201	76.5	4.6	2496	2	US-08-757-656-2	Sequence 2, Appli	c1274	76.5	4.6	64377	4	US-09-949-016-15216	Sequence 15216, A
1202	76.5	4.6	2496	2	US-08-593-491-2	Sequence 2, Appli	c1275	76.5	4.6	75431	4	US-09-949-016-15122	Sequence 15122, A
c1203	76.5	4.6	2496	2	US-08-756-386-2	Sequence 2, Appli	c1276	76.5	4.6	100463	4	US-09-949-016-12511	Sequence 12511, A
1204	76.5	4.6	2496	2	US-08-823-516-2	Sequence 2, Appli	c1277	76.5	4.6	100468	4	US-09-949-016-13725	Sequence 13725, A
c1205	76.5	4.6	2496	3	US-08-682-853A-2	Sequence 2, Appli	c1278	76.5	4.6	112874	4	US-09-949-016-13180	Sequence 13180, A
1206	76.5	4.6	2496	3	US-08-759-038-2	Sequence 2, Appli	1279	76.5	4.6	767677	4	US-09-949-016-12147	Sequence 12147, A
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1208	76.5	4.6	2496	3	US-08-758-314-2	Sequence 2, Appli	c1281	76	4.6	601	4	US-09-949-016-138697	Sequence 138697, A
c1209	76.5	4.6	2496	3	US-08-520-946-2	Sequence 2, Appli	c1282	76	4.6	750	4	US-09-107-433-906	Sequence 906, App
1210	76.5	4.6	2496	4	US-09-684-938-2	Sequence 2, Appli	1283	76	4.6	965	4	US-09-248-796A-6043	Sequence 6043, Ap
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1212	76.5	4.6	2496	4	US-09-758-282B-2	Sequence 2, Appli	c1285	76	4.6	1038	4	US-09-543-681A-1978	Sequence 1978, Ap
c1213	76.5	4.6	2496	4	US-09-655-378A-2	Sequence 2, Appli	c1286	76	4.6	1074	4	US-09-489-039A-6272	Sequence 6272, Ap
1214	76.5	4.6	2496	4	US-09-940-244-2	Sequence 2, Appli	c1287	76	4.6	1086	4	US-09-540-236-24	Sequence 244, App
c1215	76.5	4.6	2496	4	US-09-333-145-2	Sequence 2, Appli	1288	76	4.6	1119	4	US-09-602-777A-27	Sequence 27, Appl
1216	76.5	4.6	2496	4	US-09-577-304A-2	Sequence 2, Appli	1289	76	4.6	1122	4	US-09-902-540-4288	Sequence 4288, Ap
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1218	76.5	4.6	2735	4	US-09-620-312D-842	Sequence 842, App	1291	76	4.6	1161	4	US-09-328-352-596	Sequence 596, App
c1219	76.5	4.6	2850	2	US-08-224-482-7	Sequence 7, Appli	1292	76	4.6	1173	4	US-09-902-540-2437	Sequence 2437, Ap
c1220	76.5	4.6	3162	4	US-09-543-681A-1809	Sequence 1809, Ap	c1293	76	4.6	1185	4	US-09-252-991A-11261	Sequence 11261, A
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c1222	76.5	4.6	3192	3	US-08-860-886-1	Sequence 1, Appli	1295	76	4.6	1211	2	US-08-997-362-40	Sequence 40, Appl
1223	76.5	4.6	3818	4	US-09-949-016-5445	Sequence 5445, Ap	1296	76	4.6	1211	3	US-08-873-370-40	Sequence 40, Appl
c1224	76.5	4.6	3889	3	US-09-484-970B-39	Sequence 39, Appl	1297	76	4.6	1211	3	US-09-095-855-40	Sequence 40, Appl
1225	76.5	4.6	4289	4	US-09-949-016-627	Sequence 627, App	1298	76	4.6	1211	3	US-08-705-347A-40	Sequence 40, Appl
c1226	76.5	4.6	4403	2	US-08-284-941-1	Sequence 1, Appli	1299	76	4.6	1211	3	US-09-324-542-40	Sequence 40, Appl
1227	76.5	4.6	4403	2	US-08-447-642-1	Sequence 1, Appli	1300	76	4.6	1211	3	US-09-205-426-40	Sequence 40, Appl
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1229	76.5	4.6	4403	4	US-09-949-016-369	Sequence 369, App	1302	76	4.6	1295	1	US-08-433-854-3	Sequence 3, Appli
c1230	76.5	4.6	4403	5	PCT-US93-02147A-1	Sequence 1, Appli	1303	76	4.6	1295	1	US-08-174-745A-3	Sequence 3, Appli
1231	76.5	4.6	5063	4	US-09-949-016-1375	Sequence 1375, Ap	1304	76	4.6	1295	2	US-08-195-947-3	Sequence 3, Appli
c1232	76.5	4.6	7052	4	US-09-526-193A-22	Sequence 22, Appl	1305	76	4.6	1295	2	US-08-433-885-3	Sequence 3, Appli
1233	76.5	4.6	7109	4	US-09-902-540-922	Sequence 922, App	1306	76	4.6	1295	2	US-08-433-908B-3	Sequence 3, Appli
c1234	76.5	4.6	9775	3	US-09-647-540A-1	Sequence 1, Appli	1307	76	4.6	1295	3	US-08-410-614-3	Sequence 3, Appli
c1235	76.5	4.6	9775	3	US-09-647-540A-3	Sequence 3, Appli	1308	76	4.6	1307	4	US-09-774-639-49	Sequence 49, Appli

1309	76	4.6	1308	4	US-09-801-861-4	Sequence 4, Appli	1391	76	4.6	4183	4	US-09-895-547-1	Sequence 1, Appli
1310	76	4.6	1308	4	US-10-224-562-4	Sequence 4, Appli	1392	76	4.6	4464	2	US-08-400-159-7	Sequence 7, Appli
1311	76	4.6	1311	4	US-09-252-991A-1607	Sequence 1607, Ap	1393	76	4.6	4483	3	US-08-611-729A-7	Sequence 7, Appli
1312	76	4.6	1320	4	US-09-949-016-1481	Sequence 1481, Ap	1394	76	4.6	4483	4	US-09-195-524-7	Sequence 7, Appli
1313	76	4.6	1347	4	US-09-252-991A-10926	Sequence 10926, A	1395	76	4.6	4597	4	US-09-949-016-5173	Sequence 5173, Ap
1314	76	4.6	1365	4	US-09-252-991A-11429	Sequence 11429, A	1396	76	4.6	4792	3	US-08-781-891-205	Sequence 205, App
1315	76	4.6	1313	4	US-09-252-991A-10988	Sequence 10988, A	1397	76	4.6	4792	4	US-09-618-166-205	Sequence 205, App
1316	76	4.6	1495	4	US-09-252-991A-11269	Sequence 11269, A	1398	76	4.6	5724	4	US-09-976-594-768	Sequence 768, App
1317	76	4.6	1467	4	US-09-620-312D-662	Sequence 662, App	1399	76	4.6	6122	1	US-08-403-545-1	Sequence 1, Appli
1318	76	4.6	1502	4	US-09-620-312D-362	Sequence 362, App	1400	76	4.6	6122	3	US-08-404-381-1	Sequence 1, Appli
1319	76	4.6	1554	4	US-09-902-540-8489	Sequence 8489, Ap	1401	76	4.6	7147	3	US-08-961-527-23	Sequence 23, Appl
1320	76	4.6	1629	4	US-09-489-039A-4586	Sequence 4586, Ap	1402	76	4.6	7390	4	US-09-566-921-95	Sequence 95, Appl
1321	76	4.6	1659	4	US-09-252-991A-6121	Sequence 6121, Ap	c1403	76	4.6	7529	4	US-09-902-540-893	Sequence 893, App
1322	76	4.6	1669	4	US-09-902-540-3010	Sequence 3010, Ap	1404	76	4.6	8517	3	US-08-827-208-1	Sequence 1, Appli
1323	76	4.6	1755	4	US-09-252-991A-11461	Sequence 11461, A	1405	76	4.6	8517	3	US-09-500-358-1	Sequence 1, Appli
1324	76	4.6	1776	3	US-09-377-155-10	Sequence 10, Appl	1406	76	4.6	8517	3	US-09-498-809-1	Sequence 1, Appli
1325	76	4.6	1776	3	US-09-377-155-20	Sequence 20, Appl	1407	76	4.6	11707	3	US-09-136-574A-1	Sequence 1, Appli
1326	76	4.6	1776	3	US-09-669-974-10	Sequence 10, Appl	1408	76	4.6	14352	4	US-09-902-540-1070	Sequence 1070, Ap
1327	76	4.6	1776	3	US-09-669-974-20	Sequence 20, Appl	c1409	76	4.6	14899	4	US-09-902-540-1107	Sequence 1107, Ap
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1330	76	4.6	1776	4	US-09-302-826B-3	Sequence 3, Appli	c1412	76	4.6	16738	4	US-09-949-016-14678	Sequence 12305, A
1331	76	4.6	1776	4	US-09-700-293-3	Sequence 3, Appli	1413	76	4.6	28030	4	US-09-949-016-16948	Sequence 16948, A
1332	76	4.6	1818	4	US-09-148-545-87	Sequence 87, Appl	c1414	76	4.6	33478	4	US-09-949-016-13615	Sequence 13615, A
1333	76	4.6	1822	4	US-09-397-243D-1	Sequence 1, Appli	c1415	76	4.6	36412	4	US-08-311-731A-132	Sequence 132, App
1334	76	4.6	1857	4	US-09-023-655-902	Sequence 902, App	1416	76	4.6	41965	4	US-09-949-016-13067	Sequence 13067, A
1335	76	4.6	1857	4	US-09-949-016-120	Sequence 120, App	c1417	76	4.6	43550	4	US-09-949-016-12400	Sequence 12400, A
1336	76	4.6	1878	4	US-09-252-991A-6434	Sequence 6434, Ap	c1418	76	4.6	43555	4	US-09-949-016-13993	Sequence 13993, A
1337	76	4.6	1925	4	US-09-148-545-86	Sequence 86, Appl	c1419	76	4.6	43795	3	US-08-742-185-101	Sequence 101, App
1338	76	4.6	1926	4	US-09-148-545-21	Sequence 21, Appl	c1420	76	4.6	43986	4	US-09-949-016-17155	Sequence 17155, A
1339	76	4.6	1941	4	US-09-248-796A-2598	Sequence 2598, Ap	1421	76	4.6	62909	4	US-09-596-002-32	Sequence 32, Appl
1340	76	4.6	2011	4	US-09-949-016-4534	Sequence 4534, Ap	c1422	76	4.6	68702	4	US-09-949-016-16328	Sequence 16328, A
1341	76	4.6	2091	4	US-09-107-532A-1551	Sequence 1551, Ap	c1423	76	4.6	71989	3	US-09-443-501A-2	Sequence 2, Appli
1342	76	4.6	2203	4	US-09-801-861-1	Sequence 1, Appli	1424	76	4.6	19746	4	US-09-877-177A-10	Sequence 10, Appl
1343	76	4.6	2203	4	US-10-224-562-1	Sequence 1, Appli	1425	75.5	4.6	594	4	US-09-252-991A-7647	Sequence 7647, Ap
1344	76	4.6	2452	2	US-08-524-051-1	Sequence 1, Appli	1426	75.5	4.6	601	4	US-09-949-016-78056	Sequence 78056, A
1345	76	4.6	2565	4	US-09-902-540-8756	Sequence 8756, Ap	c1427	75.5	4.6	693	4	US-09-252-991A-697	Sequence 697, App
1346	76	4.6	2699	3	US-09-460-145-3	Sequence 3, Appli	1428	75.5	4.6	775	3	US-08-961-083-89	Sequence 89, Appl
1347	76	4.6	2699	3	US-09-895-547-3	Sequence 3, Appli	1429	75.5	4.6	775	4	US-09-536-784-89	Sequence 89, Appl
1348	76	4.6	2881	4	US-09-949-016-5391	Sequence 5391, Ap	c1430	75.5	4.6	808	4	US-09-513-999C-8666	Sequence 8666, Ap
1349	76	4.6	2955	4	US-09-248-796A-1987	Sequence 1987, Ap	1431	75.5	4.6	815	3	US-09-383-586-9	Sequence 9, Appli
1350	76	4.6	3045	4	US-09-596-248D-24	Sequence 24, Appl	1432	75.5	4.6	884	4	US-09-823-038A-9	Sequence 9, Appli
1360	76	4.6	3085	3	US-08-827-208-2	Sequence 2, Appli	c1433	75.5	4.6	888	4	US-09-513-999C-8665	Sequence 8665, Ap
1361	76	4.6	3085	3	US-08-827-208-4	Sequence 4, Appli	c1434	75.5	4.6	921	4	US-09-252-991A-16185	Sequence 16185, Ap
1362	76	4.6	3085	3	US-09-500-358-2	Sequence 2, Appli	1435	75.5	4.6	1011	4	US-09-252-991A-16405	Sequence 16405, A
1363	76	4.6	3085	3	US-09-500-358-4	Sequence 4, Appli	1436	75.5	4.6	1032	4	US-09-734-237B-34	Sequence 34, Appl
1364	76	4.6	3085	3	US-09-498-809-2	Sequence 2, Appli	1437	75.5	4.6	1086	3	US-09-146-980-1	Sequence 1, Appli
1365	76	4.6	3085	3	US-09-498-809-4	Sequence 4, Appli	1438	75.5	4.6	1086	4	US-09-016-434-1281	Sequence 1281, Ap
1366	76	4.6	3096	4	US-09-902-540-637	Sequence 637, App	1439	75.5	4.6	1143	2	US-08-387-942C-19	Sequence 19, Appl
1367	76	4.6	3117	2	US-08-747-536-1	Sequence 1, Appli	c1440	75.5	4.6	1185	4	US-09-902-540-4942	Sequence 4942, Ap
1368	76	4.6	3200	4	US-09-596-248D-46	Sequence 46, Appl	1441	75.5	4.6	1212	4	US-09-602-777A-93	Sequence 93, Appl
1369	76	4.6	3468	1	US-07-931-715A-2	Sequence 2, Appli	1442	75.5	4.6	1257	3	US-09-252-991A-1027	Sequence 1027, Ap
1370	76	4.6	3468	1	US-07-931-715A-4	Sequence 4, Appli	1443	75.5	4.6	1308	4	US-09-500-569-13	Sequence 13, Appl
1371	76	4.6	3468	2	US-08-459-448A-2	Sequence 2, Appli	c1444	75.5	4.6	1308	4	US-09-971-823B-13	Sequence 13, Appl
1372	76	4.6	3468	2	US-08-459-448A-4	Sequence 4, Appli	1445	75.5	4.6	1350	4	US-09-475-515-55	Sequence 55, Appl
1373	76	4.6	3468	2	US-08-459-595A-2	Sequence 2, Appli	1446	75.5	4.6	1356	3	US-09-134-001C-1624	Sequence 1624, Ap
1374	76	4.6	3468	3	US-08-459-595A-4	Sequence 4, Appli	c1447	75.5	4.6	1467	4	US-09-252-991A-1331	Sequence 1331, Ap
1375	76	4.6	3468	3	US-08-459-504B-2	Sequence 2, Appli	c1448	75.5	4.6	1507	1	US-07-906-871-13	Sequence 13, Appl
1376	76	4.6	3468	3	US-08-459-504B-4	Sequence 4, Appli	1449	75.5	4.6	1530	4	US-09-902-540-4172	Sequence 4172, Ap
1377	76	4.6	3468	3	US-08-459-444-2	Sequence 2, Appli	1450	75.5	4.6	1532	4	US-09-270-767-12050	Sequence 12050, A
1378	76	4.6	3468	3	US-08-459-444-4	Sequence 4, Appli	1451	75.5	4.6	1599	4	US-09-475-515-54	Sequence 54, Appl
1379	76	4.6	3468	3	US-09-053-549-3	Sequence 3, Appli	c1452	75.5	4.6	1606	4	US-09-799-451-245	Sequence 245, App
1380	76	4.6	3468	3	US-09-053-549-5	Sequence 5, Appli	1453	75.5	4.6	1641	4	US-09-235-153-4	Sequence 4, Appli
1381	76	4.6	3468	3	US-09-547-422-2	Sequence 2, Appli	c1454	75.5	4.6	1680	2	US-08-759-581B-3	Sequence 3, Appli
1382	76	4.6	3468	3	US-09-547-422-4	Sequence 4, Appli	c1455	75.5	4.6	1680	3	US-09-304-711-3	Sequence 3, Appli
1383	76	4.6	3468	4	US-09-988-462-2	Sequence 2, Appli	c1456	75.5	4.6	1680	3	US-09-173-281-3	Sequence 3, Appli
1384	76	4.6	3468	4	US-09-988-462-4	Sequence 4, Appli	1457	75.5	4.6	1696	3	US-08-961-083-217	Sequence 217, App
1385	76	4.6	3604	4	US-09-016-434-1180	Sequence 1180, Ap	1458	75.5	4.6	1696	4	US-09-936-784-217	Sequence 217, App
1386	76	4.6	3660	3	US-09-517-467B-3	Sequence 3, Appli	1459	75.5	4.6	1715	4	US-09-023-655-984	Sequence 984, App
1387	76	4.6	3747	1	US-08-044-618-5	Sequence 5, Appli	1460	75.5	4.6	1818	4	US-09-475-515-59	Sequence 59, Appl
1388	76	4.6	4014	4	US-09-119-014D-5	Sequence 5, Appli	1461	75.5	4.6	1818	4	US-09-475-515-61	Sequence 61, Appl
1389	76	4.6	4032	4	US-09-949-016-5588	Sequence 5588, Ap	1462	75.5	4.6	1818	4	US-09-475-515-62	Sequence 62, Appl
1390	76	4.6	4183	3	US-09-460-145-1	Sequence 1, Appli	1463	75.5	4.6	1863	4	US-09-475-515-63	Sequence 63, Appl

1464	75.5	4.6	2031	4	US-09-475-515-60	Sequence 60, Appl
1465	75.5	4.6	2112	4	US-09-475-515-56	Sequence 56, Appl
1466	75.5	4.6	2112	4	US-09-475-515-57	Sequence 57, Appl
1467	75.5	4.6	2181	4	US-09-475-515-58	Sequence 58, Appl
1468	75.5	4.6	2192	1	US-08-035-392-1	Sequence 1, Appl
1469	75.5	4.6	2192	1	US-08-504-511A-1	Sequence 1, Appl
c1470	75.5	4.6	2203	4	US-09-902-540-4252	Sequence 4252, Ap
1471	75.5	4.6	2205	1	US-08-035-392-3	Sequence 3, Appl
1472	75.5	4.6	2205	1	US-08-504-511A-3	Sequence 3, Appl
c1473	75.5	4.6	2205	4	US-09-328-352-286	Sequence 286, App
1474	75.5	4.6	2340	4	US-09-475-515-67	Sequence 67, Appl
1475	75.5	4.6	2385	4	US-09-475-515-68	Sequence 68, Appl
1476	75.5	4.6	2412	1	US-08-437-027-18	Sequence 18, Appl
1477	75.5	4.6	2502	1	US-08-073-384C-7	Sequence 7, Appl
1478	75.5	4.6	2502	1	US-08-254-359A-7	Sequence 7, Appl
1479	75.5	4.6	2502	1	US-08-483-043-7	Sequence 7, Appl
1480	75.5	4.6	2502	1	US-08-481-238-7	Sequence 7, Appl
1481	75.5	4.6	2502	2	US-08-471-066B-7	Sequence 7, Appl
1482	75.5	4.6	2502	2	US-08-484-956-7	Sequence 7, Appl
1483	75.5	4.6	2502	2	US-08-757-653-7	Sequence 7, Appl
1484	75.5	4.6	2502	2	US-08-599-491-7	Sequence 7, Appl
1485	75.5	4.6	2502	2	US-08-756-386-7	Sequence 7, Appl
1486	75.5	4.6	2502	2	US-08-823-516-7	Sequence 7, Appl
1487	75.5	4.6	2502	3	US-08-682-853A-7	Sequence 7, Appl
1488	75.5	4.6	2502	3	US-08-759-038-7	Sequence 7, Appl
1489	75.5	4.6	2502	3	US-08-758-314-7	Sequence 7, Appl
1490	75.5	4.6	2502	3	US-09-350-309-7	Sequence 7, Appl
1491	75.5	4.6	2502	3	US-08-520-946-7	Sequence 7, Appl
1492	75.5	4.6	2502	4	US-09-684-938-7	Sequence 7, Appl
1493	75.5	4.6	2502	4	US-09-308-825A-7	Sequence 7, Appl
1494	75.5	4.6	2502	4	US-09-758-282B-7	Sequence 7, Appl
1495	75.5	4.6	2502	4	US-09-655-378A-7	Sequence 7, Appl
1496	75.5	4.6	2502	4	US-09-940-244-7	Sequence 7, Appl
1497	75.5	4.6	2502	4	US-09-333-145-7	Sequence 7, Appl
1498	75.5	4.6	2502	4	US-09-577-304A-7	Sequence 7, Appl
1499	75.5	4.6	2538	4	US-09-475-515-65	Sequence 65, Appl
1500	75.5	4.6	2553	4	US-09-475-515-66	Sequence 66, Appl

RESULT 1  
US-09-232-160-13  
; Sequence 13, Application US/09232160  
; Patent No. 6368794  
; GENERAL INFORMATION:  
; APPLICANT: Steve Daniel  
; APPLICANT: James Gilmore  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Laura Stuve  
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL  
; FILE REFERENCE: PA-0003 US  
; CURRENT APPLICATION NUMBER: US/09/232,160  
; CURRENT FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PERL Program  
; SEQ ID NO 13  
; LENGTH: 2029  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE: -  
; OTHER INFORMATION: 3044710  
US-09-232-160-13

Alignment Scores:	1.97e-183	Length:	2029
Pred. No.:	322	Matches:	322
Score:	1657.00	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:	3		

RESULT 2  
US-09-949-016-1894  
; Sequence 1894, Application US/09949016  
; Patent No. 6812339

1	MetalaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
183	ATGCCAGAGTCTTTCAGCTGGTCTTCTCACTTCCATCTGCAGCACCGAGGCTCTGT	242
21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
243	GTCCAAAGCTCTTTGGCGTCAGAAAGAGCTTTTCCATCAGGTGTCTATGAGAAATATATGGG	302
41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
303	ATCACCTTGTGAGCAAAAGGCGAACAGCTGAATTTTACAGAAAGCTTAAGGAGGCC	362
61	CysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
363	TGTAGGTGCTGGGACTTAAGTTTGGCGCGCAAGGACCAAGTTGAACAGCTTGAAGCT	422
81	SerPheGluThrCysSerTyTrpValGlyAspGlyPheValValIleSerArgIle	100
423	AGCTTTGAAACTTTCAGCTATGGCTGGTGGAGATGGATTCGTGGTCTATCTTAGGATT	482
101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
483	AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGTCTCTGATTGGAAAGTTCCAGTG	542
121	SerArgGlnPheAlaAlaTyTrpCysTyAsnSerSerAspThrTrpThrAsnSerCysIle	140
543	AGCCGACAGTTTGCAGCTATTGTTCACACTCATCTGATCTTGCAGCTTAACCTCGTCAAT	602
141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
603	CCAGAAATATACACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACAACA	662
161	GluPheIleValSerAspSerThrTyTrpSerValAlaSerProTyTrpSerIleProAla	180
663	GAATTTATTGTCAGTGACAGTACTCTCGTGGCATCCCTTACTCTACATACTGCTGCC	722
181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
723	CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCACGCGAGAAAAAATTGATT	782
201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
783	TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCACTTTGTT	842
221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
843	GAATAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACCGCTCTG	902
241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyTrpValLys	260
903	CTAGTGTCTCTCTCTCTCTTCTTGTGGTGTGCAGCTGGTCTTGGATTTTGCTATGTCAA	962
261	ArgTyTrpValLysAlaPhePheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
963	AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGAGAAAGAAATGATGAAACC	1022
281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
1023	AAAGTAGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1082
301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
1083	GATAAAACCCAGAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCA	1142
321	GluVal 322	
1143	GAAAGTT 1148	

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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 1894
; LENGTH: 2301
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1894

Alignment Scores:
Pred. No.: 2,44e-183 Length: 2301
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 92 ATGCCAGGTCCTTCAGCCTGGTGTGCTTCTCATTCCATCGGACCACGAGCTCTG 151

Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 152 GTCCAAAGGCTCTTTGCGTCGAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATATGGGG 211

Qy 41 IleThrLeuValSerIleValAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 212 ATCACCCCTTGAGCAAAAAGGCGAACCCAGCAGTGAATTTCCAGAAAGCTAGAGGCCC 271

Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 272 TGTAGGCTGTGGGACTAAGTTTGGCGCGCAAGCAACCAAGTGAACAGCCTTGAAAGCT 331

Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 332 AGCTTTGAAACTTTCAGCATATGGCTGGGTTGGAGATGGATTCGGTGGTCACTCTAGGATT 391

Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 392 AGCCCAAAACCCCAAGTGTGGGAAAAATTTGGGTGGGTGCTCTGATTTGGAAAGGTTCCAGTG 451

Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 452 AGCCGACAGTTTGCAGCCTATTTGTACAACTCATCTCATCTTGGACTAATCTCGTGCAAT 511

Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 512 CCAGAAATTTATCACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 571

Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 572 GAATTTAATGTGACGTACAGTACCTCTCGGTGGCATCCCTTACTCTCAAACTACCTGCC 631

Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 632 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTCATT 691

Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 692 TGTGTACAGAAGTTTTTTATGGAAACTAGCACCATGTGTACAGAAACTGAACCATTTGTT 751
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Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 752 GAAAAATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 811

Qy 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 812 CTAGTGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 871

Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 872 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAATGATCGAAACC 931

Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 932 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 991

Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 992 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGCATGCCTGGAAGCT 1051

Qy 321 GluVal 322
Db 1052 GAAAGTT 1057

RESULT 3
; Sequence 200, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
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; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
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; PRIOR FILING DATE: 1999-09-13
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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

Alignment Scores:
Pred. No.: 2,568-183 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20
Db 160 ATGCCAGGCTCTTTCAGCTGGTGTCTTCTCACTTCATCGACACAGGCTCTCTG 219

Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTCAGCTGGTGTCTTCTCACTTCATCGACACAGGCTCTCTG 279

Qy 41 IleThrLeuValSerLeuValAlaAsnGlnGlnLeuAsnPheThrGluAlaIysGluAla 60
Db 280 ATCAACCTTTGTGAGCAAAAGCGCAACAGAGCTGTAATTTACAGAGCTTAAGAGGCC 339

Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyIysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTCTGGGACTAAGTTTGGCCGCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399

Qy 81 SerPheGluThrCysSerTyrcGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGCTGGTGGGTGGAGATGGATTCTCTAGGATT 459

Qy 101 SerProAnProLysCysGlyIysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCCTGATTGGAAGGTTCCAGTG 519

Qy 121 SerArgGlnPheAlaAlaTyrcCysTyrrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGACTTAACCTCGTGCATT 579

Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACCAACAACA 639

Qy 161 GluPheIleValSerAspSerThrTyrcSerValAlaSerProTyrcSerThrIleProAla 180
Db 640 GAATTTATTGTTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAACTACCTGCC 699

Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProAlaArgArgLysLeuIle 200
Db 700 CCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759

Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCTACAGAAAGTTTATGGAACACTAGCACCATGCTACAGAAACCTGAAACCTATT 819

Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATTAAGCAGCATTCAGAATCAAGCTGCTGGTGTGGAGGTGTCCTCCACGGCTCTG 879

Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrcValLys 260
Db 880 CTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939

Qy 261 ArgTyrcValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 999

Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1059

Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGAGTCCAGAGTCCAAAGCAAAACTACCGTGGCATGCTCGAAGCT 1119

Qy 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 6
; Sequence 200, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700

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; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

Alignment Scores:
Pred. No.: 2.56e-183 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrrpThrThrArgLeuLeu 20
Db 160 ATGCCCAAGGCTCTTCAGCGTGGTGTCTCTCACTTCCATCTGGACACGAGGCTCCTG 219
Qy 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTTCGTCGACAGAGAGCTTTCATTCAGGTGTATCGAGAAATATGGGG 279
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAAGCGCAACAGCAGCTGAATTTACAGAAAGCTTAAGGAGGCC 339
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGAGCTAAGTTTGGCCGCAAGGACCAAGTTGAACAGCCCTTCGAAAGCT 399
Qy 81 SerPheGluThrCysSerTyrGlyTrrpValGlyAspGlyPheValIleSerArgIle 100
Db 400 AGCTTTGAAACTTCGACGCTATGGCTGGGTGGAGATGGATTCTGGTCACTCTAGAGATT 459
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrpLysValProVal 120
Db 460 AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTGTGATTTGGAAAGGTTCCAGTG 519

121 SerArgGlnPheAlaIaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACACTCATCTGATACTTGGACTAACTCTGTGATT 579
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTTATCACACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 639
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAAATTTATTGTCAGTGACAGTACTCTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
Qy 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAGAGTTTATGGAACCTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTTCAAGAAATGAAGCTGTGGTGGTGGAGGTGTCCCGCCGCTCTG 879
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCTTTCCTCTTTTACAAACAAGAAATCAGCAGAAAGAAATGATCGAAACC 999
Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAAACT 1059
Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCACAGAGAGTCCAGAGTCCAAAGGCAAGAACTACCGTGGATGCTTGGAAAGCT 1119
Qy 321 GluVal 322
Db 1120 GAAATT 1125

RESULT 7
; Sequence 200, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
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; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
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; PRIOR APPLICATION NUMBER: PCT/US99/20594
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; PRIOR FILING DATE: 1999-09-13
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; PRIOR APPLICATION NUMBER: PCT/US99/30911
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; PRIOR APPLICATION NUMBER: PCT/US00/00219
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; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens

Alignment Scores:
Pred. No.:      2,56e-183      Length:      2372
Score:          1657.00      Matches:      322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              4              Gaps:        0

Qy      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160 ATGCCAGGCTCTTCAGCGTGGTGTGCTTCTCACTTCCATCGACGAGGCTCTG 219
Qy      21 ValGlnGlySerLeuArgAlaGlnLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCAAGGCTCTTTCGCGTGCAGAGAGCTTTCCATCCAGGCTCATCGAGAAATTATGGGG 279
Qy      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280 ATCACTCTTGAGCAAAAGCGACACGAGCTGAATTCACAGAGCTTAAGAGGCC 339
Qy      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGGCTCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAACAGCGCTTGAAGCT 399
Qy      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      1119 GATAAAACCCGAGAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAGT 1119
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Db      400 AGCTTTGAAACTTCAGCTATGGCTGGTTCGAGATGAGATTCTCGGTGCATCTCTAGGATT 459
Qy      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460 AGCCCAACCCCAAGTGTGGGAAAAATGGGCTGGTGTCTGATTTGGAAGTTCCAGTG 519
Qy      121 SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGACGCTTATTTTACAACCTCATCTGATCTTGGACTTAACCTCGTGCAAT 579
Qy      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGluThrThr 160
Db      580 CCAGAAATTATCACCAACCAAGATCCCATATTTCAACTCAACTCAACTGCAACCAACAACA 639
Qy      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTTATTTGTCAGTGACAGTACCTACTCGGTGCACTCCCTTACTCTACAAATACCTGCC 699
Qy      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle 200
Db      700 CCTACTACTCTCTCTCTCCAGCTTCCACTTCTATTTCCACGAGAGAAAAAATTCGATT 759
Qy      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760 TGTGTACAGAAAGTTTTTATGGAACCTAGCACCATGCTACAGAACTGAAACCAATTTGTT 819
Qy      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAATAAAGCAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCACCGCTCTG 879
Qy      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTGTCTGCTCTCTCTCTTTTGGTGTCTGAGCTGCTTCTTGGATTTCATATGTCATAA 939
Qy      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAGAGAAATGATCGAAACC 999
Qy      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000 AAAGTAGTAAGGAGGAGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAGAACT 1059
Qy      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060 GATAAAACCCGAGAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAGT 1119
Qy      321 GluVal 322
Db      1120 GAAGTT 1125

RESULT 8
; Sequence 200, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
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; APPLICANT: Paoni, Nicholas F. ; APPLICANT: Roy, Margaret Ann ; APPLICANT: Stewart, Timothy A. ; APPLICANT: Tumas, Daniel ; APPLICANT: Williams, P. Mickey ; APPLICANT: Wood, William, I. ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ; FILE REFERENCE: 10466-14 ; CURRENT APPLICATION NUMBER: US/09/904,920A ; CURRENT FILING DATE: 2001-07-13 ; PRIOR APPLICATION NUMBER: PCT/US00/04414 ; PRIOR FILING DATE: 2000-02-22 ; PRIOR APPLICATION NUMBER: US 60/143,048 ; PRIOR FILING DATE: 1999-07-07 ; PRIOR APPLICATION NUMBER: US 60/145,698 ; PRIOR FILING DATE: 1999-07-26 ; PRIOR APPLICATION NUMBER: US 60/146,222 ; PRIOR FILING DATE: 1999-07-28 ; PRIOR APPLICATION NUMBER: PCT/US99/20594 ; PRIOR FILING DATE: 1999-09-08 ; PRIOR APPLICATION NUMBER: PCT/US99/20944 ; PRIOR FILING DATE: 1999-09-13 ; PRIOR APPLICATION NUMBER: PCT/US99/21090 ; PRIOR FILING DATE: 1999-09-15 ; PRIOR APPLICATION NUMBER: PCT/US99/21547 ; PRIOR FILING DATE: 1999-09-15 ; PRIOR APPLICATION NUMBER: PCT/US99/23089 ; PRIOR FILING DATE: 1999-10-05 ; PRIOR APPLICATION NUMBER: PCT/US99/28214 ; PRIOR FILING DATE: 1999-11-29 ; PRIOR APPLICATION NUMBER: PCT/US99/28313 ; PRIOR FILING DATE: 1999-11-30 ; PRIOR APPLICATION NUMBER: PCT/US99/28564 ; PRIOR FILING DATE: 1999-12-02 ; PRIOR APPLICATION NUMBER: PCT/US99/28565 ; PRIOR FILING DATE: 1999-12-02 ; PRIOR APPLICATION NUMBER: PCT/US99/30095 ; PRIOR FILING DATE: 1999-12-16 ; PRIOR APPLICATION NUMBER: PCT/US99/30911 ; PRIOR FILING DATE: 1999-12-20 ; PRIOR APPLICATION NUMBER: PCT/US99/30999 ; PRIOR FILING DATE: 1999-12-20 ; PRIOR APPLICATION NUMBER: PCT/US00/00219 ; PRIOR FILING DATE: 2000-01-05 ; NUMBER OF SEQ ID NOS: 423 ; SEQ ID NO 200 ; LENGTH: 2372 ; TYPE: DNA ; ORGANISM: Homo sapiens	1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTCCATCTGACACAGAGGCTCTG 219 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40 220 GTCCAAGGCTCTTGGCGTGCAGAAAGAGCTTCCATCCAGGTGTATGCAGAAATTATGGG 279 41 IleThrIeuValSerIleLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60 280 ATCAACCTTGTGAGCAAAAGGCAACAGCAGCTGAATTTCAAGAGCTTAAGGAGGCC 339 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80	Alignment Scores: Pred. No.: 2,56e-183 Length: 2372 Score: 1657.00 Matches: 322 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 4 Gaps: 0	; Sequence 200, Application US/09909064 ; Patent No. 6818449 ; GENERAL INFORMATION: ; APPLICANT: Genentech, Inc. ; APPLICANT: Ashkenazi, Avi ; APPLICANT: Botstein, David ; APPLICANT: Desnoyers, Luc ; APPLICANT: Eaton, Dan L. ; APPLICANT: Ferrara, Napoleone ; APPLICANT: Filvaroff, Ellen ; APPLICANT: Fong, Sherman ; APPLICANT: Gao, Wei-Qiang ; APPLICANT: Gerber, Hanspeter ; APPLICANT: Gerritsen, Mary E. ; APPLICANT: Goddard, A. ; APPLICANT: Godowski, Paul J. ; APPLICANT: Grimaldi, Christopher J.	RESULT 9 ; Sequence 200, Application US/09909064 ; Patent No. 6818449 ; GENERAL INFORMATION: ; APPLICANT: Genentech, Inc. ; APPLICANT: Ashkenazi, Avi ; APPLICANT: Botstein, David ; APPLICANT: Desnoyers, Luc ; APPLICANT: Eaton, Dan L. ; APPLICANT: Ferrara, Napoleone ; APPLICANT: Filvaroff, Ellen ; APPLICANT: Fong, Sherman ; APPLICANT: Gao, Wei-Qiang ; APPLICANT: Gerber, Hanspeter ; APPLICANT: Gerritsen, Mary E. ; APPLICANT: Goddard, A. ; APPLICANT: Godowski, Paul J. ; APPLICANT: Grimaldi, Christopher J.	340 TGTAGGCTGCTGGAGCTAAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTTGAAAGCT 399 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100 400 AGCTTTGAAACATTGACAGCTATGCTGGGTGGAGATGGATTCGTGTCATCTCTAGATT 459 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120 460 AGCCCAAAACCCNAAGTGTGGAAAAATGGGTGGGTGCTCTGATTTTGGAAGGTTCCAGTG 519 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTTGGACTAACTCGTGCAAT 579 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160 580 CCAGAAATATTATCACCAAGATCCCATTTCAACACTCAAACTGCAACACAAACAACA 639 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180 640 GAATTTTGTGTCAGTCACAGTACCTACTCGGTGGCATCCCTTACTCTACATACCTGCC 699 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200 700 CCTACTACTACTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 759 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220 760 TGTGTACAGAGAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240 820 GAAAAATAAGCAGCATTTCAAGATGAAGCTGTGGGTGGGTGGGTGGGTGGGTGGGTGG 879 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260 880 CTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280 940 AGTATGTGAAGGCTTTCCCTTTTCAAAACAAGATCAGCAGAGGAAATGATCGAAACC 999 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300 1000 AAAGTAGTAAAGGAGGAGGAGGCCAATGATGACACCTAATCAGGAATCAAGAAAACT 1059 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320 1060 GATAAAAAACCCAGAGAGTCCAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGCATCGCTGGAAGCT 1119 321 GluVal 322 1120 GAAGTT 1125
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APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/909,064  
CURRENT FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 200  
LENGTH: 2372  
TYPE: DNA  
ORGANISM: Homo sapiens

Alignment Scores:  
Pred. No.: 2,56e-183 Length: 2372  
Score: 1657,00 Matches: 322  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

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Db 160 ATGCCAGGCTCTTCAGCGTGGTGTCTTCATCTGACACACAGGCTCTGTG 219  
Qy 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysAtgIleMetGly 40  
Db 220 GTCCAGGCTCTTTCGCGTGCAGAGAGCTTTCCATCCAGGGTGTATGAGG 279

Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
Db 280 ATCAACCTTGTGAGCAAAAGGCGAACAGCAGCTGAATTTACAGAGCTTAAGAGGCC 339  
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
Db 340 TGTAGGCTCTGGGACTAAGTTTGGCGGCAAGGCAAGTTGAACAGCTTTGAAGCT 399  
Qy 81 SerPheGluThrCysSerTyrGlyTrrValGlyAspGlyPheValValIleSerArgIle 100  
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCGTGGTCATCTCTAGGATT 459  
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrPLeuValProVal 120  
Db 460 AGCCCAAAACCCCAAGTGTGGGAAATGGGTGGGTGTCTCTGATTTGGAAGGTTCCAGTG 519  
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrPThrAsnSerCysIle 140  
Db 520 AGCCGACAGTTTGCAGCTATTTGTTACACTCATCTGATCTTGACTTAATCTGTGCTATT 579  
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
Db 580 CCAGAAATTTATCACCAACCAAGATCCCATATTTCAACTCAAACTCAAACTCAAACTCAAACTCA 639  
Qy 161 GluPheIleValSerAspSerThrTrrSerValIleSerProTrrSerThrIleProAla 180  
Db 640 GAATTTATTTGTCTAGTACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC 699  
Qy 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgLysLysIle 200  
Db 700 CCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759  
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
Db 760 TGTGTACAGAGTCTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819  
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
Db 820 GAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879  
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTrrValLys 260  
Db 880 CTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939  
Qy 261 ArgTrrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
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Qy 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
Db 1000 AAAGTAGTAAAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1059  
Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAG 1119  
Qy 321 GluVal 322  
Db 1120 GAAGTT 1125

RESULT 10  
; Sequence 200, Application US/09905381A  
; Patent No. 6818746  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Flivaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang

/	APPLICANT:	Gerber, Hanspeter
/	APPLICANT:	Gerritsen, Mary E.
/	APPLICANT:	Goddard, A.
/	APPLICANT:	Godowski, Paul J.
/	APPLICANT:	Grimaldi, Christopher J.
/	APPLICANT:	Gurney, Austin L.
/	APPLICANT:	Hillan, Kenneth, J.
/	APPLICANT:	Kljavin, Ivar J.
/	APPLICANT:	Mather, Jennie P.
/	APPLICANT:	Pan, James
/	APPLICANT:	Paoni, Nicholas F.
/	APPLICANT:	Roy, Margaret Ann
/	APPLICANT:	Stewart, Timothy A.
/	APPLICANT:	Tumas, Daniel
/	APPLICANT:	Williams, P. Mickey
/	APPLICANT:	Wood, William, I.
/	TITLE OF INVENTION:	Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
/	TITLE OF INVENTION:	Acids Encoding the Same
/	FILE REFERENCE:	10466-14
/	CURRENT APPLICATION NUMBER:	US/09/905.381A
/	CURRENT FILING DATE:	2001-07-13
/	PRIOR APPLICATION NUMBER:	PCT/US00/04414
/	PRIOR FILING DATE:	2000-02-22
/	PRIOR APPLICATION NUMBER:	US 60/143,048
/	PRIOR FILING DATE:	1999-07-07
/	PRIOR APPLICATION NUMBER:	US 60/145,698
/	PRIOR FILING DATE:	1999-07-26
/	PRIOR APPLICATION NUMBER:	US 60/146,222
/	PRIOR FILING DATE:	1999-07-28
/	PRIOR APPLICATION NUMBER:	PCT/US99/20594
/	PRIOR FILING DATE:	1999-09-08
/	PRIOR APPLICATION NUMBER:	PCT/US99/20944
/	PRIOR FILING DATE:	1999-09-13
/	PRIOR APPLICATION NUMBER:	PCT/US99/21090
/	PRIOR FILING DATE:	1999-09-15
/	PRIOR APPLICATION NUMBER:	PCT/US99/21547
/	PRIOR FILING DATE:	1999-09-15
/	PRIOR APPLICATION NUMBER:	PCT/US99/23089
/	PRIOR FILING DATE:	1999-10-05
/	PRIOR APPLICATION NUMBER:	PCT/US99/28214
/	PRIOR FILING DATE:	1999-11-29
/	PRIOR APPLICATION NUMBER:	PCT/US99/28313
/	PRIOR FILING DATE:	1999-11-30
/	PRIOR APPLICATION NUMBER:	PCT/US99/28564
/	PRIOR FILING DATE:	1999-12-02
/	PRIOR APPLICATION NUMBER:	PCT/US99/28565
/	PRIOR FILING DATE:	1999-12-02
/	PRIOR APPLICATION NUMBER:	PCT/US99/30095
/	PRIOR FILING DATE:	1999-12-16
/	PRIOR APPLICATION NUMBER:	PCT/US99/30911
/	PRIOR FILING DATE:	1999-12-20
/	PRIOR APPLICATION NUMBER:	PCT/US99/30999
/	PRIOR FILING DATE:	1999-12-20
/	PRIOR APPLICATION NUMBER:	PCT/US00/00219
/	PRIOR FILING DATE:	2000-01-05
/	NUMBER OF SEQ ID NOS:	423
/	SEQ ID NO 200	
/	LENGTH:	2372
/	TYPE:	DNA
/	ORGANISM:	Homo sapiens
Alignment Scores:		
Pred. No.:	2,56e-183	Length: 2372
Score:	1657.00	Matches: 322
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	4	Gaps: 0
Oy	1	MetalaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu
Db	160	ATGCCAGGTCCTTTCAGCGTGTTCTCACTTCCATCTGCACGAGGCTCCTG 2199

APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filwaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Klijavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/906,618  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
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PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 200  
LENGTH: 2372  
TYPE: DNA  
ORGANISM: Homo sapiens

Alignment Scores:  
Pred. No.: 2,566-183  
Score: 1657.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 4  
Length: 2372  
Matches: 322  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
Db 160 ATGCCAGGTCCTTTCAGCGTGGTGTCTTCTCACTTCCATCTGACCAACGAGGCTCCTG 219  
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
Db 220 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGAGTGTCTATGAGAAATATGSGG 279  
QY 41 IleThrLeuValSerLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
Db 280 ATCAACCTTTGTGACGCAAAAGGCGAACACGAGCTGAATTTTCACAGAACTAAGAGGCC 339  
QY 61 CysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399  
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
Db 400 AGCTTTGAAACTTTCAGCTATGGCTGGTGGAGATGGAATTCGTGGTCACTCTAGGATT 459  
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
Db 460 AGCCAAACCCCAAGTGTGGGAAATGGGGTGGGTGCTCTGATTGGAAAGTTCACGTG 519  
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
Db 520 AGCCGACAGTTTTCAGGCTATTGTTACAACTCATCTGATCTTGGACTTAACCTCGTCATT 579  
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
Db 580 CCAGAAATTTATCACCAAGATCCCATATTTCAACACTCAAACTGCAACCAACAACA 639  
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
Db 640 GAATTTATGTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTCTACTCTACAACTACCTGCC 699  
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle 200  
Db 700 CCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759  
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
Db 760 TGTGTACAGAAAGTTTATGGAAACTAGCACCATGCTCTACAGAACTGAACCACTTTGTT 819  
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
Db 820 GAAATTAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGCTCTG 879  
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
Db 880 CTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939  
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
Db 940 AGGTATGTGAAGGCTTTCCCTTTTACAAACAAGAAATCAGCAGAAAGAAATGATCGAAACC 999  
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
Db 1000 AAGTAGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1059  
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
Db 1060 GATPAAAAACCCAGAGAGTCCAGAGTCCAAAGCAAAACTACCGTGGCATGCTCGAAGCT 1119  
QY 321 GluVal 322  
Db 1120 GAAGTT 1125

RESULT 12  
US-08-892-880-1  
; Sequence 1, Application US/08892880

Patent No. 5942417  
GENERAL INFORMATION:  
APPLICANT: NI, JIAN  
APPLICANT: GENTZ, REINER L.  
APPLICANT: DILLON, PATRICK J.  
TITLE OF INVENTION: CD44-LIKE PROTEIN  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3914  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/892,880  
FILING DATE: HEREWITH  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/021,762  
FILING DATE: 15-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0490001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2313 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 91..1056  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 154..1056  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 91..153  
US-08-892-880-1

Alignment Scores:  
Pred. No.: 1.24e-182 Length: 2313  
Score: 1651.00 Matches: 321  
Percent Similarity: 99.69% Conservative: 0  
Best Local Similarity: 99.69% Mismatches: 1  
Query Match: 99.64% Indels: 0  
DB: 2 Gaps: 0

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrrThrThrArgLeuLeu 20  
Db 91 ATGCCAGGTGCTTCAGCCTGGTGTCTTCTCTCACTCCATCTGACCACGAGGCTCTG 150  
Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
Db 151 GTCCAAGGCTCTTTCGCTGCGAGAGAGCTTCCATCCAGGTGTCTGCAAGATTTATGGG 210  
Qy 41 IleThrLeuValSerIleValAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
Db 211 ATACCCCTTGAGCAAAAGCGCAACGAGCTGAATTCACAGAGCTTAAGAGGCC 270  
Qy 61 CysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

Db 271 TGTAGGCTGCTGGGACTAAAGTTTGGCGGCAAGCAAGTGAACAGCCTTTGAAAGCT 330  
Qy 81 SerPheGluThrCysSerTyrGlyTrrValGlyAspGlyPheValValIleSerArgIle 100  
Db 331 AGCTTTGCAACTTGCAGCTATGGCTGGGTGGGATGGATTCGTGGTTCATCTCTAGGATT 390  
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrLysValProVal 120  
Db 391 AGCCCAAAACCCCAAGTGTGGAAAAAATGGGTGGGTGCTCTGATTGGAAAGGTTCAGTG 450  
Qy 121 SerArgGlnPheAlaIleTrrCysTyrAsnSerSerAspThrTrrThrAsnSerCysIle 140  
Db 451 AGCCGACAGTTTGCAGCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTGCAATT 510  
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
Db 511 CCAGAAATTTATCACCAAGATCCCATATTCACACTCAAACTCAAACTGCAACACAAACA 570  
Qy 161 GluPheIleValSerAspSerThrTrrSerValAlaSerProTrrSerThrIleProAla 180  
Db 571 GAATTTATTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 630  
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
Db 631 CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 690  
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
Db 691 TGTGTACAGAAAGTTTTTATGGAAACTTAGCACCATGTCTACAGAAACTGAAACCATTTGTT 750  
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
Db 751 GAAATTAAGCAGCATTCAGAAATGAAGCTGCTGGGTGGAGGTGTCCCAACGGCTCTG 810  
Qy 241 LeuValLeuAlaLeuLeuPheGlyAlaAlaGlyLeuGlyPheCysTrrValLys 260  
Db 811 CTAGTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 870  
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
Db 871 AGGTATGTGAAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 930  
Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
Db 931 AAAGTAGTAAGGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 990  
Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
Db 991 GATAAAACCCAGAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAGT 1050  
Qy 321 GluVal 322  
Db 1051 GAAAGTT 1056  
RESULT 13  
US-09-724-864-28  
; Sequence 28, Application US/09724864  
; Patent No. 6380362  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Murison, James G.  
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
; by the polynucleotides and methods for their use.  
; FILE REFERENCE: 11000.105001  
; CURRENT APPLICATION NUMBER: US/09/724, 864  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 1896



; TYPE: DNA  
 ; ORGANISM: Mouse  
 US-09-724-864-28

**Alignment Scores:**

Pred. No.:	1.29e-118	Length:	1896
Score:	1103.00	Matches:	221
Percent Similarity:	79.18%	Conservative:	30
Best Local Similarity:	69.72%	Mismatches:	62
Query Match:	66.57%	Indels:	3
DB:	3	Gaps:	4

Qy	6	SerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeuValGlnGlySerLeu	25
Db	77	AGCCGTGGTGTACTCTCTCCGCTCTATTTTGGACCACTAGGCACCCAGTCGCAAGGTGCGGAC	136
Qy	26	ArgAlaGluLeuSerIleGlnValSerCysArgIleMetGlyIleThrLeuValSer	45
Db	137	CTCGTGCAGAGACCTTTCATTCTCT---ACATGCGAGAATCATGGCGTGTGCCCTTGTGGCG	193
Qy	46	LysLysAlaAsnGlnLeuAsnPheThrGluAlaLysGluAlaCysArgLeuLeuGly	65
Db	194	AGAAACAAAACCCACACATGAATTCACAGAACCCACAGGCGCTGTAAAGTGTCTGGGA	253
Qy	66	LeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAlaSerPheGluThrCys	85
Db	254	CTGACTCTGGCCAGCAGGACAGGTAGTAGTCAGCGCAGAAATCTGGCTTTTGAGACTTGC	313
Qy	86	SerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIleSerProAsnProLys	105
Db	314	AGCTATGATGGTGTGGAGACAGTTCTCTGTCATCCTCGGAATTTTCTCAAAACCCGAG	373
Qy	106	CysGlyLysAsnGlyValGlyValLeuIleTrpLysValProValSerArgGlnPheAla	125
Db	374	TGTGGGAAGATGGCAAGGTGTCTGATTTGGAAATGCTCCCTCCAGCCAAAGTTCAA	433
Qy	126	AlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIleProGluIleIleThr	145
Db	434	GCCTATTGCCACAACTCATCCGACACCTGGGTAACTCTCTGCATTCCAGAAATCGTTACC	493
Qy	146	ThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThrGluPheIleValSer	165
Db	494	ACATTTTACCCTGTGTGGCACTCAA-----ACACCCGCAACAGAGTTTCTGTGCAG	547
Qy	166	AspSerThrTyrSerValAlaSerProTyrSerThrIleProAlaProThrThrPro	185
Db	548	AGCAGCGCTACTTGGCTTTCATCCCTGACTCCACAAACCTGTCTGTGCCACACCC---	604
Qy	186	ProAlaProAlaSerThrSerIleProArgArgLysLysLeuIleCysValThrGluVal	205
Db	605	CGGGCTCCACCTTTACCTCCATGGCAGGAGAGAAAAAAGATTGTATCACGGAAGTT	664
Qy	206	PheMetGluThrSerThrMetSerThrGluThrGluProPheValGluAsnLysAlaAla	225
Db	665	TATACAGAAACCTATCACCATGGCTACAGAAACAGAAAGCATTTGTTGCAAGTGGAGCAG	724
Qy	226	PheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeuLeuValLeuAlaLeu	245
Db	725	TTCAAGAACGAGCAGCTGGGTTTGGAGGTGTCCCAACCCCTGCTGGTGGCTGCTCTC	784
Qy	246	LeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLysArgTyrValLysAla	265
Db	785	CTCTCTTTGGTGTGCGCTGTGCTGGCTGTTTGTCTACGTGAAAGGTATGTGAAGGCC	844
Qy	266	PheProPheThrAsnLysAsnGlnLysGluMetIleGluThrLysValValLysGlu	285
Db	845	TTCCCTTTTCCACCAACCAAGATCAACAGAAAGAAATGATCGAAACCAAGGTTGTTAAAGGA	904
Qy	286	GluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThrAspLysAsnProGlu	305
Db	905	GAGAAGGCTGATGAGCTCAACCGCTAATCAAGAAATCAAGAAAAACCATTTAAAAACCCAG	964



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Qy      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      279 TGTAGGTGCTNGGACTAAGTTTGGCCGCAAGGCCAGTTG---AACAGCTTGAAAGT- 334
Qy      81 SerPheGluThrCysSerTyrGlyTyrValGly----- 91
Db      335 AGCTTTGAAT-TGCAGTTTGGCTTGGTTGGGATGGTTCGNGNCATTTAGGTTAGCCCAA 393
Qy      92 -----AspGlyPheValValIleSerArgIleSerPro 102
Db      394 CCCATTTGGAAANTGGGTGGNCCNATTTGNAGTCCCTTAGCCCN 438
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Search completed: October 9, 2005, 01:24:57  
Job time : 281.474 secs

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Run on:      October 8, 2005, 16:25:15 ; Search time 672.622 Seconds
              (without alignments)
              2833.919 Million cell updates/sec

Title:       US-10-063-670-6
Perfect score: 1657
Sequence:    1 MARCFSLVLLTSLTWTRLL.....NPEESKSPKTVTCLEAEV 322
Scoring table: BLOSUM62
Searched:   4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 1500 summaries

1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

No.  Score  Match Length DB  ID  Description
RESULT 1
ID  AAF93818 standard; cDNA; 1755 BP.
DE  Human cDNA encoding a membrane or secretory protein clone PSEC0135.
PN  EP1067182-A2.
PD  10-JAN-2001.
PA  (HELI-) HELIX RES INST.
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 2
ID  ADE71449 standard; cDNA; 2027 BP.
DE  Human cDNA encoding PDEBC #2.
PN  US2003124543-A1.
PD  03-JUL-2003.
PA  (STUA/) STUART S G.
PA  (STRE/) STREETER D G.
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 3
ID  AAZ98172 standard; cDNA; 2029 BP.
DE  Human signal peptide containing protein HSPP-64 cDNA SEQ ID NO:198.
PN  WO20000610-A2.
PD  06-JAN-2000.
PA  (INCI-) INCYTE PHARM INC.
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 4
ID  ADE71445 standard; cDNA; 2029 BP.
DE  Human cDNA encoding PDEBC Incyte 3044710CB1.
PN  US2003124543-A1.
PD  03-JUL-2003.
PA  (STUA/) STUART S G.
PA  (STRE/) STREETER D G.
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 5
ID  ADR41319 standard; cDNA; 2369 BP.
DE  Human CD-like molecule HEMFC27 cDNA, SEQ ID NO:118.
PN  WO200226930-A2.
PD  04-APR-2002.
PA  (HUMA-) HUMAN GENOME SCI INC.

```

```

Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 6
ID  AAX52250 standard; DNA; 2372 BP.
DE  Protein PRO263 cDNA clone DNA34431-1171.
PN  WO9914328-A2.
PD  25-MAR-1999.
PA  (GETH) GENENTECH INC.
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 7
ID  ADC78520 standard; cDNA; 2372 BP.
DE  Human PRO263 cDNA.
PN  WO200015796-A2.
PD  23-MAR-2000.
PA  (GETH) GENENTECH INC.
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 8
ID  AAF72408 standard; cDNA; 2372 BP.
DE  Human PRO263 cDNA.
PN  WO200104311-A1.
PD  18-JAN-2001.
PA  (GETH) GENENTECH INC.
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 9
ID  AAF92060 standard; cDNA; 2372 BP.
DE  Human PRO263 cDNA.
PN  WO200116318-A2.
PD  08-MAR-2001.
PA  (GETH) GENENTECH INC.
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 10
ID  ABS74380 standard; cDNA; 2372 BP.
DE  Human cDNA encoding secreted/transmembrane protein PRO263.
PN  US2002119130-A1.
PD  29-AUG-2002.
PA  (GETH) GENENTECH INC.
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 11
ID  ABL80887 standard; cDNA; 2372 BP.
DE  Human PRO263 cDNA sequence SEQ ID NO:31.
PN  WO20020690-A2.
PD  03-JAN-2002.
PA  (GETH) GENENTECH INC.
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 12
ID  ABL95576 standard; cDNA; 2372 BP.
DE  Human angiogenesis related cDNA PRO263 SEQ ID NO: 31.
PN  WO200208284-A2.
PD  31-JAN-2002.
PA  (GETH) GENENTECH INC.
PA  (BAKE/) BAKER K P.
PA  (FERR/) FERRARA N.
PA  (GERB/) GERBER H.
PA  (GERR/) GERRITSEN M E.
PA  (GODD/) GODDARD A.
PA  (GODO/) GODOWSKI P J.
PA  (GURN/) GURNEY A L.
PA  (HILL/) HILLAN K J.
PA  (MARS/) MARSTERS S A.
PA  (PANJ/) PAN J.
PA  (PAON/) PAONI N F.
PA  (STEP/) STEPHAN J F.
PA  (WATA/) WATANABE C K.
PA  (WILL/) WILLIAMS P M.
PA  (WOOD/) WOOD W I.
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0

```

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RESULT 13
ID ACA60164 standard; cDNA; 2372 BP.
DE Human cDNA for secreted/transmembrane protein PRO263.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 14
ID ACD07564 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 15
ID ACA91166 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 16
ID ACD81543 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 17
ID ACA60365 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 18
ID ABX71612 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 19
ID ACH06944 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO263 cDNA.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 20
ID ACA58812 standard; cDNA; 2372 BP.
DE cDNA encoding human secreted polypeptide PRO263.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 21
ID ACA63988 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 22
ID ACA89291 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 23
ID ACD45151 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO263 cDNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 24
ID ABX96181 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #39.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 25
ID ACA05502 standard; cDNA; 2372 BP.
DE cDNA encoding human secreted protein PRO263.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 26
ID ACA93699 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 27
ID ACD20169 standard; cDNA; 2372 BP.
DE Human secreted / transmembrane polypeptide PRO263 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 28
ID ACA67273 standard; cDNA; 2372 BP.
DE cDNA encoding human secreted polypeptide PRO263.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 29
ID ACH66246 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 30
ID ACD02300 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 31
ID ACA89291 standard; cDNA; 2372 BP.
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DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US200303634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 32  
ID ACA6928 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 33  
ID ACA54972 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 34  
ID ACA98450 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 35  
ID ACA63375 standard; cDNA; 2372 BP.  
DE cDNA encoding human PRO polypeptide #3.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 36  
ID ACD19807 standard; cDNA; 2372 BP.  
DE Human secreted / transmembrane polypeptide PRO263 cDNA.  
PN US2003027143-A1.  
PD 08-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 37  
ID ADB29405 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003092002-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 38  
ID ADB17062 standard; cDNA; 2372 BP.  
DE Human cDNA clone (SeqID 5) encoding the transmembrane PRO protein.  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 39  
ID ACH03578 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane polypeptide PRO 263 cDNA.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 40  
ID ADA18261 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.

PN US2003039971-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 41  
ID ACD66954 standard; cDNA; 2372 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO263.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 42  
ID ADA19867 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 43  
ID ADB17250 standard; cDNA; 2372 BP.  
DE Human cDNA clone (SeqID 5) encoding the transmembrane PRO protein.  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 44  
ID ACD83115 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #36.  
PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 45  
ID ADA16236 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 46  
ID ADA20039 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 47  
ID ACD82092 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane polypeptide PRO 263 cDNA.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 48  
ID ADA42381 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003054401-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 49  
ID ACD23293 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #36.  
PN US2003064367-A1.

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PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 50
ID ADA00336 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO 263 cDNA.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 51
ID ADA16660 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 52
ID ADA13089 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 53
ID ADA41957 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 54
ID ADA17304 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 55
ID ADA42807 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 56
ID ACD23655 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #36.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 57
ID ADB85578 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 58
ID ABB77726 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 59
ID ADB74862 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 60
ID ADB68257 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 61
ID ADB68064 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 62
ID ADB90881 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 63
ID ADC28508 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 64
ID ADC39708 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 65
ID ADC40222 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 66
ID ADC19046 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 67
ID ADC34346 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 68
ID ADC29401 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 69
ID ADC28932 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 70
ID ADC40817 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 71
ID ADC19474 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 72
ID ADC06961 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 73
ID ADC17140 standard; cDNA; 2372 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 5).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 74
ID ADC33922 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 75
ID ADC12992 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 76
ID ADC14838 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 77
ID ADC52333 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 78
ID ADC12444 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 79
ID ADD10320 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 80
ID ADD11280 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 81
ID ADD04005 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 82
ID ADD03581 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 83
ID ADD37073 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 84
ID ADD36009 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 85
ID ADE34833 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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RESULT 86  
ID ADG01010 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 87  
ID ADG08563 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 88  
ID ADG08563 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 89  
ID ADH24037 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 90  
ID ADH34063 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 91  
ID ADH29896 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 92  
ID ADH23867 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 93  
ID ADG85271 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 94  
ID ADH24547 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 95

ID ADH37403 standard; cDNA; 2372 BP.  
DE Human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 96  
ID ADH01992 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 97  
ID ADH37573 standard; cDNA; 2372 BP.  
DE Human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 98  
ID ADG85611 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 99  
ID ADH24207 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 100  
ID ADH38501 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 101  
ID ADG83622 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 102  
ID ADH29430 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 103  
ID ADH27546 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 104  
ID ADH37743 standard; cDNA; 2372 BP.

DE Human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 105  
ID ADH37920 standard; cDNA; 2372 BP.  
DE Human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 106  
ID ADH57340 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 107  
ID ADH59316 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003039972-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 108  
ID ADH53482 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 109  
ID ADH53652 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 110  
ID ADH51988 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 111  
ID ADH49843 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 112  
ID ADI25353 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 113  
ID ADH90146 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.

PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 114  
ID ADI25523 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 115  
ID ADH97697 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 116  
ID ADI38095 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 117  
ID ADI03545 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 118  
ID ADI11902 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 119  
ID ADH89976 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 120  
ID ADH98377 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 121  
ID ADI11052 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 122  
ID ADI11562 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003181684-A1.

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PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 123
ID ADH98207 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 124
ID ADH98547 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 125
ID ADH98037 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 126
ID ACA59060 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #36.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 127
ID ACA58457 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 128
ID ADI05025 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 129
ID ADI03375 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 130
ID ADI04770 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 131
ID ADH78224 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 132
ID ADI19568 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 133
ID ADH90316 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 134
ID ADI03035 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 135
ID ADH77884 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 136
ID ADH97867 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 137
ID ADI01252 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 138
ID ADI01947 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 139
ID ADI03205 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 140
ID ADI11392 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 141  
ID ADI02294 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 142  
ID ADI11732 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 143  
ID ADI05369 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 144  
ID ADH79441 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 145  
ID ADI19398 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 146  
ID ADI05199 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 147  
ID ADH79611 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 148  
ID ADI01437 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 149  
ID ADI01607 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
RESULT 150  
ID ADI01777 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 151  
ID ADH79781 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 152  
ID ADI04599 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 153  
ID ADI02735 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 154  
ID ADH78054 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 155  
ID ADI25863 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 156  
ID ADI25863 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 157  
ID ADK65375 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 158  
ID ADH98717 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0

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RESULT 159
ID ADE79958 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 160
ID ADJ26363 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 161
ID ADJ93689 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 162
ID ADC52143 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 163
ID ADE79278 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 164
ID ADE79702 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 165
ID ADE73378 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 166
ID ADE41281 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 167
ID ADE73913 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 168
ID ADE99467 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 169
ID ADE98586 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 170
ID ADE99013 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 171
ID ADG40483 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN ) DESNOYERS L.
PA (GODD ) GODDARD A.
PA (GODO ) GODOWSKI P J.
PA (GURN ) GURNEY A L.
PA (MATH ) MATHER J P.
PA (WILL ) WILLIAMS P M.
PA (WOOD ) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 172
ID ADF73877 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 173
ID ADF73453 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 174
ID ADH06575 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 175
ID ADH06405 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 176
ID ADG68826 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180855-A1.
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PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 177
ID ADH27716 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 178
ID ADH25057 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 179
ID ADH33689 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 180
ID ADG92296 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 181
ID ADH02332 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 182
ID ADH07939 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 183
ID ADG69336 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 184
ID ADH39157 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 185
ID ADG92723 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 186
ID ADG83897 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 187
ID ADG85441 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 188
ID ADH06235 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 189
ID ADH30231 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 190
ID ADH24377 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 191
ID ADG69506 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 192
ID ADH07769 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 193
ID ADG85781 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 194
ID ADH39327 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
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RESULT 213
ID ADH43464 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #16.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 214
ID ADH07367 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 215
ID ADH52158 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 216
ID ADH59912 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 217
ID ADH49524 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 218
ID ADH06940 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 219
ID ADH90486 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 220
ID ADI11222 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 221
ID ADI18682 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 222
ID ADH98887 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 223
ID ADI02117 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 224
ID ADH90656 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 225
ID ADI37665 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 226
ID ADH97461 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 227
ID ADI65829 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 228
ID ADH60572 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

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RESULT 229	ID	ADJ99629 standard; cDNA; 2372 BP.
	DE	Human secreted/transmembrane protein cDNA, #40.
	PN	US2003187238-A1.
	PD	02-OCT-2003.
	PA	(GETH ) GENENTECH INC.
	Best Local Similarity:	100.00%
	Query Match:	Mismatches: 0 Indels: 0
RESULT 230	ID	ADL08822 standard; cDNA; 2372 BP.
	DE	Human secreted/transmembrane protein cDNA, #40.
	PN	US2003186358-A1.
	PD	02-OCT-2003.
	PA	(GETH ) GENENTECH INC.
	Best Local Similarity:	100.00%
	Query Match:	Mismatches: 0 Indels: 0
RESULT 231	ID	ADU98531 standard; cDNA; 2372 BP.
	DE	Novel human secreted and transmembrane protein PRO263 cDNA.
	PN	US2003187197-A1.
	PD	02-OCT-2003.
	PA	(GETH ) GENENTECH INC.
	Best Local Similarity:	100.00%
	Query Match:	Mismatches: 0 Indels: 0
RESULT 232	ID	ADU98701 standard; cDNA; 2372 BP.
	DE	Novel human secreted and transmembrane protein PRO263 cDNA.
	PN	US2003187228-A1.
	PD	02-OCT-2003.
	PA	(GETH ) GENENTECH INC.
	Best Local Similarity:	100.00%
	Query Match:	Mismatches: 0 Indels: 0
RESULT 233	ID	ADH78860 standard; cDNA; 2372 BP.
	DE	Novel human secreted and transmembrane protein PRO263 cDNA.
	PN	US2003181703-A1.
	PD	25-SEP-2003.
	PA	(GETH ) GENENTECH INC.
	Best Local Similarity:	100.00%
	Query Match:	Mismatches: 0 Indels: 0
RESULT 234	ID	ADJ99094 standard; cDNA; 2372 BP.
	DE	Novel human secreted and transmembrane protein PRO263 cDNA.
	PN	US2003186408-A1.
	PD	02-OCT-2003.
	PA	(GETH ) GENENTECH INC.
	Best Local Similarity:	100.00%
	Query Match:	Mismatches: 0 Indels: 0
RESULT 235	ID	ADJ99264 standard; cDNA; 2372 BP.
	DE	Novel human secreted and transmembrane protein PRO263 cDNA.
	PN	US2003187196-A1.
	PD	02-OCT-2003.
	PA	(GETH ) GENENTECH INC.
	Best Local Similarity:	100.00%
	Query Match:	Mismatches: 0 Indels: 0
RESULT 236	ID	ADU98882 standard; cDNA; 2372 BP.
	DE	Novel human secreted and transmembrane protein PRO263 cDNA.
	PN	US2003187242-A1.
	PD	02-OCT-2003.
	PA	(GETH ) GENENTECH INC.
	Best Local Similarity:	100.00%
	Query Match:	Mismatches: 0 Indels: 0
RESULT 237	ID	ADH79030 standard; cDNA; 2372 BP.
	DE	Novel human secreted and transmembrane protein PRO263 cDNA.
	PN	US2003181702-A1.
	PD	25-SEP-2003.
	PA	(GETH ) GENENTECH INC.
	Best Local Similarity:	100.00%
	Query Match:	Mismatches: 0 Indels: 0
RESULT 238	ID	ADK0890 standard; cDNA; 2372 BP.
	DE	Human PRO polynucleotide #3.
	PN	US2003186407-A1.
	PD	02-OCT-2003.
	PA	(GETH ) GENENTECH INC.
	Best Local Similarity:	100.00%
	Query Match:	Mismatches: 0 Indels: 0
RESULT 239	ID	ADK14411 standard; cDNA; 2372 BP.
	DE	Novel human secreted and transmembrane protein PRO263 cDNA.
	PN	US2003187229-A1.
	PD	02-OCT-2003.
	PA	(GETH ) GENENTECH INC.
	Best Local Similarity:	100.00%
	Query Match:	Mismatches: 0 Indels: 0
RESULT 240	ID	ADM25163 standard; cDNA; 2372 BP.
	DE	Human secreted/transmembrane protein cDNA, #40.
	PN	US2003096233-A1.
	PD	22-MAY-2003.
	PA	(GETH ) GENENTECH INC.
	Best Local Similarity:	100.00%
	Query Match:	Mismatches: 0 Indels: 0
RESULT 241	ID	ADM29913 standard; cDNA; 2372 BP.
	DE	Human secreted/transmembrane protein cDNA, #40.
	PN	US2003190611-A1.
	PD	09-OCT-2003.
	PA	(GETH ) GENENTECH INC.
	Best Local Similarity:	100.00%
	Query Match:	Mismatches: 0 Indels: 0
RESULT 242	ID	ADK82809 standard; cDNA; 2372 BP.
	DE	Human PRO polynucleotide #16.
	PN	US2004043927-A1.
	PD	04-MAR-2004.
	PA	(GETH ) GENENTECH INC.
	Best Local Similarity:	100.00%
	Query Match:	Mismatches: 0 Indels: 0
RESULT 243	ID	ADM80860 standard; cDNA; 2372 BP.
	DE	Human PRO polynucleotide #3.
	PN	US2004058411-A1.
	PD	25-MAR-2004.
	PA	(GETH ) GENENTECH INC.
	Best Local Similarity:	100.00%
	Query Match:	Mismatches: 0 Indels: 0
RESULT 244	ID	ADO62335 standard; cDNA; 2372 BP.
	DE	Human PRO polynucleotide #38.
	PN	US6686451-B1.
	PD	03-FEB-2004.
	PA	(GETH ) GENENTECH INC.
	Best Local Similarity:	100.00%
	Query Match:	Mismatches: 0 Indels: 0
RESULT 245	ID	AD811087 standard; cDNA; 2372 BP.
	DE	Human secreted/transmembrane protein cDNA, #40.
	PN	US2004137561-A1.
	PD	15-JUL-2004.
	PA	(GETH ) GENENTECH INC.
	Best Local Similarity:	100.00%
	Query Match:	Mismatches: 0 Indels: 0
RESULT 246	ID	ADRI7996 standard; cDNA; 2372 BP.
	DE	Human secreted/transmembrane protein cDNA, #40.
	PN	US2004147017-A1.
	PD	29-JUL-2004.
	PA	(ASHK/) ASHKENAZI A.
	PA	(BOTS/) BOTSTEIN D.
	PA	(DESN/) DESNOYERS L.
	PA	(EATO/) EATON D L.
	PA	(FERR/) FERRARA N.

PA (FILV/) FILVAROFF E.  
 PA (FONG/) FONG S.  
 PA (GAOW/) GAO W.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GRIM/) GRIMALDI C J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (KLJA/) KLJAVIN I J.  
 PA (MATH/) MATHER J P.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (ROYM/) ROY M A.  
 PA (STEW/) STEWART T A.  
 PA (TUMA/) TUMAS D.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 RESULT 247  
 ID ADT03672 standard; cDNA; 2372 BP.  
 DE Human secreted/transmembrane protein cDNA, #40.  
 PN US2003152922-A1.  
 PD 14-AUG-2003.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 RESULT 248  
 ID ADS74635 standard; cDNA; 2372 BP.  
 DE Human secreted/transmembrane cDNA #40.  
 PN US2004185531-A1.  
 PD 23-SEP-2004.  
 PA (ASHK/) ASHKENAZI A.  
 PA (BOTS/) BOTSTEIN D.  
 PA (DESN/) DESNOYERS L.  
 PA (EATO/) EATON D L.  
 PA (FERR/) FERRARA N.  
 PA (FILV/) FILVAROFF E.  
 PA (FONG/) FONG S.  
 PA (GAOW/) GAO W.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GRIM/) GRIMALDI C J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (KLJA/) KLJAVIN I J.  
 PA (MATH/) MATHER J P.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (ROYM/) ROY M A.  
 PA (STEW/) STEWART T A.  
 PA (TUMA/) TUMAS D.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 RESULT 249  
 ID ADQ25003 standard; DNA; 2667 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7823.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 RESULT 250  
 ID ABA09223 standard; cDNA; 2324 BP.  
 DE Human PRO263 homologue-encoding cDNA, SEQ ID NO:999.  
 PN WO200157188-A2.  
 PD 09-AUG-2001.

PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 99.69% Mismatches: 0  
 Query Match: 99.82% Indels: 0  
 RESULT 251  
 ID AAV22687 standard; DNA; 2313 BP.  
 DE DNA encoding a CD44-like protein.  
 PN WO9808839-A1.  
 PD 19-FEB-1998.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 99.69% Mismatches: 1  
 Query Match: 99.64% Indels: 0  
 RESULT 252  
 ID ABL90698 standard; cDNA; 2369 BP.  
 DE Human polynucleotide SEQ ID NO 1260.  
 PN WO200190304-A2.  
 PD 29-NOV-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 99.69% Mismatches: 1  
 Query Match: 99.64% Indels: 0  
 RESULT 253  
 ID ADP65684 standard; DNA; 2313 BP.  
 DE Human extracellular link domain containing 1 (XLKD1) DNA.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Best Local Similarity: 99.07% Mismatches: 2  
 Query Match: 98.85% Indels: 0  
 RESULT 254  
 ID ADM67137 standard; DNA; 2313 BP.  
 DE Human homologue of murine adipocyte specific DNA SeqID 273.  
 PN WO2004011618-A2.  
 PD 05-FEB-2004.  
 PA (HMGE-) HMGNE INC.  
 Best Local Similarity: 99.07% Mismatches: 2  
 Query Match: 98.85% Indels: 0  
 RESULT 255  
 ID ADN05865 standard; cDNA; 2313 BP.  
 DE Antiposoriatic cDNA sequence #1164.  
 PN WO2004028479-A2.  
 PD 08-APR-2004.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 99.07% Mismatches: 2  
 Query Match: 98.85% Indels: 0  
 RESULT 256  
 ID ADQ21088 standard; DNA; 2313 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3908.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Best Local Similarity: 99.07% Mismatches: 2  
 Query Match: 98.85% Indels: 0  
 RESULT 257  
 ID AAC59803 standard; DNA; 2967 BP.  
 DE Human secreted protein encoding DNA clone vb28 1.  
 PN WO200055375-A1.  
 PD 21-SEP-2000.  
 PA (ALPH-) ALPHAGENE INC.  
 Best Local Similarity: 61.69% Mismatches: 0  
 Query Match: 93.36% Indels: 200  
 RESULT 258  
 ID ADD04999 standard; cDNA; 1680 BP.  
 DE Human secreted/transmembrane protein cDNA, #40.  
 PN US2003104469-A1.  
 PD 05-JUN-2003.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 93.79% Mismatches: 0  
 Query Match: 92.40% Indels: 20  
 RESULT 259  
 ID ACA10111 standard; cDNA; 1127 BP.  
 DE Human NOVX polynucleotide #1.  
 PN WO200290504-A2.  
 PD 14-NOV-2002.  
 PA (CURA-) CURAGEN CORP.

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Best Local Similarity: 92.24% Mismatches: 0
Query Match: 91.22% Indels: 25
RESULT 260
ID ADO08254 standard; cDNA; 1127 BP.
DE Human NOVX polynucleotide #1.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATI/) PATTURAJAN M.
PA (PENA/) PENNA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VOSS/) VOSS E Z.
PA (ZERR/) ZERHUSEN B D.
Best Local Similarity: 92.24% Mismatches: 0
Query Match: 91.22% Indels: 25
RESULT 261
ID AAD10132 standard; cDNA; 1896 BP.
DE Mouse lymphatic endothelium-specific hyaluronan receptor LYVE-1 cDNA.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Best Local Similarity: 69.72% Mismatches: 62
Query Match: 66.57% Indels: 4
RESULT 262
ID ABL35066 standard; cDNA; 1896 BP.
DE Murine cDNA isolated from skin cells SEQ ID NO: 595.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Best Local Similarity: 69.72% Mismatches: 62
Query Match: 66.57% Indels: 4
RESULT 263
ID ADM67136 standard; DNA; 1516 BP.
DE Murine adipocyte specific DNA SeqID 272.
PN WO200401618-A2.
PD 05-FEB-2004.
PA (HMG-) HMGNE INC.
Best Local Similarity: 69.09% Mismatches: 64
Query Match: 66.08% Indels: 4
RESULT 264
ID ABT09892 standard; cDNA; 596 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 26.
PN WO200259271-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 97.88% Mismatches: 4
Query Match: 54.38% Indels: 3
RESULT 265
ID AAF94017 standard; DNA; 716 BP.
DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 451.

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PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Best Local Similarity: 94.77% Mismatches: 6
Query Match: 48.46% Indels: 3
RESULT 266
ID ACH20895 standard; cDNA; 411 BP.
DE Human adult liver cDNA #507.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 40.62% Indels: 0
RESULT 267
ID ADE71446 standard; cDNA; 559 BP.
DE Rat cDNA encoding PDEBC variant Incyte 702127782H1.
PN US2003124543-A1.
PD 03-JUL-2003.
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
Best Local Similarity: 69.57% Mismatches: 40
Query Match: 35.94% Indels: 7
RESULT 268
ID AAX41156 standard; cDNA; 451 BP.
DE Human secreted protein 5' EST SEQ ID NO:100.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST ) GENSET.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 35.73% Indels: 0
RESULT 269
ID ACH22904 standard; cDNA; 486 BP.
DE Human adult ovary cDNA #1284.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.55% Indels: 0
RESULT 270
ID ADE71447 standard; cDNA; 279 BP.
DE Rat cDNA encoding PDEBC variant Incyte 701647942H1.
PN US2003124543-A1.
PD 03-JUL-2003.
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
Best Local Similarity: 87.64% Mismatches: 10
Query Match: 23.30% Indels: 0
RESULT 271
ID ABA54110 standard; DNA; 469 BP.
DE Human foetal liver single exon nucleic acid probe #2415.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 98.41% Mismatches: 0
Query Match: 18.47% Indels: 1
RESULT 272
ID AAI33763 standard; DNA; 469 BP.
DE Probe #2449 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 98.41% Mismatches: 0
Query Match: 18.47% Indels: 1
RESULT 273
ID ABA23859 standard; DNA; 469 BP.

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DE Probe #2325 for gene expression analysis in human heart cell sample.  
 PN WO200157274-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 98.41% Mismatches: 0  
 Query Match: 18.47% Indels: 1  
 RESULT 274  
 ID AAK27829 standard; DNA; 469 BP.  
 DE Human bone marrow expressed single exon probe SEQ ID NO: 2386.  
 PN WO200157276-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 98.41% Mismatches: 0  
 Query Match: 18.47% Indels: 1  
 RESULT 275  
 ID ABS27409 standard; DNA; 469 BP.  
 DE Human liver single exon probe, SEQ ID No 2399.  
 PN WO200157273-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 98.41% Mismatches: 0  
 Query Match: 18.47% Indels: 1  
 RESULT 276  
 ID ABS02280 standard; DNA; 469 BP.  
 DE Human genome-derived single exon probe from lung SEQ ID No 2271.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 98.41% Mismatches: 0  
 Query Match: 18.47% Indels: 1  
 RESULT 277  
 ID AAX41003 standard; cDNA; 363 BP.  
 DE Human secreted protein 5', EST SEQ ID NO: 215.  
 PN WO9906554-A2.  
 PD 11-FEB-1999.  
 PA (GEST) GENSET.  
 Best Local Similarity: 91.30% Mismatches: 5  
 Query Match: 17.20% Indels: 1  
 RESULT 278  
 ID AAI33382 standard; DNA; 457 BP.  
 DE Probe #2068 used to measure gene expression in human placenta sample.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 84.51% Mismatches: 3  
 Query Match: 16.99% Indels: 7  
 RESULT 279  
 ID ABS01959 standard; DNA; 457 BP.  
 DE Human genome-derived single exon probe from lung SEQ ID No 1950.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 84.51% Mismatches: 3  
 Query Match: 16.99% Indels: 7  
 RESULT 280  
 ID AAX51631 standard; cDNA; 373 BP.  
 DE Human secreted protein 5', EST SEQ ID NO:210.  
 PN WO9906549-A2.  
 PD 11-FEB-1999.  
 PA (GEST) GENSET.  
 Best Local Similarity: 98.28% Mismatches: 1  
 Query Match: 16.72% Indels: 0  
 RESULT 281  
 ID AAQ06236 standard; DNA; 1537 BP.  
 DE B7 adhesion receptor cDNA clone.  
 PN WO9011365-A.  
 PD 04-OCT-1990.  
 PA (HUTC-) HUTCHINSON F CANCER.  
 Best Local Similarity: 28.01% Mismatches: 109  
 Query Match: 14.15% Indels: 111  
 RESULT 282  
 ID ABN86523 standard; cDNA; 1089 BP.  
 DE Nucleotide sequence of hamster CD44 cDNA.

PN WO200238794-A2.  
 PD 16-MAY-2002.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
 Best Local Similarity: 26.30% Mismatches: 147  
 Query Match: 14.09% Indels: 63  
 RESULT 283  
 ID ABN86507 standard; cDNA; 2747 BP.  
 DE Rat glycoprotein CD44 polypeptide encoding cDNA.  
 PN WO200238794-A2.  
 PD 16-MAY-2002.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
 Best Local Similarity: 23.92% Mismatches: 158  
 Query Match: 13.94% Indels: 66  
 RESULT 284  
 ID ABK63681 standard; cDNA; 2747 BP.  
 DE Rat sequence differentially expressed in response to a hepatotoxin #1588.  
 PN WO200210453-A2.  
 PD 07-FEB-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Best Local Similarity: 23.92% Mismatches: 158  
 Query Match: 13.94% Indels: 66  
 RESULT 285  
 ID ABN86522 standard; cDNA; 1177 BP.  
 DE Nucleotide sequence of mouse CD44 cDNA.  
 PN WO200238794-A2.  
 PD 16-MAY-2002.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
 Best Local Similarity: 24.93% Mismatches: 148  
 Query Match: 13.85% Indels: 63  
 RESULT 286  
 ID AAQ14263 standard; cDNA; 3207 BP.  
 DE p-meta-1 metastasis-specific variant of CD44 glycoprotein.  
 PN DE4014510-A.  
 PD 14-NOV-1991.  
 PA (GESL) KERNFORSCHUNGSZENT KARLSRUHE.  
 PA (UYKA-) UNIV KARLSRUHE.  
 PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENT.  
 Best Local Similarity: 25.22% Mismatches: 171  
 Query Match: 13.52% Indels: 44  
 RESULT 287  
 ID AB235325 standard; cDNA; 1992 BP.  
 DE Human gene expression profile polynucleotide SEQ ID NO 436.  
 PN WO200274979-A2.  
 PD 26-SEP-2002.  
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
 Best Local Similarity: 26.28% Mismatches: 134  
 Query Match: 13.46% Indels: 67  
 RESULT 288  
 ID ABA66678 standard; DNA; 141 BP.  
 DE Human foetal liver single exon nucleic acid probe #14983.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 97.87% Mismatches: 0  
 Query Match: 13.40% Indels: 1  
 RESULT 289  
 ID AAI46891 standard; DNA; 141 BP.  
 DE Probe #15577 used to measure gene expression in human placenta sample.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 97.87% Mismatches: 0  
 Query Match: 13.40% Indels: 1  
 RESULT 290  
 ID ABA33740 standard; DNA; 141 BP.  
 DE Probe #12206 for gene expression analysis in human heart cell sample.  
 PN WO200157274-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 97.87% Mismatches: 0  
 Query Match: 13.40% Indels: 1  
 RESULT 291

ID AAK40837 standard; DNA; 141 BP.  
DE Human bone marrow expressed single exon probe SEQ ID NO: 15394.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 97.87% Mismatches: 0  
Query Match: 13.40% Indels: 1  
RESULT 292  
ID AAS40414 standard; DNA; 141 BP.  
DE Human liver single exon probe, SEQ ID No 15404.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 97.87% Mismatches: 0  
Query Match: 13.40% Indels: 1  
RESULT 293  
ID ABS14788 standard; DNA; 141 BP.  
DE Human genome-derived single exon probe ORF from lung SEQ ID No 14779.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 97.87% Mismatches: 0  
Query Match: 13.40% Indels: 1  
RESULT 294  
ID AAQ21185 standard; DNA; 1354 BP.  
DE Clone CD44.5 coding for haematopoietic CD44 Antigen.  
PN WO9201049-A.  
PD 23-JAN-1992.  
PA (GEHO) GEN HOSPITAL CORP.  
Best Local Similarity: 26.79% Mismatches: 125  
Query Match: 12.98% Indels: 78  
RESULT 295  
ID AAT14724 standard; cDNA; 1354 BP.  
DE Human haematopoietic CD44 cDNA clone CD44.5.  
PN USS506126-A.  
PD 09-APR-1996.  
PA (GEHO) GEN HOSPITAL CORP.  
Best Local Similarity: 26.79% Mismatches: 125  
Query Match: 12.98% Indels: 78  
RESULT 296  
ID AAV63461 standard; cDNA; 1354 BP.  
DE Human CD44 antigen cDNA.  
PN US5830731-A.  
PD 03-NOV-1998.  
PA (GEHO) GEN HOSPITAL CORP.  
Best Local Similarity: 26.79% Mismatches: 125  
Query Match: 12.98% Indels: 78  
RESULT 297  
ID AAV81218 standard; cDNA; 1354 BP.  
DE Human CD44 antigen cDNA.  
PN US5849898-A.  
PD 15-DEC-1998.  
PA (GEHO) GEN HOSPITAL CORP.  
Best Local Similarity: 26.79% Mismatches: 125  
Query Match: 12.98% Indels: 78  
RESULT 298  
ID AA50597 standard; cDNA; 1354 BP.  
DE Human haematopoietic CD44.5 cDNA.  
PN US6111093-A.  
PD 29-AUG-2000.  
PA (GEHO) GEN HOSPITAL CORP.  
Best Local Similarity: 26.79% Mismatches: 125  
Query Match: 12.98% Indels: 78  
RESULT 299  
ID AAS03191 standard; cDNA; 1354 BP.  
DE Human haematopoietic antigen CD44 cDNA sequence.  
PN US6218525-B1.  
PD 17-APR-2001.  
PA (GEHO) GEN HOSPITAL CORP.  
Best Local Similarity: 26.79% Mismatches: 125  
Query Match: 12.98% Indels: 78  
RESULT 300  
ID ADO49372 standard; cDNA; 1354 BP.

DE Human CD44 cDNA #1.  
PN US2004072283-A1.  
PD 15-APR-2004.  
PA (SEED/) SEED B.  
PA (ALLE/) ALLEN J.  
PA (ARUF/) ARUFFO A.  
PA (CAME/) CAMERINI D.  
PA (LAUF/) LAUFFER L.  
PA (OQUE/) OQUENDO C.  
PA (SIMM/) SIMMONS D.  
PA (STAM/) STAMENKOVIC I.  
PA (STEN/) STENGELIN S.  
PA (AMIO/) AMIOT M.  
Best Local Similarity: 26.79% Mismatches: 125  
Query Match: 12.98% Indels: 78  
RESULT 301  
ID AA52811 standard; cDNA; 1794 BP.  
DE Human CD44 cDNA.  
PN WO200035935-A1.  
PD 22-JUN-2000.  
PA (ISIS-) ISIS PHARM INC.  
Best Local Similarity: 26.79% Mismatches: 126  
Query Match: 12.85% Indels: 78  
RESULT 302  
ID ABV94385 standard; cDNA; 1794 BP.  
DE Breast carcinoma related nucleotide sequence SEQ ID NO:376.  
PN WO200246467-A2.  
PD 13-JUN-2002.  
PA (IPSO-) IPSOGEN.  
Best Local Similarity: 26.79% Mismatches: 126  
Query Match: 12.85% Indels: 78  
RESULT 303  
ID ABK84043 standard; cDNA; 1794 BP.  
DE Human cDNA differentially expressed in granulocytic cells #614.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 26.79% Mismatches: 126  
Query Match: 12.85% Indels: 78  
RESULT 304  
ID ADQ38557 standard; DNA; 4335 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 220.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 26.79% Mismatches: 126  
Query Match: 12.85% Indels: 78  
RESULT 305  
ID ADD90591 standard; cDNA; 1083 BP.  
DE Human CD44std glycoprotein encoding cDNA SEQ ID NO:1.  
PN WO2003072606-A2.  
PD 04-SEP-2003.  
PA (YEDA) YEDA RES & DEV CO LTD.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
Best Local Similarity: 26.79% Mismatches: 126  
Query Match: 12.79% Indels: 78  
RESULT 306  
ID AAD48131 standard; DNA; 1807 BP.  
DE Human CD44 antigen encoding DNA.  
PN WO200276510-A1.  
PD 03-OCT-2002.  
PA (AGYT-) AGY THERAPEUTICS INC.  
Best Local Similarity: 26.79% Mismatches: 126  
Query Match: 12.79% Indels: 78  
RESULT 307  
ID ADH18929 standard; cDNA; 1874 BP.  
DE Human cell adhesion and extracellular matrix CADECM-25 cDNA - SEQ 56.  
PN WO2003094843-A2.  
PD 20-NOV-2003.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 27.41% Mismatches: 116  
Query Match: 12.79% Indels: 78  
RESULT 308

ID ADJ56374 standard; cDNA; 1981 BP.  
 DE Human cDNA differentially expressed in MYCN activated cells SeqID 180.  
 PN US2003119009-A1.  
 PD 26-JUN-2003.  
 PA (STUA/) STUART S G.  
 PA (NUCH/) NUCHTERN J G.  
 PA (PLON/) PLON S E.  
 PA (SHOH/) SHOHET J M.  
 Best Local Similarity: 26.79% Mismatches: 126  
 Query Match: 12.79% Indels: 78  
 RESULT 309  
 ID ADE25668 standard; cDNA; 4365 BP.  
 DE Human cDNA differentially expressed in foam cells #72.  
 PN US2003194721-A1.  
 PD 16-OCT-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 26.79% Mismatches: 126  
 Query Match: 12.79% Indels: 78  
 RESULT 310  
 ID ADP10572 standard; DNA; 4633 BP.  
 DE Reference mRNA sequences for marker probe #249.  
 PN WO2004042346-A2.  
 PD 21-MAY-2004.  
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
 Best Local Similarity: 26.79% Mismatches: 126  
 Query Match: 12.79% Indels: 78  
 RESULT 311  
 ID ADL61887 standard; DNA; 5165 BP.  
 DE Human ovarian cancer DNA marker #20099.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Best Local Similarity: 26.79% Mismatches: 126  
 Query Match: 12.79% Indels: 78  
 RESULT 312  
 ID ABN86521 standard; cDNA; 1297 BP.  
 DE Nucleotide sequence of human CD44 cDNA.  
 PN WO200238794-A2.  
 PD 16-MAY-2002.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
 Best Local Similarity: 26.79% Mismatches: 126  
 Query Match: 12.67% Indels: 78  
 RESULT 313  
 ID ADI31550 standard; cDNA; 1297 BP.  
 DE Human cDNA #876.  
 PN US6607879-B1.  
 PD 19-AUG-2003.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 26.79% Mismatches: 126  
 Query Match: 12.67% Indels: 78  
 RESULT 314  
 ID ADQ38556 standard; DNA; 5452 BP.  
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 219.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Best Local Similarity: 29.29% Mismatches: 96  
 Query Match: 12.64% Indels: 17  
 RESULT 315  
 ID ADP65670 standard; DNA; 3091 BP.  
 DE Human mRNA for transmembrane glycoprotein (CD44 gene) DNA.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Best Local Similarity: 23.22% Mismatches: 110  
 Query Match: 12.40% Indels: 96  
 RESULT 316  
 ID ADP65087 standard; DNA; 3091 BP.  
 DE Human CD44 antigen (homing function and Indian blood group DNA sequence.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Best Local Similarity: 23.22% Mismatches: 110

Query Match: 12.40% Indels: 96  
 RESULT 317  
 ID ADR67138 standard; DNA; 3091 BP.  
 DE Human bladder cancer associated nucleotide sequence.  
 PN WO2004076613-A2.  
 PD 10-SEP-2004.  
 PA (HERR/) HERR A.  
 PA (HINZ/) HINZMANN B.  
 PA (DAHL/) DAHL E.  
 PA (STAU/) STAUB E.  
 PA (PILA/) PILARSKY C.  
 PA (SPEC/) SPECHT T.  
 Best Local Similarity: 23.22% Mismatches: 110  
 Query Match: 12.40% Indels: 96  
 RESULT 318  
 ID ADQ38561 standard; DNA; 4633 BP.  
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 224.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Best Local Similarity: 25.21% Mismatches: 123  
 Query Match: 12.40% Indels: 100  
 RESULT 319  
 ID ADQ38554 standard; DNA; 4723 BP.  
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 217.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Best Local Similarity: 23.74% Mismatches: 120  
 Query Match: 12.37% Indels: 134  
 RESULT 320  
 ID ACN39193 standard; cDNA; 3083 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA325446, SEQ ID NO:3187.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 23.22% Mismatches: 110  
 Query Match: 12.34% Indels: 96  
 RESULT 321  
 ID AAA91130 standard; DNA; 1483 BP.  
 DE CD44Hextra/tmfascyto coding sequence.  
 PN WO200100854-A2.  
 PD 04-JAN-2001.  
 PA (ANGI-) ANGIOGENE PHARM LTD.  
 Best Local Similarity: 25.38% Mismatches: 130  
 Query Match: 12.25% Indels: 78  
 RESULT 322  
 ID ADQ38563 standard; DNA; 3091 BP.  
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 226.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Best Local Similarity: 22.25% Mismatches: 129  
 Query Match: 12.25% Indels: 92  
 RESULT 323  
 ID ADQ38562 standard; DNA; 5468 BP.  
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 225.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Best Local Similarity: 22.78% Mismatches: 130  
 Query Match: 12.25% Indels: 84  
 RESULT 324  
 ID ADQ38555 standard; DNA; 5674 BP.  
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 218.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Best Local Similarity: 22.25% Mismatches: 129  
 Query Match: 12.25% Indels: 92  
 RESULT 325  
 ID ADQ38558 standard; DNA; 5739 BP.  
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 221.

PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Best Local Similarity: 22.25% Mismatches: 129  
 Query Match: 12.25% Indels: 92  
 RESULT 326  
 ID AAA911129 standard; DNA; 1468 BP.  
 DE CD44HextraFASTm/cyto coding sequence.  
 PN WO200100854-A2.  
 PD 04-JAN-2001.  
 PA (ANGI-) ANGIOGENE PHARM LTD.  
 Best Local Similarity: 24.70% Mismatches: 130  
 Query Match: 12.22% Indels: 77  
 RESULT 327  
 ID ASN86520 standard; cDNA; 1737 BP.  
 DE Nucleotide sequence of human CD44R cDNA.  
 PN WO200238794-A2.  
 PD 16-MAY-2002.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
 Best Local Similarity: 22.19% Mismatches: 138  
 Query Match: 12.04% Indels: 105  
 RESULT 328  
 ID ADK61304 standard; DNA; 1737 BP.  
 DE Ovarian cancer-related DNA #459 with altered ovarian cancer expression.  
 PN WO2003068054-A2.  
 PD 21-AUG-2003.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 PA (SLOK) SLOAN KETTERING INST CANCER RES.  
 Best Local Similarity: 22.19% Mismatches: 138  
 Query Match: 12.04% Indels: 105  
 RESULT 329  
 ID ABZ70446 standard; cDNA; 1824 BP.  
 DE Human CD44 variant CD44vRA associated with rheumatoid arthritis.  
 PN WO2003014160-A2.  
 PD 20-FEB-2003.  
 PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 Best Local Similarity: 22.92% Mismatches: 136  
 Query Match: 12.04% Indels: 78  
 RESULT 330  
 ID AAA91011 standard; DNA; 2100 BP.  
 DE Human CD44 splice variant (RA-CD44) coding sequence.  
 PN WO200075312-A1.  
 PD 14-DEC-2000.  
 PA (YISS) YISSUM RES & DEV CO.  
 Best Local Similarity: 22.92% Mismatches: 136  
 Query Match: 12.04% Indels: 78  
 RESULT 331  
 ID ADD90593 standard; cDNA; 2100 BP.  
 DE Human CD44v glycoprotein encoding cDNA SEQ ID NO:3.  
 PN WO2003072606-A2.  
 PD 04-SEP-2003.  
 PA (YEDA) YEDA RES & DEV CO LTD.  
 PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 Best Local Similarity: 22.92% Mismatches: 136  
 Query Match: 12.04% Indels: 78  
 RESULT 332  
 ID AAS03192 standard; cDNA; 2307 BP.  
 DE Human epithelial antigen CD44 cDNA sequence.  
 PN US6218525-B1.  
 PD 17-APR-2001.  
 PA (GEHO) GEN HOSPITAL CORP.  
 Best Local Similarity: 23.57% Mismatches: 100  
 Query Match: 12.04% Indels: 75  
 RESULT 333  
 ID AAQ21186 standard; DNA; 2308 BP.  
 DE Clone CD44 coding for epithelial CD44 Antigen.  
 PN WO9201049-A.  
 PD 23-JAN-1992.  
 PA (GEHO) GEN HOSPITAL CORP.  
 Best Local Similarity: 23.57% Mismatches: 100  
 Query Match: 12.04% Indels: 75  
 RESULT 334  
 ID AAT14725 standard; cDNA; 2308 BP.

DE Human epithelial CD44 cDNA.  
 PN US5506136-A.  
 PD 09-APR-1996.  
 PA (GEHO) GEN HOSPITAL CORP.  
 Best Local Similarity: 23.57% Mismatches: 100  
 Query Match: 12.04% Indels: 75  
 RESULT 335  
 ID AAV63462 standard; cDNA; 2308 BP.  
 DE Human CD44 antigen cDNA.  
 PN US5830731-A.  
 PD 03-NOV-1998.  
 PA (GEHO) GEN HOSPITAL CORP.  
 Best Local Similarity: 23.57% Mismatches: 100  
 Query Match: 12.04% Indels: 75  
 RESULT 336  
 ID AAV81219 standard; cDNA; 2308 BP.  
 DE Human CD44 antigen cDNA.  
 PN US5849898-A.  
 PD 15-DEC-1998.  
 PA (GEHO) GEN HOSPITAL CORP.  
 Best Local Similarity: 23.57% Mismatches: 100  
 Query Match: 12.04% Indels: 75  
 RESULT 337  
 ID AAA50598 standard; cDNA; 2308 BP.  
 DE Human epithelial CD44 cDNA.  
 PN US6111093-A.  
 PD 29-AUG-2000.  
 PA (GEHO) GEN HOSPITAL CORP.  
 Best Local Similarity: 23.57% Mismatches: 100  
 Query Match: 12.04% Indels: 75  
 RESULT 338  
 ID ABO49374 standard; cDNA; 2308 BP.  
 DE Human CD44 cDNA #2.  
 PN US2004072283-A1.  
 PD 15-APR-2004.  
 PA (SEED) SEED B.  
 PA (ALLE) ALLEN J.  
 PA (ARUF) ARUFFO A.  
 PA (CAME) CAMERINI D.  
 PA (LAUF) LAUFFER L.  
 PA (OQUE) OQUENDO C.  
 PA (SIMM) SIMMONS D.  
 PA (STAM) STAMENKOVIC I.  
 PA (STEN) STENGELIN S.  
 PA (AMIO) AMIOT M.  
 Best Local Similarity: 23.57% Mismatches: 100  
 Query Match: 12.04% Indels: 75  
 RESULT 339  
 ID ABX77520 standard; cDNA; 4674 BP.  
 DE Differentially expressed breast cancer associated cDNA #15.  
 PN US2002156263-A1.  
 PD 24-OCT-2002.  
 PA (CHEN) CHEN H.  
 Best Local Similarity: 22.19% Mismatches: 138  
 Query Match: 12.04% Indels: 105  
 RESULT 340  
 ID ADJ56375 standard; cDNA; 4674 BP.  
 DE Human cDNA differentially expressed in MYCN activated cells SeqID 181.  
 PN US2003119009-A1.  
 PD 26-JUN-2003.  
 PA (STUA) STUART S G.  
 PA (NUCH) NUCHTERN J G.  
 PA (PLON) PLON S E.  
 PA (SHOH) SHOHEIT J M.  
 Best Local Similarity: 22.19% Mismatches: 138  
 Query Match: 12.04% Indels: 105  
 RESULT 341  
 ID ADM86790 standard; cDNA; 4674 BP.  
 DE Human cDNA #51 differentially expressed in lung cancer.  
 PN US2003175704-A1.  
 PD 18-SEP-2003.  
 PA (LASE) LASEK A K W.  
 PA (SHYJ) SHYJAN A W.



PA (TURN/) TURNER C M. Mismatches: 138  
 Query Match: 12.04% Indels: 105  
 RESULT 342  
 ID ADI61729 standard; cDNA; 4675 BP.  
 DE Human cDNA upregulated in Alzheimer's disease, INCYTE 234630.26.  
 PN US668288-B1.  
 PD 27-JAN-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 22.19% Mismatches: 138  
 Query Match: 12.04% Indels: 105  
 RESULT 343  
 ID ADO318553 standard; DNA; 5053 BP.  
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 216.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Best Local Similarity: 25.96% Mismatches: 109  
 Query Match: 11.95% Indels: 63  
 RESULT 344  
 ID ADD90595 standard; cDNA; 2097 BP.  
 DE Human CD44v glycoprotein encoding cDNA SEQ ID NO:5.  
 PN WO2003072606-A2.  
 PD 04-SEP-2003.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 Best Local Similarity: 23.32% Mismatches: 128  
 Query Match: 11.89% Indels: 69  
 RESULT 345  
 ID ACN42246 standard; cDNA; 2342 BP.  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1121.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 25.96% Mismatches: 109  
 Query Match: 11.89% Indels: 63  
 RESULT 346  
 ID ABX76192 standard; DNA; 2387 BP.  
 DE Lung cancer-associated polynucleotide #63.  
 PN WO200286443-A2.  
 PD 31-OCT-2002.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Best Local Similarity: 23.32% Mismatches: 128  
 Query Match: 11.89% Indels: 69  
 RESULT 347  
 ID ADL61117 standard; DNA; 2387 BP.  
 DE Human protein tyrosine kinase biomarker CD44 antigen DNA.  
 PN WO2004020583-A2.  
 PD 11-MAR-2004.  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 Best Local Similarity: 23.32% Mismatches: 128  
 Query Match: 11.89% Indels: 69  
 RESULT 348  
 ID ABX63495 standard; cDNA; 2905 BP.  
 DE Human cDNA #495 differentially expressed in activated vascular tissue.  
 PN US2002137081-A1.  
 PD 26-SEP-2002.  
 PA (BAND/) BANDMAN O.  
 Best Local Similarity: 23.32% Mismatches: 128  
 Query Match: 11.89% Indels: 69  
 RESULT 349  
 ID ADA10891 standard; cDNA; 3474 BP.  
 DE Human cDNA differentially expressed in colon cancer #7.  
 PN US2002160382-A1.  
 PD 31-OCT-2002.  
 PA (LASE/) LASEK A W.  
 PA (JONE/) JONES D A.  
 Best Local Similarity: 23.32% Mismatches: 128  
 Query Match: 11.89% Indels: 69  
 RESULT 350  
 ID ADO38560 standard; DNA; 4874 BP.  
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 223.  
 PN WO2004058052-A2.

PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Best Local Similarity: 30.86% Mismatches: 84  
 Query Match: 11.89% Indels: 14  
 RESULT 351  
 ID ADI60527 standard; DNA; 1190 BP.  
 DE Secreted polypeptide encoding gene #66.  
 PN WO2003025142-A2.  
 PD 27-MAR-2003.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 30.86% Mismatches: 84  
 Query Match: 11.83% Indels: 14  
 RESULT 352  
 ID ACC43051 standard; DNA; 339 BP.  
 DE Nucleotide sequence of a chicken CD44-hyaluronic acid binding domain.  
 PN WO2003018044-A1.  
 PD 06-MAR-2003.  
 PA (STRO/) STROEMBLAD S.  
 PA (KOG/) KOGERMAN P.  
 PA (PAEL/) PAELL T.  
 Best Local Similarity: 36.28% Mismatches: 53  
 Query Match: 11.56% Indels: 1  
 RESULT 353  
 ID ACC43049 standard; DNA; 336 BP.  
 DE Nucleotide sequence of a human CD44-hyaluronic acid binding domain.  
 PN WO2003018044-A1.  
 PD 06-MAR-2003.  
 PA (STRO/) STROEMBLAD S.  
 PA (KOG/) KOGERMAN P.  
 PA (PAEL/) PAELL T.  
 Best Local Similarity: 36.04% Mismatches: 51  
 Query Match: 11.47% Indels: 2  
 RESULT 354  
 ID ACC43052 standard; DNA; 336 BP.  
 DE Nucleotide sequence of a CD44-hyaluronic acid binding domain.  
 PN WO2003018044-A1.  
 PD 06-MAR-2003.  
 PA (STRO/) STROEMBLAD S.  
 PA (KOG/) KOGERMAN P.  
 PA (PAEL/) PAELL T.  
 Best Local Similarity: 36.04% Mismatches: 51  
 Query Match: 11.35% Indels: 2  
 RESULT 355  
 ID ACC43053 standard; DNA; 336 BP.  
 DE Nucleotide sequence of a CD44-hyaluronic acid binding domain.  
 PN WO2003018044-A1.  
 PD 06-MAR-2003.  
 PA (STRO/) STROEMBLAD S.  
 PA (KOG/) KOGERMAN P.  
 PA (PAEL/) PAELL T.  
 Best Local Similarity: 36.04% Mismatches: 51  
 Query Match: 11.23% Indels: 2  
 RESULT 356  
 ID ACC43054 standard; DNA; 336 BP.  
 DE Nucleotide sequence of a CD44-hyaluronic acid binding domain.  
 PN WO2003018044-A1.  
 PD 06-MAR-2003.  
 PA (STRO/) STROEMBLAD S.  
 PA (KOG/) KOGERMAN P.  
 PA (PAEL/) PAELL T.  
 Best Local Similarity: 36.04% Mismatches: 51  
 Query Match: 11.10% Indels: 2  
 RESULT 357  
 ID ACC43050 standard; DNA; 336 BP.  
 DE Nucleotide sequence of a dog CD44-hyaluronic acid binding domain.  
 PN WO2003018044-A1.  
 PD 06-MAR-2003.  
 PA (STRO/) STROEMBLAD S.  
 PA (KOG/) KOGERMAN P.  
 PA (PAEL/) PAELL T.  
 Best Local Similarity: 34.23% Mismatches: 51  
 Query Match: 10.98% Indels: 2  
 RESULT 358

ID AAS81254 standard; cDNA; 2764 BP.  
DE DNA encoding novel human diagnostic protein #17058.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC. Mismatches: 119  
Query Match: 10.89% Indels: 74  
Best Local Similarity: 26.03%  
RESULT 359  
ID AAS81258 standard; cDNA; 2273 BP.  
DE DNA encoding novel human diagnostic protein #17062.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC. Mismatches: 129  
Query Match: 21.83% Indels: 88  
Best Local Similarity: 10.80%  
RESULT 360  
ID AAI4523 standard; DNA; 106 BP.  
DE Probe #15209 used to measure gene expression in human placenta sample.  
PN W0200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC. Mismatches: 0  
Query Match: 10.26% Indels: 0  
Best Local Similarity: 100.00%  
RESULT 361  
ID ABS14478 standard; DNA; 106 BP.  
DE Human genome-derived single exon probe ORF from lung SEQ ID NO 14469.  
PN W0200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC. Mismatches: 0  
Query Match: 100.00% Indels: 0  
Best Local Similarity: 10.26%  
RESULT 362  
ID ACH49200 standard; cDNA; 399 BP.  
DE Human leukocyte cDNA #794.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Best Local Similarity: 37.36% Mismatches: 41  
Query Match: 10.05% Indels: 1  
RESULT 363  
ID ADE71448 standard; cDNA; 820 BP.  
DE Dog cDNA encoding PDEBC variant Incyte 704113673J1.  
PN US2003124543-A1.  
PD 03-JUL-2003.  
PA (STUA/) STUART S G.  
PA (STRE/) STREETER D G.  
Best Local Similarity: 78.79% Mismatches: 11  
Query Match: 9.96% Indels: 5  
RESULT 364  
ID ABZ34973 standard; cDNA; 549 BP.  
DE Human gene expression profile polynucleotide SEQ ID NO 85.  
PN W0200274979-A2.  
PD 26-SEP-2002.  
PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC. Mismatches: 61  
Query Match: 34.92% Indels: 8  
Best Local Similarity: 9.54%  
RESULT 365  
ID ABZ91738 standard; DNA; 549 BP.  
DE Human nucleic acid sequence.  
PN W0200285308-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC. Mismatches: 61  
Query Match: 34.92% Indels: 8  
Best Local Similarity: 9.54%  
RESULT 366  
ID ADK61306 standard; DNA; 549 BP.  
DE Ovarian cancer-related DNA #461 with altered ovarian cancer expression.  
PN W02003068054-A2.  
PD 21-AUG-2003.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (SLOK ) SLOAN KETTERING INST CANCER RES. Mismatches: 61  
Best Local Similarity: 34.92% Indels: 8  
Query Match: 9.54%  
RESULT 367  
ID ABD27968 standard; DNA; 549 BP.  
DE AA282906 DNA fragment.  
PN W0200285309-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC. Mismatches: 61  
Best Local Similarity: 34.92% Indels: 8  
Query Match: 9.54%  
RESULT 368  
ID ADB62456 standard; cDNA; 2863 BP.  
DE Human cDNA encoding clone FEBRA20038970.  
PN EPI308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 21.26% Mismatches: 98  
Query Match: 9.11% Indels: 102  
RESULT 369  
ID ACH48521 standard; cDNA; 425 BP.  
DE Human leukocyte cDNA #115.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Best Local Similarity: 36.59% Mismatches: 36  
Query Match: 8.96% Indels: 1  
RESULT 370  
ID ABX74436 standard; cDNA; 781 BP.  
DE Human cDNA sequence #8 up-regulated in CC-RCC patients.  
PN W0200279411-A2.  
PD 10-OCT-2002.  
PA (VAND-) VAN ANDEL INST.  
Best Local Similarity: 30.22% Mismatches: 62  
Query Match: 8.78% Indels: 13  
RESULT 371  
ID ADL13961 standard; DNA; 834 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #493.  
PN W02003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC. Mismatches: 62  
Best Local Similarity: 30.22% Indels: 13  
Query Match: 8.78%  
RESULT 372  
ID ABX63446 standard; cDNA; 1144 BP.  
DE Human cDNA #446 differentially expressed in activated vascular tissue.  
PN US2002137081-A1.  
PD 28-SEP-2002.  
PA (BAND/) BANDMAN O.  
Best Local Similarity: 30.22% Mismatches: 62  
Query Match: 8.78% Indels: 13  
RESULT 373  
ID ABE25720 standard; cDNA; 1144 BP.  
DE Human cDNA differentially expressed in foam cells #124.  
PN US2003194721-A1.  
PD 16-OCT-2003.  
PA (INCY-) INCYTE GENOMICS INC. Mismatches: 62  
Best Local Similarity: 30.22% Indels: 13  
Query Match: 8.78%  
RESULT 374  
ID ADL13963 standard; DNA; 1414 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #495.  
PN W02003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC. Mismatches: 123  
Best Local Similarity: 22.79% Indels: 59  
Query Match: 8.78%

RESULT 375  
ID ABX76382 standard; DNA; 1422 BP.  
DE Lung cancer-associated polynucleotide #246.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 22.79% Mismatches: 123  
Query Match: 8.78% Indels: 59  
RESULT 376  
ID ACC72678 standard; cDNA; 1422 BP.  
DE Human cancer related protein encoding cDNA SEQ ID NO:17.  
PN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 22.79% Mismatches: 123  
Query Match: 8.78% Indels: 59  
RESULT 377  
ID ADN38973 standard; cDNA; 1422 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:291.  
PN WO2003042861-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 22.79% Mismatches: 123  
Query Match: 8.78% Indels: 59  
RESULT 378  
ID ADN39702 standard; cDNA; 1430 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C74.  
PN WO2003042861-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 30.22% Mismatches: 62  
Query Match: 8.78% Indels: 13  
RESULT 379  
ID ADQ21505 standard; DNA; 1440 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4325.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Best Local Similarity: 22.79% Mismatches: 123  
Query Match: 8.78% Indels: 59  
RESULT 380  
ID ADQ25341 standard; DNA; 1461 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8161.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Best Local Similarity: 30.22% Mismatches: 62  
Query Match: 8.78% Indels: 13  
RESULT 381  
ID ABX63445 standard; cDNA; 1728 BP.  
DE Human CDNA #445 differentially expressed in activated vascular tissue.  
PN US2002137081-A1.  
PD 26-SEP-2002.  
PA (BAND/) BANDMAN O.  
Best Local Similarity: 30.22% Mismatches: 62  
Query Match: 8.78% Indels: 13  
RESULT 382  
ID ADK67833 standard; cDNA; 7840 BP.  
DE Human BRCC300 gene coding sequence.  
PN WO2004012755-A1.  
PD 12-FEB-2004.  
PA (WIST-) WISTAR INST.  
Best Local Similarity: 21.71% Mismatches: 107  
Query Match: 8.78% Indels: 66  
RESULT 383  
ID ABV95472 standard; cDNA; 351 BP.  
DE Human pancreatic cancer expressed cDNA SEQ ID NO 880.  
PN WO200260317-A2.  
PD 08-AUG-2002.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 32.95% Mismatches: 41  
Query Match: 8.75% Indels: 2  
RESULT 384

ID ADM80849 standard; cDNA; 813 BP.  
DE Human CAECM-36 encoding cDNA SEQ ID NO:78.  
PN WO2004015396-A2.  
PD 19-FEB-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 32.95% Mismatches: 41  
Query Match: 8.75% Indels: 2  
RESULT 385  
ID AAQ27190 standard; cDNA; 1414 BP.  
DE Tumour necrosis factor-induced glycoprotein TSG-6 gene.  
PN WO200212175-A1.  
PD 23-JUL-1992.  
PA (UYNY) UNIV NEW YORK STATE.  
Best Local Similarity: 32.95% Mismatches: 41  
Query Match: 8.75% Indels: 2  
RESULT 386  
ID AAV71778 standard; cDNA; 1414 BP.  
DE Tumour necrosis factor stimulated gene 6 (TSG-6) protein encoding cDNA.  
PN US5846763-A.  
PD 08-DEC-1998.  
PA (UYNY) UNIV NEW YORK STATE.  
Best Local Similarity: 32.95% Mismatches: 41  
Query Match: 8.75% Indels: 2  
RESULT 387  
ID AAD06019 standard; cDNA; 1414 BP.  
DE Human tumour necrosis factor (TNF) stimulated gene-6 (TSG-6) cDNA.  
PN US6210905-B1.  
PD 03-APR-2001.  
PA (UYNY) UNIV NEW YORK STATE.  
Best Local Similarity: 32.95% Mismatches: 41  
Query Match: 8.75% Indels: 2  
RESULT 388  
ID ABS54635 standard; cDNA; 1414 BP.  
DE Human CDNA encoding tumour necrosis factor stimulated gene 6, TSG-6.  
PN US2002090708-A1.  
PD 11-JUL-2002.  
PA (UYNY) UNIV NEW YORK STATE.  
Best Local Similarity: 32.95% Mismatches: 41  
Query Match: 8.75% Indels: 2  
RESULT 389  
ID ADS85080 standard; DNA; 1605 BP.  
DE Mouse atopic dermatitis-related gene sequence SeqID82.  
PN WO2004033386-A1.  
PD 15-APR-2004.  
PA (GENO-) GENOX RES INC.  
PA (UYJU-) UNIV JUNTENDO.  
Best Local Similarity: 32.95% Mismatches: 41  
Query Match: 8.69% Indels: 2  
RESULT 390  
ID AAD48132 standard; DNA; 3366 BP.  
DE Rat CD44i DNA.  
PN WO200276510-A1.  
PD 03-OCT-2002.  
PA (AGYT-) AGY THERAPEUTICS INC.  
Best Local Similarity: 26.69% Mismatches: 93  
Query Match: 8.69% Indels: 63  
RESULT 391  
ID ACH30555 standard; cDNA; 396 BP.  
DE Human testis cDNA #941.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Best Local Similarity: 31.58% Mismatches: 58  
Query Match: 8.66% Indels: 13  
RESULT 392  
ID ABT08487 standard; cDNA; 8444 BP.  
DE Human novel protein NOV1a coding sequence SEQ ID NO: 1.  
PN WO200259315-A2.  
PD 01-AUG-2002.

PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 21.59%  
 Query Match: 8.60%  
 Mismatches: 151  
 Indels: 38  
 RESULT 393  
 ID ADO09835 standard; cDNA; 8444 BP.  
 DE Human NOV1a cDNA.  
 PN US2004018970-A1.  
 PD 29-JAN-2004.  
 PA (SHIM/) SHIMKETS R A.  
 PA (PATT/) PATTURAJAN M.  
 PA (VERN/) VERNET C A M.  
 PA (CASM/) CASMAN S J.  
 PA (MALY/) MALYANKAR U M.  
 PA (WALY/) MALYANKAR U M.  
 PA (SHEN/) SHENOY S G.  
 PA (SPYT/) SPYTEK K A.  
 PA (GANG/) GANGOLLI E A.  
 PA (MILL/) MILLER C E.  
 PA (BOLD/) BOLDOG F L.  
 PA (LILL/) LI L.  
 PA (TAUP/) TAUPIER R J.  
 PA (KEKU/) KEKUDA R.  
 PA (SMIT/) SMITHSON G.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (LIUX/) LIU X.  
 PA (COLM/) COLMAN S D.  
 PA (TCHE/) TCHERNEV V T.  
 PA (SIJG/) SI J.  
 PA (EDIN/) EDINGER S R.  
 PA (SCIO/) SCIORE P.  
 PA (STON/) STONE D J.  
 PA (MILL/) MILLER I.  
 PA (ROTH/) ROTHENBERG M E.  
 Best Local Similarity: 21.59%  
 Query Match: 8.60%  
 Mismatches: 151  
 Indels: 38  
 RESULT 394  
 ID AAF87120 standard; DNA; 3625 BP.  
 DE NOV9 coding sequence.  
 PN WO200136638-A2.  
 PD 25-MAY-2001.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 24.44%  
 Query Match: 8.54%  
 Mismatches: 134  
 Indels: 59  
 RESULT 395  
 ID ADH71325 standard; DNA; 3625 BP.  
 DE Human gene of the invention NOV9h SEQ ID NO:221.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 24.44%  
 Query Match: 8.54%  
 Mismatches: 134  
 Indels: 59  
 RESULT 396  
 ID ABT08488 standard; cDNA; 8495 BP.  
 DE Human novel protein NOV1b coding sequence SEQ ID NO: 3.  
 PN WO200259315-A2.  
 PD 01-AUG-2002.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 24.44%  
 Query Match: 8.54%  
 Mismatches: 134  
 Indels: 59  
 RESULT 397  
 ID ADH71331 standard; DNA; 8495 BP.  
 DE Human gene of the invention NOV9k SEQ ID NO:227.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 24.44%  
 Query Match: 8.54%  
 Mismatches: 134  
 Indels: 59  
 RESULT 398  
 ID ADO09837 standard; cDNA; 8495 BP.  
 DE Human NOV1b cDNA.  
 PN US2004018970-A1.  
 PD 29-JAN-2004.  
 PA (SHIM/) SHIMKETS R A.  
 PA (PATT/) PATTURAJAN M.

PA (VERN/) VERNET C A M.  
 PA (CASM/) CASMAN S J.  
 PA (MALY/) MALYANKAR U M.  
 PA (SHEN/) SHENOY S G.  
 PA (SPYT/) SPYTEK K A.  
 PA (GANG/) GANGOLLI E A.  
 PA (MILL/) MILLER C E.  
 PA (BOLD/) BOLDOG F L.  
 PA (LILL/) LI L.  
 PA (TAUP/) TAUPIER R J.  
 PA (KEKU/) KEKUDA R.  
 PA (SMIT/) SMITHSON G.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (LIUX/) LIU X.  
 PA (COLM/) COLMAN S D.  
 PA (TCHE/) TCHERNEV V T.  
 PA (SIJG/) SI J.  
 PA (EDIN/) EDINGER S R.  
 PA (STON/) STONE D J.  
 PA (SCIO/) SCIORE P.  
 PA (MILL/) MILLER I.  
 PA (ROTH/) ROTHENBERG M E.  
 Best Local Similarity: 24.44%  
 Query Match: 8.54%  
 Mismatches: 134  
 Indels: 59  
 RESULT 399  
 ID AAH23114 standard; DNA; 1411 BP.  
 DE Osteoarthritis tissue-derived nucleic acid sequence #44.  
 PN WO200153531-A2.  
 PD 28-JUL-2001.  
 PA (PHAA) PHARMACIA CORP.  
 Best Local Similarity: 31.62%  
 Query Match: 8.36%  
 Mismatches: 62  
 Indels: 13  
 RESULT 400  
 ID ADO09967 standard; cDNA; 3256 BP.  
 DE Human NOVIC cDNA.  
 PN US2004018970-A1.  
 PD 29-JAN-2004.  
 PA (SHIM/) SHIMKETS R A.  
 PA (PATT/) PATTURAJAN M.  
 PA (VERN/) VERNET C A M.  
 PA (CASM/) CASMAN S J.  
 PA (MALY/) MALYANKAR U M.  
 PA (SPYT/) SPYTEK K A.  
 PA (GANG/) GANGOLLI E A.  
 PA (MILL/) MILLER C E.  
 PA (BOLD/) BOLDOG F L.  
 PA (LILL/) LI L.  
 PA (TAUP/) TAUPIER R J.  
 PA (KEKU/) KEKUDA R.  
 PA (SMIT/) SMITHSON G.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (LIUX/) LIU X.  
 PA (COLM/) COLMAN S D.  
 PA (TCHE/) TCHERNEV V T.  
 PA (SIJG/) SI J.  
 PA (EDIN/) EDINGER S R.  
 PA (STON/) STONE D J.  
 PA (SCIO/) SCIORE P.  
 PA (ROTH/) ROTHENBERG M E.  
 Best Local Similarity: 22.03%  
 Query Match: 8.27%  
 Mismatches: 134  
 Indels: 90  
 RESULT 401  
 ID ABT08489 standard; cDNA; 3260 BP.  
 DE Human novel protein NOVIC coding sequence SEQ ID NO: 210.  
 PN WO200259315-A2.  
 PD 01-AUG-2002.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 22.03%  
 Query Match: 8.27%  
 Mismatches: 134  
 Indels: 90  
 RESULT 402  
 ID ADH71311 standard; DNA; 3260 BP.

DE Human gene of the invention NOV9a SEQ ID NO:207.  
PD WO2003102155-A2.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 22.03% Mismatches: 134  
Query Match: 8.27% Indels: 90  
RESULT 403  
ID ADH71355 standard; DNA: 4527 BP.  
DE Human gene of the invention NOV9w SEQ ID NO:251.  
PD WO2003102155-A2.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 22.03% Mismatches: 134  
Query Match: 8.27% Indels: 90  
RESULT 404  
ID ABA04662 standard; cDNA: 4576 BP.  
DE Human Hyaluronic Acid Receptor for Endocytosis, HARE, coding sequence.  
PD WO200181544-A2.  
PA (WEIG/) WEIGEL P A.  
PA (ZHOU/) ZHOU B.  
PA (WEIG/) WEIGEL J A.  
Best Local Similarity: 22.03% Mismatches: 134  
Query Match: 8.27% Indels: 90  
RESULT 405  
ID ABX13822 standard; cDNA: 4642 BP.  
DE cDNA encoding human 190kDa Hyaluronan receptor for endocytosis #1.  
PD WO200286093-A2.  
PA (WEIG/) WEIGEL P H.  
PA (WEIG/) WEIGEL J A.  
Best Local Similarity: 22.03% Mismatches: 134  
Query Match: 8.27% Indels: 90  
RESULT 406  
ID ABX13823 standard; cDNA: 4962 BP.  
DE cDNA encoding human 190kDa Hyaluronan receptor for endocytosis #2.  
PD WO200286093-A2.  
PA (WEIG/) WEIGEL P H.  
PA (WEIG/) WEIGEL J A.  
Best Local Similarity: 22.03% Mismatches: 134  
Query Match: 8.27% Indels: 90  
RESULT 407  
ID ADH71357 standard; DNA: 5416 BP.  
DE Human gene of the invention NOV9x SEQ ID NO:253.  
PD WO2003102155-A2.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 22.03% Mismatches: 134  
Query Match: 8.27% Indels: 90  
RESULT 408  
ID ADM90626 standard; DNA: 5688 BP.  
DE Human DNA encoding a pharmaceutically useful protein SeqID 19.  
PD WO2004020595-A2.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.  
PA (DNAF-) DNAFORM KK.  
Best Local Similarity: 22.03% Mismatches: 134  
Query Match: 8.27% Indels: 90  
RESULT 409  
ID ADM91044 standard; DNA: 5688 BP.  
DE Human DNA encoding a pharmaceutically useful protein SeqID 437.  
PD WO2004020595-A2.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.  
PA (DNAF-) DNAFORM KK.  
Best Local Similarity: 22.03% Mismatches: 134  
Query Match: 8.27% Indels: 90  
RESULT 410  
ID ADH71359 standard; DNA: 7670 BP.  
DE Human gene of the invention NOV9y SEQ ID NO:255.

PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 22.03% Mismatches: 134  
Query Match: 8.27% Indels: 90  
RESULT 411  
ID ABA04648 standard; cDNA: 4706 BP.  
DE Rat Hyaluronic Acid Receptor for Endocytosis, HARE, coding sequence.  
PD WO200181544-A2.  
PA (WEIG/) WEIGEL P A.  
PA (ZHOU/) ZHOU B.  
PA (WEIG/) WEIGEL J A.  
Best Local Similarity: 22.42% Mismatches: 138  
Query Match: 8.21% Indels: 80  
RESULT 412  
ID ABX13821 standard; cDNA: 4706 BP.  
DE cDNA encoding rat 175kDa Hyaluronan receptor for endocytosis (HARE).  
PD WO200286093-A2.  
PA (WEIG/) WEIGEL P H.  
PA (WEIG/) WEIGEL J A.  
Best Local Similarity: 22.42% Mismatches: 138  
Query Match: 8.21% Indels: 80  
RESULT 413  
ID AAF29464 standard; cDNA: 3153 BP.  
DE Murine brevidin cDNA.  
PD WO200100638-A2.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 24.88% Mismatches: 97  
Query Match: 8.18% Indels: 30  
RESULT 414  
ID ACD66770 standard; cDNA: 3153 BP.  
DE Secreted polypeptide-related cDNA #76.  
PD US200302279-A1.  
PD 30-JAN-2003.  
PA (FRAS/) FRASER C C.  
PA (BARN/) BARNES T M.  
PA (SHAR/) SHARP J D.  
PA (KIRS/) KIRST S J.  
PA (MYER/) MYERS P S.  
PA (LEIB/) LEIBY K R.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (WRIG/) WRIGHTON N.  
PA (MACK/) MACKAY C R.  
PA (GOOD/) GOODEARL A D J.  
Best Local Similarity: 24.88% Mismatches: 97  
Query Match: 8.18% Indels: 30  
RESULT 415  
ID ADB90788 standard; cDNA: 3153 BP.  
DE Mouse cDNA encoding brevicin protein.  
PD US2003082586-A1.  
PD 01-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 24.88% Mismatches: 97  
Query Match: 8.18% Indels: 30  
RESULT 416  
ID ADF71523 standard; cDNA: 3153 BP.  
DE Murine brevidin protein cDNA.  
PD US2003175733-A1.  
PD 18-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 24.88% Mismatches: 97  
Query Match: 8.18% Indels: 30  
RESULT 417  
ID ADQ10339 standard; cDNA: 3153 BP.  
DE Human polynucleotide #61.  
PD US2004121396-A1.  
PD 24-JUN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 24.88% Mismatches: 97

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Query Match: 8.18% Indels: 30
RESULT 418
ID ABS70406 standard; cDNA; 1734 BP.
DE Human bone remodelling gene #63.
PN US6426186-B1.
PD 30-JUL-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 30.00% Mismatches: 61
Query Match: 8.06% Indels: 14
RESULT 419
ID ADB63670 standard; cDNA; 2160 BP.
DE Human cDNA encoding clone THYMU20143230.
PN B1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 25.93% Mismatches: 105
Query Match: 8.00% Indels: 49
RESULT 420
ID ACN42826 standard; cDNA; 7678 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1701.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 27.43% Mismatches: 54
Query Match: 8.00% Indels: 59
RESULT 421
ID ACN42825 standard; cDNA; 7975 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1700.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 27.43% Mismatches: 54
Query Match: 8.00% Indels: 59
RESULT 422
ID AB281727 standard; cDNA; 2652 BP.
DE Rat mutant brain-enriched hyaluronan binding protein coding sequence.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYVA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (MATT/) MATTHEWS R T.
Best Local Similarity: 24.26% Mismatches: 81
Query Match: 7.94% Indels: 39
RESULT 423
ID ADK67780 standard; DNA; 2652 BP.
DE Rat brain-enriched hyaluronan binding (BEHAB) mutant coding sequence.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYVA) UNIV YALE.
Best Local Similarity: 24.26% Mismatches: 81
Query Match: 7.94% Indels: 39
RESULT 424
ID AAF29460 standard; cDNA; 2013 BP.
DE Human TANGO 332 cDNA open reading frame.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 425
ID ACB66767 standard; cDNA; 2013 BP.
DE Secreted polypeptide-related cDNA #51.
PN US200302279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 426
ID ADB90774 standard; cDNA; 2730 BP.
DE Human cDNA encoding TANGO 332.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 427
ID ADF71510 standard; cDNA; 2013 BP.
DE Human TANGO 332 CDS.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 428
ID ADQ10328 standard; cDNA; 2013 BP.
DE Human polynucleotide #58.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 429
ID AAF29459 standard; cDNA; 2730 BP.
DE Human TANGO 332 cDNA.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 430
ID ACD66766 standard; cDNA; 2730 BP.
DE Secreted polypeptide-related cDNA #50.
PN US200302279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 431
ID ADB90774 standard; cDNA; 2730 BP.
DE Human cDNA encoding TANGO 332.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 432
ID ADF71509 standard; cDNA; 2730 BP.
DE Human TANGO 332 cDNA.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 20.39% Mismatches: 105
Query Match: 7.91% Indels: 90
RESULT 433
ID ADQ10327 standard; cDNA; 2730 BP.
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DE Human polynucleotide #57.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 434
ID ACN37482 standard; cDNA; 3275 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA323924, SEQ ID NO:394.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 435
ID ADH18923 standard; cDNA; 3293 BP.
DE Human cell adhesion and extracellular matrix CADECM-19 cDNA - SEQ 50.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 436
ID ADI28068 standard; cDNA; 3438 BP.
DE ECMAD gene clone 6755002CB1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 437
ID AA91017 standard; DNA; 3476 BP.
DE Human secreted protein PRO6018 coding sequence.
PN WO200075317-A2.
PD 14-DEC-2000.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 438
ID ABR69986 standard; DNA; 3476 BP.
DE cDNA encoding human Pro peptide #26.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 439
ID ADA01319 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 440
ID ADA43748 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 441
ID ADA43516 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 442
ID ADA01191 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 443
ID ADA01075 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 444
ID ADA43632 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 445
ID ADA06894 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 446
ID ADA08382 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 447
ID ADB99675 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide SEQ ID 51.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 448
ID ADB86958 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 449
ID ADB66113 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 450
ID ADB99791 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide SEQ ID 51.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 451
ID ADB99446 standard; cDNA; 3476 BP.
DE Novel human secreted and transmembrane protein PRO6018 cDNA.
PN US2003082731-A1.
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PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 452
ID ADB65997 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 453
ID ADC23395 standard; cDNA; 3476 BP.
DE Human cDNA clone (SeqID 51) encoding the transmembrane PRO protein.
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 454
ID ADC26088 standard; cDNA; 3476 BP.
DE Human PRO6018 cDNA.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 455
ID ADE04915 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 456
ID ADE11221 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 457
ID ADD88152 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 458
ID ADD95447 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 459
ID ADE06377 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 460
ID ADE38152 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 461
ID ADD88268 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 462
ID ADD90849 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 463
ID ADF99404 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 464
ID ADG06497 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 465
ID ADG05448 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 466
ID ADG82449 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 467
ID ADE51702 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 468
ID ADE51818 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%
Query Match: 7.91%
Mismatches: 105
Indels: 90
RESULT 469
ID ADE37676 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 470
ID ADE37560 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 471
ID ADD95331 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 472
ID ADE38031 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 473
ID ADE76120 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003124655-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 474
ID ADE39443 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 475
ID ADE04247 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 476
ID ADE39844 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 477
ID ADE19709 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 478
ID ADE77287 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 479
ID ADE65395 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 480
ID ADE76004 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 481
ID ADE37915 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 482
ID ADE64525 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 483
ID ADE38960 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 484
ID ADE51934 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 485
ID ADD90965 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 486
ID ADE38744 standard; cDNA; 3476 BP.
DE Human PRO polynucleotide #26.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
RESULT 487
ID ADE37444 standard; cDNA; 3476 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 20.39%      Mismatches: 105
Query Match: 7.91%                Indels: 90
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RESULT 488  
ID ADE06261 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138898-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 489  
ID ADE39327 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003138904-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 490  
ID ADE38628 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119086-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 491  
ID ADE39559 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119118-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 492  
ID ADD89164 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138897-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 493  
ID ADD88931 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138899-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 494  
ID ADE19825 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138900-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 495  
ID ADE77403 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003124667-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 496  
ID ADE65279 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119113-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 497  
ID ADE65279 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119113-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90

ID ADE39327 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119115-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 498  
ID ADE38512 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104559-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 499  
ID ADG11065 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003170809-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 500  
ID ADG10949 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003077743-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 501  
ID ADH31477 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119139-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 502  
ID ADH38725 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119140-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 503  
ID ADH29360 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119137-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 504  
ID ADH23663 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119143-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 505  
ID ADH26993 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119135-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39%  
Query Match: 7.91%  
Mismatches: 105  
Indels: 90  
RESULT 506  
ID ADH38261 standard; cDNA; 3476 BP.

DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119124-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 507  
ID ADH26877 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119134-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 508  
ID ADH38145 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119123-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 509  
ID ADH38841 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119141-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 510  
ID ADH23779 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119142-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 511  
ID ADH40155 standard; cDNA; 3476 BP.  
DE Human PRO6018 cDNA.  
PN US2003119132-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 512  
ID ADH40039 standard; cDNA; 3476 BP.  
DE Human PRO6018 cDNA.  
PN US2003119133-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 513  
ID ADH31361 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119138-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 514  
ID ADH29239 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119136-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 515  
ID ADH49454 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.

PN US2003119127-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 516  
ID ADH51918 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119125-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 517  
ID ADH49773 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119128-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 518  
ID ADH52374 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119130-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 519  
ID ADH52490 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119129-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 520  
ID ADH58487 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119121-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 521  
ID ADH51802 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119126-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 522  
ID ADH58363 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119122-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 523  
ID ADH13560 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119131-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.39% Mismatches: 105  
Query Match: 7.91% Indels: 90  
RESULT 524  
ID ADK00816 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003186373-A1.

PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 105  
Best Local Similarity: 20.39% Indels: 90  
Query Match: 7.91%  
RESULT 525  
ID ADL08557 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003186372-A1.  
PD 02-OCT-2003  
PA (GETH ) GENENTECH INC. Mismatches: 105  
Best Local Similarity: 20.39% Indels: 90  
Query Match: 7.91%  
RESULT 526  
ID ABZ81728 standard; cDNA; 2652 BP.  
DE Rat brain-enriched hyaluronan binding protein coding sequence.  
PN WO2003007880-A2.  
PD 30-JAN-2003.  
PA (UYIA ) UNIV YALE.  
PA (HOCK/) HOCKFIELD S.  
PA (WATT/) MATTHEWS R T.  
Best Local Similarity: 23.32% Mismatches: 101  
Query Match: 7.88% Indels: 37  
RESULT 527  
ID ADK67781 standard; DNA; 2652 BP.  
DE Rat glycosylation-variant BEHAB isoform coding sequence.  
PN WO2004013356-A1.  
PD 12-FEB-2004.  
PA (UYIA ) UNIV YALE.  
Best Local Similarity: 23.32% Mismatches: 101  
Query Match: 7.88% Indels: 37  
RESULT 528  
ID ADB59097 standard; DNA; 3077 BP.  
DE Toxicity-related gene, SEQ ID 4123.  
PN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC. Mismatches: 101  
Best Local Similarity: 23.32% Indels: 37  
Query Match: 7.88%  
RESULT 529  
ID ADP72861 standard; DNA; 3077 BP.  
DE Renal toxin progression gene marker #1450.  
PN WO2004048598-A2.  
PD 10-JUN-2004.  
PA (GENE-) GENE LOGIC INC. Mismatches: 101  
Best Local Similarity: 23.32% Indels: 37  
Query Match: 7.88%  
RESULT 530  
ID ABL90758 standard; cDNA; 3681 BP.  
DE Human polynucleotide SEQ ID NO 1320.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 101  
Best Local Similarity: 23.32% Indels: 37  
Query Match: 7.88%  
RESULT 531  
ID ADL13490 standard; DNA; 6951 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #22.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC. Mismatches: 55  
Best Local Similarity: 27.43% Indels: 59  
Query Match: 7.88%  
RESULT 532  
ID ADL13489 standard; DNA; 7137 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #21.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC. Mismatches: 55  
Best Local Similarity: 27.43% Indels: 59  
Query Match: 7.88%  
RESULT 533  
ID ADP65694 standard; DNA; 7137 BP.  
DE Human aggrecan 1 (chondroitin sulfate proteoglycan 1, large DNA.

PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT. Mismatches: 55  
Best Local Similarity: 27.43% Indels: 59  
Query Match: 7.88%  
RESULT 534  
ID ADP65777 standard; DNA; 7137 BP.  
DE Human large aggregating cartilage proteoglycan core protein mRNA, DNA.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT. Mismatches: 55  
Best Local Similarity: 27.43% Indels: 59  
Query Match: 7.88%  
RESULT 535  
ID ACN37944 standard; cDNA; 7871 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA324323, SEQ ID NO:1163.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC. Mismatches: 122  
Best Local Similarity: 20.62% Indels: 97  
Query Match: 7.88%  
RESULT 536  
ID ACF04000 standard; cDNA; 7879 BP.  
DE Human CLEVER-1 encoding cDNA SEQ ID NO:1.  
PN WO2003057130-A2.  
PD 17-JUL-2003.  
PA (JALK/) JALKANEN S.  
PA (IRJA/) IRJALA H.  
PA (SALM/) SALMI M.  
Best Local Similarity: 20.73% Mismatches: 133  
Query Match: 7.85% Indels: 124  
RESULT 537  
ID ADQ22919 standard; DNA; 8038 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5739.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC. Mismatches: 133  
Best Local Similarity: 20.73% Indels: 124  
Query Match: 7.85%  
RESULT 538  
ID AAAS7363 standard; DNA; 1522 BP.  
DE DNA encoding a human hyaluronan-binding protein, designated WF-HABP.  
PN WO200039166-A1.  
PD 06-JUL-2000.  
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 112  
PA (AMNA-) AMERICAN NAT RED CROSS. Indels: 89  
Best Local Similarity: 20.88%  
Query Match: 7.82%  
RESULT 539  
ID AAAS7362 standard; DNA; 6761 BP.  
DE DNA encoding a human hyaluronan-binding protein, designated WF-HABP.  
PN WO200039166-A1.  
PD 06-JUL-2000.  
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 112  
PA (AMNA-) AMERICAN NAT RED CROSS. Indels: 89  
Best Local Similarity: 20.88%  
Query Match: 7.82%  
RESULT 540  
ID AAT05627 standard; cDNA; 3259 BP.  
DE Bovine brevicain core protein cDNA.  
PN WO9526201-A1.  
PD 05-OCT-1995.  
PA (LJOL-) LA JOLLA CANCER RES FOUND. Mismatches: 100  
Best Local Similarity: 21.97% Indels: 97  
Query Match: 7.75%  
RESULT 541  
ID ACH15082 standard; cDNA; 488 BP.  
DE Human adult brain cDNA #2294.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.

PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W. Mismatches: 39  
 Best Local Similarity: 35.56% Indels: 4  
 Query Match: 7.69%  
 RESULT 542  
 ID ADPO7636 standard; DNA; 859 BP.  
 DE Human secreted protein encoding DNA, seq id 119.  
 PN WO2004042000-A2.  
 PD 21-MAY-2004.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 543  
 ID AA158121 standard; cDNA; 1365 BP.  
 DE Human polynucleotide SEQ ID NO 324.  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 544  
 ID ADL91792 standard; cDNA; 1844 BP.  
 DE Human PRO271 encoding cDNA SEQ ID NO:13.  
 PN WO2004042076-A2.  
 PD 25-MAR-2004.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 545  
 ID ADQ23710 standard; DNA; 1925 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6530.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 546  
 ID AAX52252 standard; DNA; 1984 BP.  
 DE Protein PRO271 cDNA clone DNA39423-1182.  
 PN WO9914328-A2.  
 PD 25-MAR-1999.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 547  
 ID ADC78532 standard; cDNA; 1984 BP.  
 DE Human PRO271 cDNA.  
 PN WO200015796-A2.  
 PD 23-MAR-2000.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 548  
 ID ADL18008 standard; cDNA; 1984 BP.  
 DE Human secreted/transmembrane protein cDNA, #42.  
 PN US2004147017-A1.  
 PD 29-JUL-2004.  
 PA (ASHK/) ASHKENAZI A.  
 PA (BOTS/) BOTSTEIN D.  
 PA (DESN/) DESNOYERS L.  
 PA (EATO/) EATON D L.  
 PA (FERR/) FERRARA N.  
 PA (FILV/) FILVAROFF E.  
 PA (FONG/) FONG S.  
 PA (GAOW/) GAO W.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GRIM/) GRIMALDI C J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (KLJA/) KLJAVIN I J.

PA (MATH/) MATHER J P.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (ROYM/) ROY M A.  
 PA (STEW/) STEWART T A.  
 PA (TUMA/) TUMAS D.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 549  
 ID AAF72410 standard; cDNA; 1985 BP.  
 DE Human PRO271 cDNA.  
 PN WO200104311-A1.  
 PD 18-JAN-2001.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 550  
 ID AAS45938 standard; cDNA; 1985 BP.  
 DE Human DNA encoding PRO polypeptide sequence #14.  
 PN WO200168848-A2.  
 PD 20-SEP-2001.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 551  
 ID ACA60174 standard; cDNA; 1985 BP.  
 DE Human cDNA for secreted/transmembrane protein PRO271.  
 PN US2003030350-A1.  
 PD 02-JAN-2003.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 552  
 ID ACA89388 standard; cDNA; 1985 BP.  
 DE cDNA encoding human PRO polypeptide #14.  
 PN US2003036141-A1.  
 PD 20-FEB-2003.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 553  
 ID ACA73398 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003036146-A1.  
 PD 20-FEB-2003.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 554  
 ID ACA05713 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003036162-A1.  
 PD 20-FEB-2003.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 555  
 ID ACA66547 standard; cDNA; 1985 BP.  
 DE cDNA encoding human PRO protein #14.  
 PN US2003036137-A1.  
 PD 20-FEB-2003.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 556  
 ID ACD07574 standard; cDNA; 1985 BP.  
 DE Novel human secreted and transmembrane protein PRO271 cDNA.  
 PN US2002197671-A1.  
 PD 26-DEC-2002.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 557  
 ID ACD07574 standard; cDNA; 1985 BP.  
 DE Novel human secreted and transmembrane protein PRO271 cDNA.  
 PN US2002197671-A1.  
 PD 26-DEC-2002.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4



PN US2003044916-A1.  
PD 06-MAR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 578  
ID ACH06954 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane polypeptide PRO271 cDNA.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 579  
ID ABX98166 standard; cDNA; 1985 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 27.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 580  
ID ACD13917 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 581  
ID ACD09697 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 582  
ID ACC88442 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 583  
ID ACD21182 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 584  
ID ABX75554 standard; cDNA; 1985 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO271.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 585  
ID ABX97757 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 586  
ID ACA97233 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 587  
ID ACA57696 standard; cDNA; 1985 BP.  
DE Human PRO271 cDNA.  
PN US2003036143-A1.

PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 588  
ID ACD14224 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 589  
ID ACC91007 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 590  
ID ACC88749 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 591  
ID ACD06946 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 592  
ID ACA67397 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 593  
ID ACC81452 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 594  
ID ACC89056 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 595  
ID ACC86412 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 596  
ID ACC89670 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 597  
ID ACC92849 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032135-A1.  
PD 13-FEB-2003.

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PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 598
ID ACA72477 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003022295-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 599
ID ACA88995 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003022297-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 600
ID ACA69731 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032105-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 601
ID ACA96874 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 602
ID ACA90870 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032111-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 603
ID ACA70652 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032119-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 604
ID ACA95162 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 605
ID ACC89977 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027263-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 606
ID ACC89977 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027271-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 607
ID ACD12585 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036125-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4

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Query Match: 7.69%
Indel: 4
RESULT 608
ID ACF19815 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040068-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 609
ID ABX76759 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003027280-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 610
ID ABX96191 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 611
ID ACA73091 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 612
ID ACA05512 standard; cDNA; 1985 BP.
DE cDNA encoding human secreted protein PRO271.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 613
ID ACA68634 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 614
ID ACA74478 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003036138-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 615
ID ACA70345 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032109-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 616
ID ACD14531 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003040066-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 617
ID ACD20179 standard; cDNA; 1985 BP.
DE Human secreted / transmembrane polypeptide PRO271 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4

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Query Match: 7.69% Indels: 4
RESULT 618
ID ACA68203 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 619
ID ABX98668 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 620
ID ACC81145 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032120-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 621
ID ACA95469 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 622
ID ACD04387 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 623
ID ACC87828 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 624
ID ACP12490 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040058-A1.
PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 625
ID ACA96205 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003017540-A1.
PD 23-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 626
ID ACA64979 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032106-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 627
ID ACA73705 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032129-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 628
ID ACA91349 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 629
ID ACA96512 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032103-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 630
ID ACD10618 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003032107-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 631
ID ACC91314 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032139-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 632
ID ACD02649 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003022301-A1.
PD 30-JAN-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 633
ID ACC87214 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 634
ID ACC85798 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027262-A1.
PD 06-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 635
ID ACA65286 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032110-A1.
PD 13-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 636
ID ACA94103 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036142-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 637
ID ACA97847 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003036145-A1.
PD 20-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 638
ID ACA91349 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
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PN US2003036154-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 639  
ID ACA90563 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 640  
ID ACD16110 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 641  
ID ACD17271 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 642  
ID AC91928 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 643  
ID ACA74785 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 644  
ID ACA91656 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 645  
ID ACA71300 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 646  
ID ACC90700 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 647  
ID ACA65710 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO protein #14.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 648  
ID ACA54982 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 649  
ID ACA94855 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 650  
ID ACD16417 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 651  
ID ACD15496 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 652  
ID ABX16599 standard; cDNA; 1985 BP.  
DE Human cDNA encoding secreted/transmembrane protein #14.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 653  
ID ACA97540 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 654  
ID ACA98989 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 655  
ID ACC91621 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 656  
ID ACD11032 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 657  
ID ACD14882 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 658  
ID ACD19817 standard; cDNA; 1985 BP.  
DE Human secreted / transmembrane polypeptide PRO271 cDNA.  
PN US2003027143-A1.  
PD 06-FEB-2003.

PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 659  
 ID ACD11646 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003032118-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 660  
 ID ACC95775 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003036135-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 661  
 ID ACF16338 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003054455-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 662  
 ID ACF02456 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003049741-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 663  
 ID ACF02763 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003049743-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 664  
 ID ACF21350 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003049769-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 665  
 ID ACF10034 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003068743-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 666  
 ID ACF77927 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003054479-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 667  
 ID ACD46632 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003068685-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4

RESULT 668  
 ID ACD49395 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003068725-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 669  
 ID ACF28162 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003068752-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 670  
 ID ACD88852 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003068682-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 671  
 ID ACD84247 standard; cDNA; 1985 BP.  
 DE Human PRO polynucleotide #14.  
 PN US2003068701-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 672  
 ID ACD99021 standard; cDNA; 1985 BP.  
 DE cDNA encoding human PRO polypeptide #14.  
 PN US2003068755-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 673  
 ID ADA77779 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003073180-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 674  
 ID ACF48763 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003104539-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 675  
 ID ADB29417 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein cDNA, #42.  
 PN US2003092002-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 676  
 ID ACD09083 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003036131-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 35.56% Mismatches: 39  
 Query Match: 7.69% Indels: 4  
 RESULT 677  
 ID ACF11876 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.



RESULT 696  
ID ACD45404 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 697  
ID ACF53061 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 698  
ID ACF27241 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 699  
ID ACF45079 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 700  
ID ACF29697 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 701  
ID ACD89773 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 702  
ID ACD84554 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 703  
ID ACD98714 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 704  
ID ACF77006 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 705  
ID ACF76699 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 706  
ID ACF49684 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 707  
ID ACF49991 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 708  
ID ACD09390 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 709  
ID ACD08469 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 710  
ID ACF12183 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 711  
ID ACC94691 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 712  
ID ACD22410 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 713  
ID ACF15110 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 714  
ID ACC97205 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 715  
ID ADA18273 standard; cDNA; 1985 BP.

DE Human secreted/transmembrane protein cdNA, #42.  
PN US2003039971-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 716  
ID ACD66964 standard; cdNA; 1985 BP.  
DE Human cdNA encoding secreted/transmembrane protein PRO271.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 717  
ID AC92235 standard; cdNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cdNA, SEQ ID NO:27.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 718  
ID ACF13882 standard; cdNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cdNA, SEQ ID NO:27.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 719  
ID ACF14189 standard; cdNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cdNA, SEQ ID NO:27.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 720  
ID ACF09420 standard; cdNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cdNA, SEQ ID NO:27.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 721  
ID ACD45711 standard; cdNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cdNA #14.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 722  
ID ACD47860 standard; cdNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cdNA #14.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 723  
ID ACD67591 standard; cdNA; 1985 BP.  
DE cdNA encoding human PRO polypeptide #14.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 724  
ID ACF25399 standard; cdNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cdNA, SEQ ID NO:27.

PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 725  
ID ACF29083 standard; cdNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cdNA, SEQ ID NO:27.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 726  
ID ACD84861 standard; cdNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cdNA #14.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 727  
ID ACD83940 standard; cdNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 728  
ID ACD87931 standard; cdNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cdNA #14.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 729  
ID ACF30618 standard; cdNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cdNA, SEQ ID NO:27.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 730  
ID ACF32221 standard; cdNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cdNA, SEQ ID NO:27.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 731  
ID ACH11881 standard; cdNA; 1985 BP.  
DE cdNA encoding human PRO polypeptide #14.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 732  
ID ACH12188 standard; cdNA; 1985 BP.  
DE cdNA encoding human PRO polypeptide #14.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 733  
ID ACD40580 standard; cdNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cdNA #14.  
PN US2003032134-A1.

PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 734  
ID ACF18052 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 735  
ID ACF08499 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 736  
ID ACF31300 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 737  
ID ACF52140 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 738  
ID ACD50009 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 739  
ID ACF38712 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 740  
ID ACF26627 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 741  
ID ACF24727 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 742  
ID ACF46307 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 743  
ID ACF27855 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 744  
ID ACD89159 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 745  
ID ACF63731 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 746  
ID ACF60371 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 747  
ID ACH12495 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 748  
ID ACH09918 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 749  
ID ACD03773 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 750  
ID ACD10311 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 751  
ID ACD11953 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 752  
ID ACD83125 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #38.

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PN US2003044793-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 753
ID ACF42338 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054480-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 754
ID ADA16248 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003049621-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 755
ID ACF18359 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059885-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 756
ID ACF02149 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049740-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 757
ID ACF21657 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049770-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 758
ID ACF10341 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073169-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 759
ID ACF37393 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064457-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 760
ID ACF44755 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068711-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 761
ID ACD90387 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049745-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 762
ID ACD91000 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049751-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 763
ID ACF30311 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003087478-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 764
ID ACD87010 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003086773-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 765
ID ACF60064 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073185-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 766
ID ACF46614 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003087373-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 767
ID ACF75471 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096353-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 768
ID ADA79571 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073173-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 769
ID ACF17131 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054458-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 770
ID ACF22885 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059886-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 771
ID ACF07885 standard; cDNA; 1985 BP.
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DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 772  
ID ACF08192 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 773  
ID ACF40496 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 774  
ID ACF53675 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 775  
ID ACF46939 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 776  
ID ACF47842 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 777  
ID ACF47228 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 778  
ID ACF46000 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 779  
ID ACF86089 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 780  
ID ACF52447 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003082715-A1.  
PD 01-MAY-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 781  
ID ACF52754 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 782  
ID ACF64747 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 783  
ID ACF76392 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 784  
ID ACF61292 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 785  
ID ACF61599 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 786  
ID ACD30630 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 787  
ID ACD31551 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 788  
ID ACD32472 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 789  
ID ACF17438 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 790  
ID ACF52447 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

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RESULT 790
ID ACF07271 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted/transmembrane protein cDNA, #42.
RESULT 791
ID ACF20429 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted/transmembrane protein cDNA, #42.
RESULT 792
ID ACF21043 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted/transmembrane protein (PRO) cDNA #14.
RESULT 793
ID ACF20736 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted/transmembrane protein (PRO) cDNA #14.
RESULT 794
ID ACD47553 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted/transmembrane protein (PRO) cDNA #14.
RESULT 795
ID ACF47535 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted/transmembrane protein (PRO) cDNA #14.
RESULT 796
ID ACF53368 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068579-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted/transmembrane protein (PRO) cDNA #14.
RESULT 797
ID ACD86703 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted/transmembrane protein (PRO) cDNA #14.
RESULT 798
ID ACH04951 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted/transmembrane protein (PRO) cDNA, SEQ ID NO:27.
RESULT 799
ID ACF44448 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted/transmembrane protein (PRO) cDNA, SEQ ID NO:27.
RESULT 800
ID ADA42393 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted/transmembrane protein (PRO) cDNA #14.
RESULT 801
ID ADA81298 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted/transmembrane protein (PRO) cDNA #14.
RESULT 802
ID ACD22103 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted/transmembrane protein (PRO) cDNA #14.
RESULT 803
ID ACD24450 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted/transmembrane protein (PRO) cDNA #14.
RESULT 804
ID ACD39653 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted/transmembrane protein (PRO) cDNA, SEQ ID NO:27.
RESULT 805
ID ACD39960 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted/transmembrane protein (PRO) cDNA, SEQ ID NO:27.
RESULT 806
ID ACF13268 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
RESULT 807
ID ACF03070 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
RESULT 808
ID ACD23303 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #38.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Indels: 4
Query Match:
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
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Query Match: 7.69% Indels: 4
RESULT 809
ID ACF78541 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACF83633 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACF11262 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACF50605 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACF34100 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACD46325 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACD48167 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACP27548 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACF24420 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACD85475 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACF01228 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040059-A1.
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DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 819
ID ACD83633 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACF49070 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACH07155 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACH07462 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACH08076 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACH11267 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACH11574 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACH10225 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
ID ACF01228 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040059-A1.
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PD 27-FEB-2003.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 828
ID ACF40803 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 829
ID ACD24143 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 830
ID ACD31244 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 831
ID ACF17745 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 832
ID ACF32528 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 833
ID ACF40189 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 834
ID ACF48149 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 835
ID ACF38098 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 836
ID ACF25034 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 837
ID ACC92542 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 838
ID ACF26934 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 839
ID ACD87624 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 840
ID ACF49377 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 841
ID ACF43834 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 842
ID ACH06179 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 843
ID ACH06486 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 844
ID ADA83096 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 845
ID ACC92542 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. Mismatches: 39
Best Local Similarity: 35.56% Indels: 4
Query Match: 7.69%
RESULT 846
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PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 847  
ID ACC931156 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO2711-encoding cDNA, SEQ ID NO:27.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 848  
ID ACF19201 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO2711-encoding cDNA, SEQ ID NO:27.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 849  
ID ACD12892 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 850  
ID ACF06350 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO2711-encoding cDNA, SEQ ID NO:27.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 851  
ID ACC94384 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO2711-encoding cDNA, SEQ ID NO:27.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 852  
ID ACC97812 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO2711-encoding cDNA, SEQ ID NO:27.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 853  
ID ACC94077 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO2711-encoding cDNA, SEQ ID NO:27.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 854  
ID ACF42031 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO2711-encoding cDNA, SEQ ID NO:27.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 855  
ID ACD30937 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 856  
ID ACD42966 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003054463-A1.  
PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 857  
ID ACD43273 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 858  
ID ACF14803 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO2711-encoding cDNA, SEQ ID NO:27.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 859  
ID ACF01535 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO2711-encoding cDNA, SEQ ID NO:27.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 860  
ID ACF31607 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO2711-encoding cDNA, SEQ ID NO:27.  
PN US2003064469-A1.  
PD 03-APR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 861  
ID ACD67284 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003064453-A1.  
PD 03-APR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 862  
ID ACD48474 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003064466-A1.  
PD 03-APR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 863  
ID ACD48781 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003064468-A1.  
PD 03-APR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 864  
ID ACF51219 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO2711-encoding cDNA, SEQ ID NO:27.  
PN US2003068760-A1.  
PD 10-APR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 865  
ID ACF53982 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO2711-encoding cDNA, SEQ ID NO:27.  
PN US2003068769-A1.  
PD 10-APR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 866  
ID ACD42966 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003054463-A1.  
PD 20-MAR-2003.



DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 885  
ID ACC96389 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 886  
ID ACC98419 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 887  
ID ADAL16672 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 888  
ID ACF41724 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 889  
ID ACF16645 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 890  
ID ADAL13101 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049622-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 891  
ID ACD32165 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 892  
ID ACD30323 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 893  
ID ACD41194 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 894

ID ACF07578 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 895  
ID ACF30993 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 896  
ID ACF77313 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 897  
ID ACF10955 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 898  
ID ACF32835 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 899  
ID ACF26013 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 900  
ID ACD83326 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 901  
ID ACF34399 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 902  
ID ACF42913 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 903  
ID ACF43220 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

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PN US2003104551-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 904
ID ACH05872 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049761-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 905
ID ACH08690 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049757-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 906
ID ADA11969 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003082540-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 907
ID ACC90284 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027273-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 908
ID ACF10648 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036119-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 909
ID ACC93463 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036120-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 910
ID ACD24757 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044921-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 911
ID ACD47246 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068697-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 912
ID ADA17316 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003017498-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 913
ID ACF01842 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049739-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 914
ID ACF21964 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059882-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 915
ID ACF22578 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059884-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 916
ID ACF08806 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068687-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 917
ID ACF33142 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073186-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 918
ID ACF54596 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064443-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 919
ID ACF48456 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064444-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 920
ID ACD47246 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068697-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 921
ID ACD49088 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068710-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 922
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ID ACF37791 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 923
ID ACF30004 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 924
ID ACD87317 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 925
ID ACF61906 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 926
ID ACH10839 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 927
ID ADA42819 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 928
ID ACD10004 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 929
ID ACD16729 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 930
ID ACC99026 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 931
ID ACF00420 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054456-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 932
ID ACD40887 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 933
ID ACF14496 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 934
ID ACF22271 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 935
ID ACF78848 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 936
ID ACF11569 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 937
ID ACF51526 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 938
ID ACF33449 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 939
ID ACD49702 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 940
ID ACF37484 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068683-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
RESULT 941
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatches: 39
Indels: 4
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ID ACF28469 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 942  
ID ACD88545 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068681-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 943  
ID ACF75164 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 944  
ID ACF60985 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 945  
ID ACF41141 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 946  
ID ACH08383 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 947  
ID ACC93770 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 948  
ID ACD20875 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 949  
ID ACF06657 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 950  
ID ACD20568 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044919-A1.  
PD 06-MAR-2003.

Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 951  
ID ACD22717 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 952  
ID ACF41417 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 953  
ID ACF06964 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 954  
ID ACD23665 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #38.  
PN US2003064923-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 955  
ID ACF77620 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 956  
ID ACD46018 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 957  
ID ACF46921 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 958  
ID ACF54289 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 959  
ID ACF45693 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 960

ID ACF45386 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 961

ID ACF38405 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 962

ID ACD89466 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 963

ID ACD85168 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 964

ID ACD85782 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 965

ID ACF75778 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 966

ID ACF60678 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 967

ID ACH05565 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 968

ID ADA82462 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 969

ID ACF55824 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 970

ID ACF55210 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 971

ID ADB77738 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 972

ID ADB74874 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 973

ID ADB85770 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 974

ID ACF56131 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 975

ID ACF56438 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 976

ID ACF55517 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 977

ID ACF54903 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 978

ID ADC28520 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003059772-A1.

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PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 979
ID ADC39720 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 980
ID ADC40234 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 981
ID ADC19058 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 982
ID ADC34358 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 983
ID ADC29413 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 984
ID ADC28944 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 985
ID ADC40829 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 986
ID ADC19486 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 987
ID ADC33934 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 988
ID ADC13004 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 989
ID ADC12456 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 990
ID ADD05500 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 991
ID ADD05011 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 992
ID ADD04017 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 993
ID ADD03593 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 994
ID ADE34845 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 995
ID ADG02495 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56% Mismatches: 39
Query Match: 7.69% Indels: 4
RESULT 996
ID ADG01202 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 997  
ID ADF95377 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 998  
ID ADG12192 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 999  
ID ADH08852 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1000  
ID ADH59328 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003039972-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1001  
ID ADJ38107 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1002  
ID ABX78541 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1003  
ID ACA59070 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #38.  
PN US2002146709-A1.  
PD 10-OCT-2002.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1004  
ID ACA75513 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1005  
ID ACA70993 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1006  
ID ACC87521 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003027278-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1007  
ID ACC86907 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1008  
ID ACD04080 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1009  
ID ACA69411 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1010  
ID ACA90256 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1011  
ID ACA58467 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #38.  
PN US2002192659-A1.  
PD 19-DEC-2002.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1012  
ID ACC89363 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1013  
ID ACA98154 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1014  
ID ACA93796 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1015  
ID ACD15189 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1016  
ID ACD08776 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040062-A1.  
PD 27-FEB-2003.

Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1017  
ID ACC96696 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1018  
ID ACF15417 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1019  
ID ACA72784 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1020  
ID ACD02956 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1021  
ID ACD01771 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1022  
ID ACA91963 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1023  
ID ADJ26375 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003054349-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1024  
ID ADL32633 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1025  
ID ADM30167 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1026  
ID ADE79290 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003135025-A1.

PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1027  
ID ADE79714 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003130489-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1028  
ID ADE73390 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003129592-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1029  
ID ADE74164 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1030  
ID ADE73925 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003148370-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1031  
ID ADE74776 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1032  
ID ADE99479 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003211576-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1033  
ID ADE98598 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003211569-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1034  
ID ADE99025 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003211568-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 35.56% Mismatches: 39  
Query Match: 7.69% Indels: 4  
RESULT 1035  
ID ADG40495 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003225253-A1.  
PD 04-DEC-2003.  
PA (DESN//) GODDARD A.

PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match: 35.56%  
Best Local Similarity: 7.69%  
Mismatch: 39  
Indel: 4  
RESULT 1036  
ID ADF73889 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003180312-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match: 35.56%  
Best Local Similarity: 7.69%  
Mismatch: 39  
Indel: 4  
RESULT 1037  
ID ADF95989 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match: 35.56%  
Best Local Similarity: 7.69%  
Mismatch: 39  
Indel: 4  
RESULT 1038  
ID ADF73465 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003166051-A1.  
PD 04-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match: 35.56%  
Best Local Similarity: 7.69%  
Mismatch: 39  
Indel: 4  
RESULT 1039  
ID ADG04260 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match: 35.56%  
Best Local Similarity: 7.69%  
Mismatch: 39  
Indel: 4  
RESULT 1040  
ID ADG00420 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match: 35.56%  
Best Local Similarity: 7.69%  
Mismatch: 39  
Indel: 4  
RESULT 1041  
ID ADG82676 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match: 35.56%  
Best Local Similarity: 7.69%  
Mismatch: 39  
Indel: 4  
RESULT 1042  
ID ADG92308 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003027145-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match: 35.56%  
Best Local Similarity: 7.69%  
Mismatch: 39  
Indel: 4  
RESULT 1043  
ID ADG92735 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003027146-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match: 35.56%  
Best Local Similarity: 7.69%  
Mismatch: 39  
Indel: 4  
RESULT 1044  
ID ADH25957 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.

PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match: 35.56%  
Best Local Similarity: 7.69%  
Mismatch: 39  
Indel: 4  
RESULT 1045  
ID ADH32926 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match: 35.56%  
Best Local Similarity: 7.69%  
Mismatch: 39  
Indel: 4  
RESULT 1046  
ID ADH20524 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2004005553-A1.  
PD 08-JAN-2004.  
PA (GETH) GENENTECH INC.  
Query Match: 35.56%  
Best Local Similarity: 7.69%  
Mismatch: 39  
Indel: 4  
RESULT 1047  
ID ADH07379 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2004006211-A1.  
PD 08-JAN-2004.  
PA (DESN) DESNOYERS L.  
PA (GODO/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match: 35.56%  
Best Local Similarity: 7.69%  
Mismatch: 39  
Indel: 4  
RESULT 1048  
ID ADH59924 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003215904-A1.  
PD 20-NOV-2003.  
PA (GETH) GENENTECH INC.  
Query Match: 35.56%  
Best Local Similarity: 7.69%  
Mismatch: 39  
Indel: 4  
RESULT 1049  
ID ADH06952 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2004005665-A1.  
PD 08-JAN-2004.  
PA (DESN) DESNOYERS L.  
PA (GODO/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match: 35.56%  
Best Local Similarity: 7.69%  
Mismatch: 39  
Indel: 4  
RESULT 1050  
ID ADI18694 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003152999-A1.  
PD 14-AUG-2003.  
PA (GETH) GENENTECH INC.  
Query Match: 35.56%  
Best Local Similarity: 7.69%  
Mismatch: 39  
Indel: 4  
RESULT 1051  
ID ADI65414 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003148419-A1.  
PD 07-AUG-2003.  
PA (GETH) GENENTECH INC.  
Query Match: 35.56%  
Best Local Similarity: 7.69%  
Mismatch: 39  
Indel: 4

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RESULT 1052
ID ADI37677 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003096340-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 1053
ID ADH97473 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003190610-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 1054
ID ADI65841 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003148371-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 1055
ID ADH60584 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2004023331-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 1056
ID ADJ99641 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003187238-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 1057
ID ADL08834 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003186358-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 1058
ID ADJ54665 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2004023321-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 1059
ID ADM25175 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003096233-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 1060
ID ADM29925 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2004185531-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 1061
ID ADJ64436 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2004038337-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 1062
ID ADM31332 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2004048334-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 1063
ID ADM36379 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2004053358-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 1064
ID ADM40184 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2004048335-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 1065
ID ADO06247 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #40.
PN US6686451-B1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 1066
ID ADN37792 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2004091959-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 1067
ID ADR11099 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2004137561-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 1068
ID ADT03684 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003152922-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4
RESULT 1069
ID ADS74647 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2004185531-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 35.56%
Query Match: 7.69%
Mismatch: 39
Indel: 4

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PD 23-SEP-2004.  
 PA (ASHK/) ASHKENAZI A.  
 PA (BOTS/) BOTSTEIN D.  
 PA (DESN/) DESNOYERS L.  
 PA (EATO/) EATON D L.  
 PA (FERR/) FERRARA N.  
 PA (FILV/) FILVAROFF E.  
 PA (FONG/) FONG S.  
 PA (GAOW/) GAO W.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GRIM/) GRIMALDI C J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (KLJA/) KLJAVIN I J.  
 PA (MATH/) MATHER J P.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (ROYM/) ROY M A.  
 PA (STEW/) STEWART T A.  
 PA (TUMA/) TUMAS D.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Best Local Similarity: 35.56%  
 Query Match: 7.69%  
 Mismatches: 39  
 Indels: 4  
 RESULT 1070  
 ID AAD48133 standard; DNA; 2878 BP.  
 DE Human chondroitin sulphate proteoglycan BEHAB/brevican DNA.  
 PN WO200276510-A1.  
 PD 03-OCT-2002.  
 PA (AGYT-) AGY THERAPEUTICS INC.  
 Best Local Similarity: 24.65%  
 Query Match: 7.69%  
 Mismatches: 76  
 Indels: 53  
 RESULT 1071  
 ID ADN38941 standard; cDNA; 2878 BP.  
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:259.  
 PN WO2003042661-A2.  
 PD 22-MAY-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Best Local Similarity: 24.65%  
 Query Match: 7.69%  
 Mismatches: 76  
 Indels: 53  
 RESULT 1072  
 ID ADK67783 standard; DNA; 2878 BP.  
 DE Human glycosylation-variant BEHAB isoform coding sequence.  
 PN WO2004013356-A1.  
 PD 12-FEB-2004.  
 PA (UYVA) UNIV YALE.  
 Best Local Similarity: 24.65%  
 Query Match: 7.69%  
 Mismatches: 76  
 Indels: 53  
 RESULT 1073  
 ID ADQ83194 standard; cDNA; 3467 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #8.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Best Local Similarity: 24.65%  
 Query Match: 7.69%  
 Mismatches: 76  
 Indels: 53  
 RESULT 1074  
 ID ADQ85107 standard; cDNA; 3467 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #1921.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Best Local Similarity: 24.65%  
 Query Match: 7.69%  
 Mismatches: 76  
 Indels: 53  
 RESULT 1075  
 ID ACN42086 standard; cDNA; 4353 BP.

DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:961.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 24.65%  
 Query Match: 7.69%  
 Mismatches: 76  
 Indels: 53  
 RESULT 1076  
 ID ACN42083 standard; cDNA; 4545 BP.  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:958.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 24.65%  
 Query Match: 7.69%  
 Mismatches: 76  
 Indels: 53  
 RESULT 1077  
 ID ACN42082 standard; cDNA; 4659 BP.  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:957.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 24.65%  
 Query Match: 7.69%  
 Mismatches: 76  
 Indels: 53  
 RESULT 1078  
 ID ABK62593 standard; cDNA; 2465 BP.  
 DE Rat sequence differentially expressed in response to a hepatotoxin #500.  
 PN WO200210453-A2.  
 PD 07-FEB-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Best Local Similarity: 27.14%  
 Query Match: 7.66%  
 Mismatches: 69  
 Indels: 11  
 RESULT 1079  
 ID ADB47730 standard; cDNA; 2753 BP.  
 DE Novel human secreted protein cDNA #3.  
 PN US2003054443-A1.  
 PD 20-MAR-2003.  
 PA (RUBE/) RUBEN S M.  
 PA (SOPP/) SOPPET D R.  
 PA (EBNE/) EBNER R.  
 PA (OLSE/) OLSEN H S.  
 PA (YOUN/) YOUNG P E.  
 PA (GREE/) GREENE J M.  
 PA (FERR/) FERRIE A M.  
 PA (YUGG/) YU G.  
 PA (NIJU/) NI J.  
 PA (ROSE/) ROSEN C A.  
 PA (BREW/) BREWER L A.  
 PA (JANA/) JANAT F.  
 PA (BIRS/) BIRSE C E.  
 Best Local Similarity: 20.62%  
 Query Match: 7.63%  
 Mismatches: 123  
 Indels: 97  
 RESULT 1080  
 ID ADJ5285 standard; cDNA; 2753 BP.  
 DE Novel human secreted protein cDNA #3.  
 PN US2004023283-A1.  
 PD 05-FEB-2004.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 20.62%  
 Query Match: 7.63%  
 Mismatches: 123  
 Indels: 97  
 RESULT 1081  
 ID ADQ45337 standard; DNA; 201 BP.  
 DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 7000.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Best Local Similarity: 42.65%  
 Query Match: 7.60%  
 Mismatches: 30  
 Indels: 2  
 RESULT 1082  
 ID ADQ45257 standard; DNA; 201 BP.  
 DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6920.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Best Local Similarity: 42.65%  
 Query Match: 7.60%  
 Mismatches: 30  
 Indels: 2

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Query Match: 7.54% Indels: 2
RESULT 1083
ID ADO45308 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6971.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 7.54% Indels: 2
RESULT 1084
ID ADO45241 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6904.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 7.54% Indels: 2
RESULT 1085
ID ADO45225 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6888.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 7.54% Indels: 2
RESULT 1086
ID ADO45323 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6986.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 7.54% Indels: 2
RESULT 1087
ID ADO45215 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6878.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 7.54% Indels: 2
RESULT 1088
ID ADO45264 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6927.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 7.54% Indels: 2
RESULT 1089
ID ADO45280 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6943.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 7.54% Indels: 2
RESULT 1090
ID ADO45298 standard; DNA; 201 BP.
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6961.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 42.65% Mismatches: 30
Query Match: 7.54% Indels: 2
RESULT 1091
ID ADL13960 standard; DNA; 834 BP.
DE Osteoarthritis-associated polymorphic nucleotide #492.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1092
ID ABL68341 standard; DNA; 1414 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6678.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1093
ID ABK83989 standard; cDNA; 1414 BP.
DE Human cDNA differentially expressed in granulocytic cells #560.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1094
ID ABX76383 standard; DNA; 1414 BP.
DE Lung cancer-associated polynucleotide #247.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1095
ID ACC72679 standard; cDNA; 1414 BP.
DE Human cancer related protein encoding cDNA SEQ ID NO:18.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1096
ID ADL13959 standard; DNA; 1414 BP.
DE Osteoarthritis-associated polymorphic nucleotide #491.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1097
ID ADN38975 standard; cDNA; 1414 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:293.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1098
ID ADO24484 standard; cDNA; 1414 BP.
DE Human PRO87343 encoding cDNA SEQ ID NO:123.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH-) GENENTECH INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1099
ID ADO24438 standard; cDNA; 1414 BP.
DE Human PRO87335 encoding cDNA SEQ ID NO:77.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH-) GENENTECH INC.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1100
ID ADR14116 standard; DNA; 1414 BP.
DE Human NF-kappaB pathway-associated gene SeqID117.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Best Local Similarity: 32.97% Mismatches: 39
Query Match: 7.54% Indels: 8
RESULT 1101
```

ID ACH45565 standard; cDNA; 474 BP.  
DE Human foetal cDNA #6290.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Best Local Similarity: 34.52%  
Query Match: 7.48%  
Mismatch: 41  
Indels: 2  
RESULT 1102  
ID ADM80846 standard; cDNA; 795 BP.  
DE Human CADSCM-33 encoding cDNA SEQ ID NO:75.  
PN WO2004015396-A2.  
PD 19-FEB-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 34.94%  
Query Match: 7.33%  
Mismatch: 37  
Indels: 3  
RESULT 1103  
ID AAV41923 standard; cDNA; 1587 BP.  
DE Nucleotide sequence of the cDNA clone BEF (HSXCK41).  
PN WO9831800-A2.  
PD 23-JUL-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (AUCC-) AUCCLAND UNISERVICES LTD.  
Best Local Similarity: 24.06%  
Query Match: 7.30%  
Mismatch: 81  
Indels: 48  
RESULT 1104  
ID AAO57710 standard; cDNA; 5191 BP.  
DE Neurocan DNA.  
PN WO9403601-A2.  
PD 17-FEB-1994.  
PA (UINY) UNIV NEW YORK STATE.  
Best Local Similarity: 23.61%  
Query Match: 7.27%  
Mismatch: 95  
Indels: 43  
RESULT 1105  
ID ABX34625 standard; cDNA; 1761 BP.  
DE Human mddt cDNA SEQ ID 186.  
PN WO200279449-A2.  
PD 10-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 23.87%  
Query Match: 7.24%  
Mismatch: 95  
Indels: 54  
RESULT 1106  
ID ADQ83195 standard; cDNA; 1771 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #9.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Best Local Similarity: 23.87%  
Query Match: 7.24%  
Mismatch: 95  
Indels: 54  
RESULT 1107  
ID ADM87060 standard; cDNA; 1783 BP.  
DE Human protein encoding cDNA SEQ ID NO:153.  
PN WO2004009834-A2.  
PD 29-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Best Local Similarity: 22.67%  
Query Match: 7.15%  
Mismatch: 68  
Indels: 89  
RESULT 1108  
ID ABL62702 standard; cDNA; 11185 BP.  
DE Colon adenocarcinoma related gene sequence SEQ ID NO:1039.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Best Local Similarity: 25.47%  
Query Match: 7.15%  
Mismatch: 69  
Indels: 27  
RESULT 1109  
ID ABN96814 standard; cDNA; 11185 BP.  
DE Gene #3312 used to diagnose liver cancer.

PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 25.47%  
Query Match: 7.15%  
Mismatch: 69  
Indels: 27  
RESULT 1110  
ID ADN95527 standard; cDNA; 11185 BP.  
DE Human BEC/LEC-related gene sequence SeqID450.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN) LICENTIA LTD.  
Best Local Similarity: 25.47%  
Query Match: 7.15%  
Mismatch: 69  
Indels: 27  
RESULT 1111  
ID ADJ75063 standard; cDNA; 11185 BP.  
DE Marker Gene SEQ ID NO:315.  
PN EPI394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Best Local Similarity: 25.47%  
Query Match: 7.15%  
Mismatch: 69  
Indels: 27  
RESULT 1112  
ID ADN04530 standard; cDNA; 11185 BP.  
DE Antiprosclerotic cDNA sequence #467.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 25.47%  
Query Match: 7.15%  
Mismatch: 69  
Indels: 27  
RESULT 1113  
ID ADP23737 standard; cDNA; 11185 BP.  
DE PRO polypeptide encoding cDNA SEQ ID NO:915.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 25.47%  
Query Match: 7.15%  
Mismatch: 69  
Indels: 27  
RESULT 1114  
ID AAS94985 standard; cDNA; 12319 BP.  
DE Human DNA sequence #240 expressed during foam cell differentiation.  
PN WO200177389-A2.  
PD 18-OCT-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 25.47%  
Query Match: 7.15%  
Mismatch: 69  
Indels: 27  
RESULT 1115  
ID ADJ75926 standard; cDNA; 7375 BP.  
DE Marker gene SEQ ID NO:1178.  
PN EPI394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Best Local Similarity: 28.93%  
Query Match: 7.12%  
Mismatch: 57  
Indels: 11  
RESULT 1116  
ID ADP71272 standard; cDNA; 573 BP.  
DE Human LP2 B-B' domain gene region SeqID7.  
PN JP2004154038-A.  
PD 03-JUN-2004.  
PA (SEKK) SEIKAGAKU KOGYO CO LTD.  
Best Local Similarity: 26.45%  
Query Match: 7.06%  
Mismatch: 63  
Indels: 36  
RESULT 1117  
ID ACH29430 standard; cDNA; 410 BP.  
DE Human adult spleen cDNA #449.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Best Local Similarity: 32.39%  
Mismatch: 32

Query Match: 6.97% Indels: 1

RESULT 1118  
ID A0Q38685 standard; DNA; 7291 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 348.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 24.18% Mismatches: 82  
Query Match: 6.97% Indels: 27

RESULT 1119  
ID A0Q38687 standard; DNA; 7358 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 350.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 24.18% Mismatches: 82  
Query Match: 6.97% Indels: 27

RESULT 1120  
ID A0Q38681 standard; DNA; 12553 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 344.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 24.18% Mismatches: 82  
Query Match: 6.97% Indels: 27

RESULT 1121  
ID A0Q38682 standard; DNA; 12620 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 345.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 24.18% Mismatches: 82  
Query Match: 6.97% Indels: 27

RESULT 1122  
ID A0Q38686 standard; DNA; 8224 BP.  
DE Human breast cancer associated coding sequence SEQ ID NO: 1222.  
PN WO200259271-A2.  
PD 01-AUG-2002.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 29.75% Mismatches: 57  
Query Match: 6.82% Indels: 11

RESULT 1123  
ID A0Q31199 standard; DNA; 5191 BP.  
DE Rat neurocan gene for glucosaminoglycan reduction in glial scars.  
PN WO2004041197-A2.  
PD 21-MAY-2004.  
PA (UYCA-) UNIV CASE WESTERN RESERVE.  
Best Local Similarity: 23.15% Mismatches: 96  
Query Match: 6.91% Indels: 43

RESULT 1124  
ID ABL07438 standard; CDNA; 8924 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16796.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 22.48% Mismatches: 85  
Query Match: 6.88% Indels: 54

RESULT 1125  
ID AAA63526 standard; DNA; 285 BP.  
DE DNA encoding the domain of hyaluronic acid which interacts with CD44.  
PN WO200047163-A2.  
PD 17-AUG-2000.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
Best Local Similarity: 27.10% Mismatches: 36  
Query Match: 6.85% Indels: 27

RESULT 1126  
ID ABA02881 standard; CDNA; 2087 BP.  
DE Human versican isoform V3 encoding CDNA SEQ ID NO 1.  
PN WO200179284-A2.  
PD 25-OCT-2001.  
PA (WIGH/) WIGHT T N.  
PA (MERR/) MERRILEES M.  
Best Local Similarity: 29.75% Mismatches: 57

Query Match: 6.82% Indels: 11

RESULT 1127  
ID A0Q38683 standard; DNA; 4330 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 346.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 29.75% Mismatches: 57  
Query Match: 6.82% Indels: 11

RESULT 1128  
ID ACH04002 standard; CDNA; 7182 BP.  
DE Human cDNA differentially expressed in lung cancer #207.  
PN US2003065157-A1.  
PD 03-APR-2003.  
PA (LASE/) LASEK A W.  
Best Local Similarity: 29.75% Mismatches: 57  
Query Match: 6.82% Indels: 11

RESULT 1129  
ID AAO12261 standard; CDNA; 8224 BP.  
DE Versican gene.  
PN WO9108230-A.  
PD 13-JUN-1991.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
Best Local Similarity: 29.75% Mismatches: 57  
Query Match: 6.82% Indels: 11

RESULT 1130  
ID A0Q38686 standard; DNA; 8224 BP.  
DE Breast cancer associated CDNA sequence SEQ ID NO:89.  
PN WO2003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Best Local Similarity: 29.75% Mismatches: 57  
Query Match: 6.82% Indels: 11

RESULT 1131  
ID A0Q38686 standard; DNA; 9592 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 349.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 29.75% Mismatches: 57  
Query Match: 6.82% Indels: 11

RESULT 1132  
ID A0Q38684 standard; DNA; 9647 BP.  
DE Breast cancer related marker, seq id 11006.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Best Local Similarity: 29.75% Mismatches: 57  
Query Match: 6.82% Indels: 11

RESULT 1133  
ID A0Q38684 standard; DNA; 9659 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 347.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 29.75% Mismatches: 57  
Query Match: 6.82% Indels: 11

RESULT 1134  
ID ABA06490 standard; CDNA; 972 BP.  
DE Human cDNA SEQ ID NO: 156.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 25.66% Mismatches: 66

Query Match: 6.79% Indels: 25  
 RESULT 1136  
 ID ABV83827 standard; cDNA; 972 BP.  
 DE Human polynucleotide SEQ ID NO 156.  
 PN US2002090672-A1.  
 PD 11-JUL-2002.  
 PA (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 Best Local Similarity: 25.66% Mismatches: 66  
 Indels: 25  
 Query Match: 6.79%  
 RESULT 1137  
 ID AAQ51157 standard; DNA; 1190 BP.  
 DE Herpes simplex virus glycoprotein I DNA.  
 PN EP568178-A1.  
 PD 03-NOV-1993.  
 PA (CEDA-) CSDARS SINAI MEDICAL CENT.  
 Best Local Similarity: 21.63% Mismatches: 99  
 Indels: 52  
 Query Match: 6.76%  
 RESULT 1138  
 ID ACA40155 standard; DNA; 1209 BP.  
 DE Prokaryotic essential gene #21812.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 22.47% Mismatches: 114  
 Indels: 61  
 Query Match: 6.73%  
 RESULT 1139  
 ID ADP71270 standard; DNA; 600 BP.  
 DE Human aggrecan B-B' domain gene region SeqID5.  
 PN JP2004154038-A.  
 PD 03-JUN-2004.  
 PA (SEKK) SEIKAGAKU KOGYO CO LTD.  
 Best Local Similarity: 37.36% Mismatches: 35  
 Indels: 14  
 Query Match: 6.70%  
 RESULT 1140  
 ID AAJ34196 standard; DNA; 1720 BP.  
 DE Human secreted protein gene 43 clone HSXCK41.  
 PN WO9839446-A2.  
 PD 11-SEP-1998.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 23.94% Mismatches: 80  
 Indels: 49  
 Query Match: 6.70%  
 RESULT 1141  
 ID ACD08067 standard; cDNA; 1720 BP.  
 DE cDNA encoding novel human secreted protein #43.  
 PN US2003027132-A1.  
 PD 06-FEB-2003.  
 PA (RUBE/) RUBEN S M.  
 PA (ROSE/) ROSEN C A.  
 PA (FISC/) FISCHER C L.  
 PA (SOPP/) SOPPET D R.  
 PA (CART/) CARTER K C.  
 PA (BEDN/) BEDNARIK D R.  
 PA (ENDR/) ENDRESS G A.  
 PA (YUGG/) YU G.  
 PA (NIJJ/) NI J.  
 PA (FENG/) FENG P.  
 PA (YOUN/) YOUNG P E.  
 PA (GREE/) GREENE J M.  
 PA (FERR/) FERRIE A M.  
 PA (DUAN/) DUAN R.  
 PA (HUJJ/) HU J.  
 PA (FLOR/) FLORENCE K A.  
 PA (OLSE/) OLSEN H S.  
 PA (EBNE/) EBNER R. A.  
 PA (BREW/) BREWER L A.  
 PA (SHIY/) SHI Y.  
 Best Local Similarity: 23.94% Mismatches: 80  
 Indels: 49  
 Query Match: 6.70%  
 RESULT 1142  
 ID AAC76373 standard; cDNA; 1377 BP.  
 DE Human ORFX ORF1928 polynucleotide sequence SEQ ID NO:3855.

PN WO200058473-A2.  
 PD 05-OCT-2000.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 21.12% Mismatches: 121  
 Indels: 91  
 Query Match: 6.67%  
 RESULT 1143  
 ID AAA61263 standard; DNA; 1308 BP.  
 DE Human secreted protein gene 4 clone HFXHC41.  
 PN WO200029422-A1.  
 PD 25-MAY-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 28.48% Mismatches: 55  
 Indels: 42  
 Query Match: 6.64%  
 RESULT 1144  
 ID AAA57365 standard; DNA; 1259 BP.  
 DE DNA encoding a human hyaluronan-binding protein, designated BM-HABP.  
 PN WO200039166-A1.  
 PD 06-JUL-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 24.56% Mismatches: 85  
 Indels: 20  
 Query Match: 6.61%  
 RESULT 1145  
 ID AAD08974 standard; cDNA; 1354 BP.  
 DE Alternative version of human TNF stimulated gene-6 (TSG-6) cDNA.  
 PN US6210905-B1.  
 PD 03-APR-2001.  
 PA (UYNY) UNIV NEW YORK STATE.  
 Best Local Similarity: 26.79% Mismatches: 78  
 Indels: 16  
 Query Match: 6.61%  
 RESULT 1146  
 ID ACC49518 standard; cDNA; 6310 BP.  
 DE Tumour-associated antigenic target protein TAT185 cDNA SEQ ID NO:26.  
 PN WO2003024392-A2.  
 PD 27-MAR-2003.  
 PA (GETH) GENENTECH INC.  
 Best Local Similarity: 23.02% Mismatches: 102  
 Indels: 62  
 Query Match: 6.58%  
 RESULT 1147  
 ID ADN38943 standard; cDNA; 6310 BP.  
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:261.  
 PN WO2003042661-A2.  
 PD 22-MAY-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Best Local Similarity: 23.02% Mismatches: 102  
 Indels: 62  
 Query Match: 6.58%  
 RESULT 1148  
 ID ADO31195 standard; DNA; 6310 BP.  
 DE Human neurocan gene for glucosaminoglycan reduction in glial scars.  
 PN WO2004041197-A2.  
 PD 21-MAY-2004.  
 PA (UYCA-) UNIV CASE WESTERN RESERVE.  
 Best Local Similarity: 23.02% Mismatches: 102  
 Indels: 62  
 Query Match: 6.58%  
 RESULT 1149  
 ID ADP71268 standard; DNA; 585 BP.  
 DE Human LPI B-B' domain gene region SeqID3.  
 PN JP2004154038-A.  
 PD 03-JUN-2004.  
 PA (SEKK) SEIKAGAKU KOGYO CO LTD.  
 Best Local Similarity: 33.33% Mismatches: 44  
 Indels: 7  
 Query Match: 6.52%  
 RESULT 1150  
 ID ADL13630 standard; DNA; 1065 BP.  
 DE Osteoarthritis-associated polymorphic nucleotide #162.  
 PN WO2003054166-A2.  
 PD 03-JUL-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 27.40% Mismatches: 63  
 Indels: 19  
 Query Match: 6.52%  
 RESULT 1151  
 ID ABT43880 standard; DNA; 1492 BP.  
 DE 151P3D4 v-1 DNA clone-1 from placenta.

PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Best Local Similarity: 27.40% Mismatches: 63  
Query Match: 6.52% Indels: 19  
RESULT 1152  
ID ABT43881 standard; DNA; 1492 BP.  
DE DNA derived from mRNA of human cartilage link protein.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Best Local Similarity: 27.40% Mismatches: 63  
Query Match: 6.52% Indels: 19  
RESULT 1153  
ID AAS28787 standard; cDNA; 1640 BP.  
DE Human immunoglobulin encoding cDNA SEQ ID No 33.  
PN WO200155315-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 25.83% Mismatches: 74  
Query Match: 6.52% Indels: 22  
RESULT 1154  
ID ABA06583 standard; cDNA; 1640 BP.  
DE Human cDNA SEQ ID No: 249.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 25.83% Mismatches: 74  
Query Match: 6.52% Indels: 22  
RESULT 1155  
ID ABV83920 standard; cDNA; 1640 BP.  
DE Human polynucleotide SEQ ID NO 249.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Best Local Similarity: 25.83% Mismatches: 74  
Query Match: 6.52% Indels: 22  
RESULT 1156  
ID ADB31512 standard; cDNA; 1640 BP.  
DE Human cDNA encoding a novel protein SEQ ID NO 33.  
PN US2003077606-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 25.83% Mismatches: 74  
Query Match: 6.52% Indels: 22  
RESULT 1157  
ID AAS28848 standard; cDNA; 1641 BP.  
DE Human immunoglobulin encoding cDNA SEQ ID No 94.  
PN WO200155315-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 25.83% Mismatches: 74  
Query Match: 6.52% Indels: 22  
RESULT 1158  
ID ABA06754 standard; cDNA; 1641 BP.  
DE Human cDNA SEQ ID No: 420.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 25.83% Mismatches: 74  
Query Match: 6.52% Indels: 22  
RESULT 1159  
ID ABV84091 standard; cDNA; 1641 BP.  
DE Human polynucleotide SEQ ID NO 420.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Best Local Similarity: 25.83% Mismatches: 74  
Query Match: 6.52% Indels: 22

RESULT 1160  
ID ADB31573 standard; cDNA; 1641 BP.  
DE Human cDNA encoding a novel protein SEQ ID NO 94.  
PN US2003077606-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 25.83% Mismatches: 74  
Query Match: 6.52% Indels: 22  
RESULT 1161  
ID ADH71347 standard; DNA; 1668 BP.  
DE Human gene of the invention NOV9s SEQ ID NO:243.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 29.21% Mismatches: 44  
Query Match: 6.52% Indels: 2  
RESULT 1162  
ID ADL13629 standard; DNA; 1759 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #161.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 27.40% Mismatches: 63  
Query Match: 6.52% Indels: 19  
RESULT 1163  
ID ABL34375 standard; DNA; 1790 BP.  
DE Human immune system associated gene SEQ ID NO: 2348.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 24.42% Mismatches: 52  
Query Match: 6.52% Indels: 64  
RESULT 1164  
ID ABK31533 standard; DNA; 1790 BP.  
DE Signal transduction associated gene modified complementary DNA #188.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 24.42% Mismatches: 52  
Query Match: 6.52% Indels: 64  
RESULT 1165  
ID ABT43866 standard; DNA; 1957 BP.  
DE DNA of transcript variant 151P3D4 v-1.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Best Local Similarity: 27.40% Mismatches: 63  
Query Match: 6.52% Indels: 19  
RESULT 1166  
ID ABT43869 standard; cDNA; 1957 BP.  
DE 151P3D4 v-1 cDNA clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Best Local Similarity: 27.40% Mismatches: 63  
Query Match: 6.52% Indels: 19  
RESULT 1167  
ID ABT43878 standard; cDNA; 1957 BP.  
DE 151P3D4 v-10 cDNA clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Best Local Similarity: 27.40% Mismatches: 63  
Query Match: 6.52% Indels: 19  
RESULT 1168  
ID ABT43877 standard; cDNA; 1957 BP.  
DE 151P3D4 v-9 cDNA clone-1 from placenta.  
PN WO200283860-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Best Local Similarity: 27.40% Mismatches: 63  
Query Match: 6.52% Indels: 19  
RESULT 1169  
ID ABA06754 standard; cDNA; 1641 BP.  
DE Human cDNA SEQ ID No: 420.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 25.83% Mismatches: 74  
Query Match: 6.52% Indels: 22

```
ID ABT43879 standard; cDNA; 1957 BP.
DE 151P3D4 v-11 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1170
ID ABT43874 standard; cDNA; 1957 BP.
DE 151P3D4 v-6 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1171
ID ABT43876 standard; cDNA; 1957 BP.
DE 151P3D4 v-8 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1172
ID ABT43871 standard; cDNA; 1957 BP.
DE 151P3D4 v-3 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1173
ID ABT43872 standard; cDNA; 1957 BP.
DE 151P3D4 v-4 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1174
ID ABT43873 standard; cDNA; 1957 BP.
DE 151P3D4 v-5 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1175
ID ABT43875 standard; cDNA; 1957 BP.
DE 151P3D4 v-7 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1176
ID ABT43870 standard; cDNA; 2166 BP.
DE 151P3D4 v-2 cDNA clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1177
ID ABT43865 standard; DNA; 2166 BP.
DE DNA of transcript variant 151P3D4 v-2.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1178
ID ABT43867 standard; DNA; 2166 BP.
DE DNA of transcript variant 151P3D4 v-2.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1179
ID ADQ24054 standard; DNA; 2538 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6874.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Best Local Similarity: 27.40% Mismatches: 63
Query Match: 6.52% Indels: 19
RESULT 1180
ID ABL07439 standard; cDNA; 6279 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16799.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Best Local Similarity: 23.18% Mismatches: 90
Query Match: 6.49% Indels: 48
RESULT 1181
ID ADH71333 standard; DNA; 1599 BP.
DE Human gene of the invention NOV91 SEQ ID NO:229.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 6.46% Indels: 2
RESULT 1182
ID ADH71335 standard; DNA; 1611 BP.
DE Human gene of the invention NOV9m SEQ ID NO:231.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 6.46% Indels: 2
RESULT 1183
ID ADH71313 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9b SEQ ID NO:209.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 6.46% Indels: 2
RESULT 1184
ID ADH71353 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9v SEQ ID NO:249.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 6.46% Indels: 2
RESULT 1185
ID ADH71341 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9p SEQ ID NO:237.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 6.46% Indels: 2
RESULT 1186
ID ADH71345 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9r SEQ ID NO:241.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 45
Query Match: 6.46% Indels: 2
RESULT 1187
ID ADH71339 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9o SEQ ID NO:235.
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PN WO2003102155-A2.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 29.21% Mismatches: 45  
Query Match: 6.46% Indels: 2  
RESULT 1188  
ID ADH71349 standard; DNA; 1668 BP.  
DE Human gene of the invention NOV9t SEQ ID NO:245.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 29.21% Mismatches: 45  
Query Match: 6.46% Indels: 2  
RESULT 1189  
ID ADH71343 standard; DNA; 1668 BP.  
DE Human gene of the invention NOV9q SEQ ID NO:239.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 29.21% Mismatches: 45  
Query Match: 6.46% Indels: 2  
RESULT 1190  
ID ABA83182 standard; DNA; 1851 BP.  
DE HST-4 ovarian tumour marker gene sequence, SEQ ID NO:144.  
PN WO200175177-A2.  
PD 11-OCT-2001.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Best Local Similarity: 33.71% Mismatches: 41  
Query Match: 6.46% Indels: 4  
RESULT 1191  
ID AAF87113 standard; DNA; 2011 BP.  
DE NOV2 coding sequence.  
PN WO200136638-A2.  
PD 25-MAY-2001.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 25.14% Mismatches: 84  
Query Match: 6.46% Indels: 22  
RESULT 1192  
ID ADH71315 standard; DNA; 2011 BP.  
DE Human gene of the invention NOV9c SEQ ID NO:211.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 25.14% Mismatches: 84  
Query Match: 6.46% Indels: 22  
RESULT 1193  
ID AAQ71391 standard; DNA; 2589 BP.  
DE Yeast 2.6 kb agglutination gene FLO1s.  
PN WO9419475-A2.  
PD 01-SEP-1994.  
PA (SAPB ) SAPPORO BREWERIES.  
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.  
Best Local Similarity: 25.10% Mismatches: 115  
Query Match: 6.46% Indels: 38  
RESULT 1194  
ID AAQ67360 standard; DNA; 2685 BP.  
DE S. cerevisiae FLO1 gene.  
PN WO9418330-A1.  
PD 18-AUG-1994.  
PA (UNIL ) UNILEVER PLC.  
PA (UNIL ) UNILEVER NV.  
Best Local Similarity: 25.10% Mismatches: 115  
Query Match: 6.46% Indels: 38  
RESULT 1195  
ID AAQ54029 standard; DNA; 2685 BP.  
DE Flocculation protein coding sequence of Saccharomyces cerevisiae.  
PN WO9401567-A1.  
PD 20-JAN-1994.  
PA (UNIL ) UNILEVER PLC.  
PA (UNIL ) UNILEVER NV.  
Best Local Similarity: 25.10% Mismatches: 115  
Query Match: 6.46% Indels: 38  
RESULT 1196  
ID ABL25978 standard; DNA; 7782 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 29407.  
PN WO200171042-A2.

ID ADQ38559 standard; DNA; 3858 BP.  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 222.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 22.28% Mismatches: 91  
Query Match: 6.46% Indels: 31  
RESULT 1197  
ID AAQ71390 standard; DNA; 4614 BP.  
DE Yeast 4.7 kb agglutination gene FLO1L.  
PN WO9419475-A2.  
PD 01-SEP-1994.  
PA (SAPB ) SAPPORO BREWERIES.  
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.  
Best Local Similarity: 25.10% Mismatches: 115  
Query Match: 6.46% Indels: 38  
RESULT 1198  
ID AAA95422 standard; DNA; 4614 BP.  
DE S. cerevisiae FLO1 coding sequence.  
PN WO200058342-A1.  
PD 05-OCT-2000.  
PA (VALW ) VALTION TEKNIILLINEN TUTKIMUSKESKUS.  
Best Local Similarity: 25.10% Mismatches: 115  
Query Match: 6.46% Indels: 38  
RESULT 1199  
ID ADS46655 standard; cDNA; 4614 BP.  
DE Bacterial polynucleotide #1398.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Best Local Similarity: 25.10% Mismatches: 115  
Query Match: 6.46% Indels: 38  
RESULT 1200  
ID ADO31201 standard; DNA; 5259 BP.  
DE Mouse neurocan gene for glucosaminoglycan reduction in glial scars.  
PN WO2004041197-A2.  
PD 21-MAY-2004.  
PA (UYCA-) UNIV CASE WESTERN RESERVE.  
Best Local Similarity: 26.21% Mismatches: 44  
Query Match: 6.46% Indels: 16  
RESULT 1201  
ID ABL25979 standard; DNA; 5388 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 29410.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 25.81% Mismatches: 93  
Query Match: 6.46% Indels: 52  
RESULT 1202  
ID ADR32196 standard; DNA; 5613 BP.  
DE Yeast FLO1 open reading frame fragment, SEQ ID NO:1.  
PN WO2004067565-A1.  
PD 12-AUG-2004.  
PA (OSBO-) OSBORNE DISTRIBUTORA SA.  
PA (UYDO/) UNIV DE OLAVIDE PABLO.  
Best Local Similarity: 25.10% Mismatches: 115  
Query Match: 6.46% Indels: 38  
RESULT 1203  
ID ADP87474 standard; DNA; 5864 BP.  
DE S. cerevisiae glucan synthase pathway gene YAR050W (FLO1) SeqID16.  
PN WO2004057033-A1.  
PD 08-JUL-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
Best Local Similarity: 25.10% Mismatches: 115  
Query Match: 6.46% Indels: 38  
RESULT 1204  
ID ABL25978 standard; DNA; 7782 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 29407.  
PN WO200171042-A2.



PD 27-SEP-2001.  
PA (PEXE ) PE CORP NY. Mismatches: 93  
Best Local Similarity: 25.81% Indels: 52  
Query Match: 6.46%  
RESULT 1205  
ID ABO42487 standard; DNA; 1174 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 29078.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG. Mismatches: 84  
Best Local Similarity: 24.35% Indels: 45  
Query Match: 6.43%  
RESULT 1206  
ID ABO42486 standard; DNA; 1174 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 29077.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG. Mismatches: 84  
Best Local Similarity: 24.35% Indels: 45  
Query Match: 6.43%  
RESULT 1207  
ID ACA55632 standard; cDNA; 1482 BP.  
DE Human signalling pathway polynucleotide probe SEQ ID NO 230.  
PN US6500938-B1.  
PD 31-DEC-2002.  
PA (INCY-) INCYTE GENOMICS INC. Mismatches: 122  
Best Local Similarity: 20.62% Indels: 98  
Query Match: 6.43%  
RESULT 1208  
ID ADI55428 standard; DNA; 1482 BP.  
DE Human polynucleotide probe #230.  
PN US2004010136-A1.  
PD 15-JAN-2004.  
PA (INCY-) INCYTE GENOMICS INC. Mismatches: 122  
Best Local Similarity: 20.62% Indels: 98  
Query Match: 6.43%  
RESULT 1209  
ID AA45836 standard; cDNA; 2455 BP.  
DE cDNA of intestinal insect mucin isoform IIM14.  
PN WO9967373-A2.  
PD 29-DEC-1999.  
PA (BOYC-) BOYCE THOMPSON INST PLANT RES. Mismatches: 75  
Best Local Similarity: 27.03% Indels: 34  
Query Match: 6.43%  
RESULT 1210  
ID AA45837 standard; cDNA; 2821 BP.  
DE cDNA of intestinal insect mucin isoform IIM22.  
PN WO9967373-A2.  
PD 29-DEC-1999.  
PA (BOYC-) BOYCE THOMPSON INST PLANT RES. Mismatches: 75  
Best Local Similarity: 27.03% Indels: 34  
Query Match: 6.43%  
RESULT 1211  
ID ADQ45269 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6932.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. Mismatches: 24  
Best Local Similarity: 42.86% Indels: 2  
Query Match: 6.40%  
RESULT 1212  
ID ADQ45261 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6924.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. Mismatches: 24  
Best Local Similarity: 42.86% Indels: 2  
Query Match: 6.40%  
RESULT 1213  
ID ADQ45247 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6910.  
PN WO2004058052-A2.  
PD 15-JUL-2004.

PA (APPL-) APPLERA CORP. Mismatches: 24  
Best Local Similarity: 42.86% Indels: 2  
Query Match: 6.40%  
RESULT 1214  
ID ADQ45220 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6883.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. Mismatches: 24  
Best Local Similarity: 42.86% Indels: 2  
Query Match: 6.40%  
RESULT 1215  
ID ADQ45210 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6873.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. Mismatches: 24  
Best Local Similarity: 42.86% Indels: 2  
Query Match: 6.40%  
RESULT 1216  
ID ADQ45303 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6966.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. Mismatches: 24  
Best Local Similarity: 42.86% Indels: 2  
Query Match: 6.40%  
RESULT 1217  
ID ADQ45335 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6998.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. Mismatches: 24  
Best Local Similarity: 42.86% Indels: 2  
Query Match: 6.40%  
RESULT 1218  
ID ADQ45230 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6893.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. Mismatches: 24  
Best Local Similarity: 42.86% Indels: 2  
Query Match: 6.40%  
RESULT 1219  
ID ADQ45293 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6956.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. Mismatches: 24  
Best Local Similarity: 42.86% Indels: 2  
Query Match: 6.40%  
RESULT 1220  
ID ADQ45313 standard; DNA; 201 BP.  
DE Myocardial infarction-associated SNP flanking transcript, SEQ ID 6976.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP. Mismatches: 43  
Best Local Similarity: 32.63% Indels: 9  
Query Match: 6.40%  
RESULT 1221  
ID ADP71266 standard; DNA; 600 BP.  
DE Human versican B-B' domain gene region SeqID1.  
PN JP2004154038-A.  
PD 03-JUN-2004.  
PA (SEGG ) SEIKAGAKU KOGYO CO LTD. Mismatches: 43  
Best Local Similarity: 32.63% Indels: 9  
Query Match: 6.40%  
RESULT 1222  
ID ADH71337 standard; DNA; 1668 BP.  
DE Human gene of the invention NOV9n SEQ ID NO:233.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.

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Best Local Similarity: 29.21% Mismatches: 46
Query Match: 6.40% Indels: 2
RESULT 1223
ID AAL56704 standard; DNA; 36604 BP.
DE Chimpanzee adenovirus serotype Pan6 genomic DNA.
PN WO2003046124-A2.
PA (MOOR/) MOORE P A.
PA (SHIV/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Best Local Similarity: 20.96% Mismatches: 106
Query Match: 6.34% Indels: 122
RESULT 1224
ID ACH79577 standard; DNA; 538 BP.
DE Human genome derived single exon probe #12772.
PN US2003194704-A1.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Best Local Similarity: 25.37% Mismatches: 55
Query Match: 6.31% Indels: 25
RESULT 1225
ID ACN44758 standard; DNA; 172569 BP.
DE Human genomic sequence hCG20145.
PN WO2003073826-A2.
PA (SAGR-) SAGRES DISCOVERY.
Best Local Similarity: 34.21% Mismatches: 35
Query Match: 6.31% Indels: 1
RESULT 1226
ID ADR24283 standard; DNA; 484 BP.
DE Breast cancer prognosis marker #144.
PN WO2004065545-A2.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Best Local Similarity: 20.71% Mismatches: 61
Query Match: 6.28% Indels: 28
RESULT 1227
ID ADH71351 standard; DNA; 1668 BP.
DE Human gene of the invention NOV9u SEQ ID NO:247.
PN WO2003102155-A2.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 29.21% Mismatches: 46
Query Match: 6.28% Indels: 2
RESULT 1228
ID ADN41609 standard; DNA; 4767 BP.
DE Novel human secreted protein polynucleotide seqid 731.
PN US200404191-A1.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYU/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAPL/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIV/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Best Local Similarity: 25.61% Mismatches: 114
Query Match: 6.28% Indels: 71
RESULT 1229
ID ADN41608 standard; DNA; 4768 BP.
DE Novel human secreted protein polynucleotide seqid 730.
PN US200404191-A1.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (SHIV/) SHI Y.
PA (MOOR/) MOORE P A.
PA (LAPL/) LAFLEUR D W.
PA (ZENG/) ZENG Z.
PA (LIYU/) LI Y.
PA (KYAW/) KYAW H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Best Local Similarity: 25.61% Mismatches: 114
Query Match: 6.28% Indels: 71
RESULT 1230
ID AAS28917 standard; DNA; 5430 BP.
DE Human immunoglobulin encoding genomic DNA SEQ ID NO 279.
PN WO200155315-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 23.46% Mismatches: 70
Query Match: 6.28% Indels: 28
RESULT 1231
ID ADB31758 standard; DNA; 5430 BP.
DE Human novel protein DNA SEQ ID NO 279.
PN US2003077606-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 23.46% Mismatches: 70
Query Match: 6.28% Indels: 28
RESULT 1232
ID ADI39160 standard; DNA; 86941 BP.
DE Streptomyces hygroscopicus herbimycin gene cluster, SEQ ID NO:2.
PN WO2003106653-A2.
PA (KOSA-) KOSAN BIOSCIENCES INC.
PA (REID/) REID R C.
Best Local Similarity: 21.39% Mismatches: 96
Query Match: 6.28% Indels: 133
RESULT 1233
ID ASL27120 standard; DNA; 8433 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32833.
PN WO200171042-A2.
PA (PEKE ) PE CORP NY.
Best Local Similarity: 31.01% Mismatches: 39
Query Match: 6.25% Indels: 42
RESULT 1234
ID ADF80106 standard; DNA; 402 BP.
DE Leukemia-related DNA sequence #662.
PN WO2003039443-A2.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Best Local Similarity: 32.26% Mismatches: 30
Query Match: 6.22% Indels: 0
RESULT 1235
ID AAT01476 standard; cDNA; 1519 BP.
DE Cat brain-enriched hyaluronan binding protein cDNA.
PN WO9527785-A1.
PA (UYUA ) UNIV YALE.
Best Local Similarity: 21.43% Mismatches: 107
Query Match: 6.22% Indels: 83
RESULT 1236
ID AAA34893 standard; DNA; 1696 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2582.
PN WO200009525-A2.
PA (UYEC-) UNIV EAST CAROLINA.
Best Local Similarity: 22.13% Mismatches: 106
Query Match: 6.22% Indels: 125

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RESULT 1237  
 ID AAF21015 standard; DNA; 1696 BP.  
 DE Human low adenosine antisense oligonucleotide related sequence #2582.  
 PN WO200062736-A2.  
 PD 26-OCT-2000.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 Best Local Similarity: 22.13% Mismatches: 106  
 Query Match: 6.22% Indels: 125

RESULT 1238  
 ID AB296709 standard; DNA; 1696 BP.  
 DE Human nucleic acid sequence.  
 PN WO200285308-A2.  
 PD 31-OCT-2002.  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 Best Local Similarity: 22.13% Mismatches: 106  
 Query Match: 6.22% Indels: 125

RESULT 1239  
 ID ABD20558 standard; DNA; 1696 BP.  
 DE Human pulmonary and inflammatory target DNA #169.  
 PN WO200285309-A2.  
 PD 31-OCT-2002.  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 Best Local Similarity: 22.13% Mismatches: 106  
 Query Match: 6.22% Indels: 125

RESULT 1240  
 ID AAV34254 standard; DNA; 1962 BP.  
 DE Human secreted protein gene 43 clone HSKCK41.  
 PN WO9839446-A2.  
 PD 11-SEP-1998.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 20.4% Mismatches: 107  
 Query Match: 6.22% Indels: 89

RESULT 1241  
 ID ACD08125 standard; cDNA; 1962 BP.  
 DE cDNA encoding novel human secreted protein #101.  
 PN US2003027132-A1.  
 PD 06-FEB-2003.  
 PA (RUBE/) RUBEN S M.  
 PA (ROSE/) ROSEN C A.  
 PA (FISC/) FISCHER C L.  
 PA (SOPP/) SOPPET D R.  
 PA (CART/) CARTER K C.  
 PA (BEDN/) BEDNARIK D R.  
 PA (ENDR/) ENDRESS G A.  
 PA (YUGG/) YU G.  
 PA (NIJJ/) NI J.  
 PA (FENG/) FENG P.  
 PA (YOUN/) YOUNG P E.  
 PA (GREE/) GREENE J M.  
 PA (FERR/) FERRIE A M.  
 PA (DUAN/) DUAN R.  
 PA (HUJJ/) HU J.  
 PA (FLOR/) FLORENCE K A.  
 PA (OLSE/) OLSEN H S.  
 PA (EBNE/) EBNER R.  
 PA (BREW/) BREWER L A.  
 PA (SHIY/) SHI Y.  
 Best Local Similarity: 20.4% Mismatches: 107  
 Query Match: 6.22% Indels: 89

RESULT 1242  
 ID ACN42085 standard; cDNA; 4391 BP.  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:960.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 25.00% Mismatches: 51  
 Query Match: 6.22% Indels: 14

RESULT 1243  
 ID ACN42084 standard; cDNA; 4536 BP.  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:959.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.

PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 25.00% Mismatches: 51  
 Query Match: 6.22% Indels: 14

RESULT 1244  
 ID ADM43175 standard; DNA; 35167 BP.  
 DE Wild-type adenovirus serotype 24 nucleotide sequence SEQ ID NO:5.  
 PN WO2004018627-A2.  
 PD 04-MAR-2004.  
 PA (MERI) MERCK & CO INC.  
 Best Local Similarity: 23.62% Mismatches: 78  
 Query Match: 6.22% Indels: 86

RESULT 1245  
 ID ADS00140 standard; DNA; 35167 BP.  
 DE Wild-type human adenovirus serotype 24 DNA SEQ ID NO:1.  
 PN WO2004083418-A1.  
 PD 30-SEP-2004.  
 PA (MERI) MERCK & CO INC.  
 Best Local Similarity: 23.62% Mismatches: 78  
 Query Match: 6.22% Indels: 86

RESULT 1246  
 ID ABT23534 standard; DNA; 1341 BP.  
 DE Cellobiohydrolase I activity polynucleotide SEQ ID NO 43.  
 PN WO2003000941-A2.  
 PD 03-JAN-2003.  
 PA (NOVO) NOVOZYMES AS.  
 Best Local Similarity: 23.68% Mismatches: 125  
 Query Match: 6.19% Indels: 104

RESULT 1247  
 ID ABU18341 standard; DNA; 1372 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6496.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Best Local Similarity: 29.69% Mismatches: 54  
 Query Match: 6.19% Indels: 25

RESULT 1248  
 ID ABU18340 standard; DNA; 4492 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6493.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Best Local Similarity: 29.69% Mismatches: 54  
 Query Match: 6.19% Indels: 25

RESULT 1249  
 ID ABQ81848 standard; DNA; 349980 BP.  
 DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1104.  
 PN EP1227152-A1.  
 PD 31-JUL-2002.  
 PA (NEST) SOC PROD NESTLE SA.  
 Best Local Similarity: 26.64% Mismatches: 113  
 Query Match: 6.16% Indels: 29

RESULT 1250  
 ID ABO41262 standard; DNA; 1276 BP.  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 27853.  
 PN WO200218632-A2.  
 PD 07-MAR-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Best Local Similarity: 24.53% Mismatches: 95  
 Query Match: 6.13% Indels: 38

RESULT 1251  
 ID ABO41263 standard; DNA; 1276 BP.  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 27854.  
 PN WO200218632-A2.  
 PD 07-MAR-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Best Local Similarity: 24.53% Mismatches: 95  
 Query Match: 6.13% Indels: 38

RESULT 1252  
 ID AAA93621 standard; DNA; 2607 BP.  
 DE Human SLIT protein-like splice variant SECX 3352358-2 DNA.  
 PN WO200053742-A2.  
 PD 14-SEP-2000.  
 PA (CURA-) CURAGEN CORP.

Best Local Similarity: 20.58% Mismatches: 124  
 Query Match: 6.13% Indels: 79  
 RESULT 1253  
 ID ADA23288 standard; cDNA; 2607 BP.  
 DE cDNA encoding human SECK polypeptide, SEC6.  
 PN US2003054514-A1.  
 PD 20-MAR-2003.  
 PA (SHIM/) SHIMKETS R A.  
 PA (LARO/) LAROCHELLE W J.  
 Best Local Similarity: 20.58% Mismatches: 124  
 Query Match: 6.13% Indels: 79  
 RESULT 1254  
 ID ABK33981 standard; DNA; 6112 BP.  
 DE Human DNA for staging of Astrocytomas, complement, #33.  
 PN WO200202808-A2.  
 PD 10-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Best Local Similarity: 24.53% Mismatches: 95  
 Query Match: 6.13% Indels: 38  
 RESULT 1255  
 ID ADA20369 standard; DNA; 6112 BP.  
 DE Prostate tumour related genomic DNA complement sample #17.  
 PN WO2002103042-A2.  
 PD 27-DEC-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Best Local Similarity: 24.53% Mismatches: 95  
 Query Match: 6.13% Indels: 38  
 RESULT 1256  
 ID ADA84176 standard; DNA; 6112 BP.  
 DE Human renal/prostate carcinoma associated DNA SEQ ID NO:34.  
 PN WO2002103041-A2.  
 PD 27-DEC-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Best Local Similarity: 24.53% Mismatches: 95  
 Query Match: 6.13% Indels: 38  
 RESULT 1257  
 ID AAS59543 standard; DNA; 53178 BP.  
 DE Propionibacterium acnes immunogenic protein encoding DNA #38.  
 PN WO200181581-A2.  
 PD 01-NOV-2001.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 25.00% Mismatches: 91  
 Query Match: 6.13% Indels: 67  
 RESULT 1258  
 ID ACF64472 standard; DNA; 53178 BP.  
 DE Propionibacterium acnes DNA contig sequence #38.  
 PN WO2003033515-A1.  
 PD 24-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 25.00% Mismatches: 91  
 Query Match: 6.13% Indels: 67  
 RESULT 1259  
 ID AAT01475 standard; cDNA; 1084 BP.  
 DE Rat brain-enriched hyaluronan binding protein cDNA.  
 PN WO9527785-A1.  
 PD 19-OCT-1995.  
 PA (UYVA) UNIV YALE.  
 Best Local Similarity: 25.00% Mismatches: 52  
 Query Match: 6.10% Indels: 14  
 RESULT 1260  
 ID AAH90018 standard; cDNA; 2313 BP.  
 DE Human bone marrow cDNA, SEQ ID NO: 262.  
 PN WO200153453-A2.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 26.75% Mismatches: 78  
 Query Match: 6.10% Indels: 55  
 RESULT 1261  
 ID ACD05902 standard; cDNA; 2313 BP.  
 DE Novel human contig #76.  
 PN WO2003023013-A2.  
 PD 20-MAR-2003.  
 PA (HYSE-) HYSEQ INC.

Best Local Similarity: 26.75% Mismatches: 78  
 Query Match: 6.10% Indels: 55  
 RESULT 1262  
 ID ADE07990 standard; DNA; 2313 BP.  
 DE Novel DNA-related contig nucleotide sequence #512.  
 PN WO2003054152-A2.  
 PD 03-JUL-2003.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 26.75% Mismatches: 78  
 Query Match: 6.10% Indels: 55  
 RESULT 1263  
 ID ADE07629 standard; DNA; 2514 BP.  
 DE Novel coding sequence (useful for identifying genetic disorders) #695.  
 PN WO2003054152-A2.  
 PD 03-JUL-2003.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 26.75% Mismatches: 78  
 Query Match: 6.10% Indels: 55  
 RESULT 1264  
 ID AAH14562 standard; cDNA; 3118 BP.  
 DE Human cDNA sequence SEQ ID NO:12139.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Best Local Similarity: 26.75% Mismatches: 78  
 Query Match: 6.10% Indels: 55  
 RESULT 1265  
 ID ADB63178 standard; cDNA; 3175 BP.  
 DE Human cDNA encoding clone SPLEN20087370.  
 PN EP1308459-A2.  
 PD 07-MAY-2003.  
 PA (HELI-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Best Local Similarity: 23.23% Mismatches: 87  
 Query Match: 6.10% Indels: 106  
 RESULT 1266  
 ID AAH14010 standard; cDNA; 3499 BP.  
 DE Human cDNA sequence SEQ ID NO:11101.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Best Local Similarity: 26.75% Mismatches: 78  
 Query Match: 6.10% Indels: 55  
 RESULT 1267  
 ID ADO00911 standard; cDNA; 4011 BP.  
 DE Human homologue of Fruit fly AD-related cDNA CG1103 #2.  
 PN US2004067535-A1.  
 PD 08-APR-2004.  
 PA (LIFE-) LIFE SCI DEV CORP.  
 Best Local Similarity: 26.75% Mismatches: 78  
 Query Match: 6.10% Indels: 55  
 RESULT 1268  
 ID ADR07180 standard; cDNA; 5131 BP.  
 DE Full length human cDNA useful for treating neurological disease Seq 686.  
 PN EP1447413-A2.  
 PD 18-AUG-2004.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Best Local Similarity: 26.75% Mismatches: 78  
 Query Match: 6.10% Indels: 55  
 RESULT 1269  
 ID ADL13962 standard; DNA; 160198 BP.  
 DE Osteoarthritis-associated polymorphic nucleotide #494.  
 PN WO2003054166-A2.  
 PD 03-JUL-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 34.55% Mismatches: 23  
 Query Match: 6.10% Indels: 2  
 RESULT 1270  
 ID AAS17594 standard; cDNA; 1209 BP.  
 DE DNA encoding novel secreted protein #23.  
 PN WO200179454-A1.  
 PD 25-OCT-2001.  
 PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC. Mismatches: 40  
 Query Match: 30.86% Indels: 3  
 RESULT 1271  
 ID ADF58259 standard; cDNA; 1209 BP.  
 DE Human polynucleotide sequence SEQ ID NO:626.  
 PN WO2003080795-A2.  
 PD 02-OCT-2003.  
 PA (HYSE-) HYSEQ INC. Mismatches: 40  
 Best Local Similarity: 30.86% Indels: 3  
 Query Match: 6.07%  
 RESULT 1272  
 ID AAA37671 standard; DNA; 1241 BP.  
 DE Human peptidase, HPEP-15 coding sequence.  
 PN WO200042201-A2.  
 PD 20-JUL-2000.  
 PA (INCY-) INCYTE PHARM INC. Mismatches: 76  
 Best Local Similarity: 23.50% Indels: 45  
 Query Match: 6.07%  
 RESULT 1273  
 ID ABK1078 standard; cDNA; 1475 BP.  
 DE cDNA encoding LP polypeptide #1.  
 PN WO200216578-A2.  
 PD 28-FEB-2002.  
 PA (ELIL ) LILLY & CO ELI. Mismatches: 40  
 Best Local Similarity: 30.86% Indels: 3  
 Query Match: 6.07%  
 RESULT 1274  
 ID ABU24247 standard; DNA; 4140 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 24214.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY. Mismatches: 94  
 Best Local Similarity: 20.16% Indels: 59  
 Query Match: 6.07%  
 RESULT 1275  
 ID ADF74225 standard; cDNA; 5409 BP.  
 DE Human novel brain/hippocampus cDNA #43.  
 PN JP2003009886-A.  
 PD 14-JAN-2003.  
 PA (KAZU-) ZH KAZUSA DNA KENKYUSHO. Mismatches: 40  
 Best Local Similarity: 30.86% Indels: 3  
 Query Match: 6.07%  
 RESULT 1276  
 ID AAD56128 standard; DNA; 7596 BP.  
 DE Mouse Notch carcinoma associated (CA) gene coding region.  
 PN WO2003035837-A2.  
 PD 01-MAY-2003.  
 PA (SAGR-) SAGRES DISCOVERY. Mismatches: 65  
 Best Local Similarity: 25.99% Indels: 47  
 Query Match: 6.07%  
 RESULT 1277  
 ID ADA02491 standard; cDNA; 7596 BP.  
 DE Mouse Notch1 carcinoma associated coding sequence, SEQ ID NO:1009.  
 PN WO2003057146-A2.  
 PD 17-JUL-2003.  
 PA (SAGR-) SAGRES DISCOVERY. Mismatches: 65  
 Best Local Similarity: 25.99% Indels: 47  
 Query Match: 6.07%  
 RESULT 1278  
 ID ADB72229 standard; cDNA; 7596 BP.  
 DE Mouse Notch1 cDNA.  
 PN WO2003008583-A2.  
 PD 30-JAN-2003.  
 PA (SAGR-) SAGRES DISCOVERY. Mismatches: 65  
 Best Local Similarity: 25.99% Indels: 47  
 Query Match: 6.07%  
 RESULT 1279  
 ID AAD56127 standard; DNA; 8064 BP.  
 DE Mouse Notch carcinoma associated (CA) DNA.  
 PN WO2003035837-A2.  
 PD 01-MAY-2003.

PA (SAGR-) SAGRES DISCOVERY. Mismatches: 65  
 Best Local Similarity: 25.99% Indels: 47  
 Query Match: 6.07%  
 RESULT 1280  
 ID ADA02490 standard; cDNA; 8064 BP.  
 DE Mouse Notch1 carcinoma associated cDNA, SEQ ID NO:1008.  
 PN WO2003057146-A2.  
 PD 17-JUL-2003.  
 PA (SAGR-) SAGRES DISCOVERY. Mismatches: 65  
 Best Local Similarity: 25.99% Indels: 47  
 Query Match: 6.07%  
 RESULT 1281  
 ID ADB72228 standard; mRNA; 8064 BP.  
 DE Mouse Notch1 mRNA.  
 PN WO2003008583-A2.  
 PD 30-JAN-2003.  
 PA (SAGR-) SAGRES DISCOVERY. Mismatches: 65  
 Best Local Similarity: 25.99% Indels: 47  
 Query Match: 6.07%  
 RESULT 1282  
 ID ABQ14105 standard; DNA; 645 BP.  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 696.  
 PN WO200218632-A2.  
 PD 07-MAR-2002.  
 PA (EPIG-) EPIGENOMICS AG. Mismatches: 68  
 Best Local Similarity: 21.39% Indels: 64  
 Query Match: 6.04%  
 RESULT 1283  
 ID ABQ14104 standard; DNA; 645 BP.  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 695.  
 PN WO200218632-A2.  
 PD 07-MAR-2002.  
 PA (EPIG-) EPIGENOMICS AG. Mismatches: 68  
 Best Local Similarity: 21.39% Indels: 64  
 Query Match: 6.04%  
 RESULT 1284  
 ID ADS55917 standard; cDNA; 1386 BP.  
 DE Bacterial polynucleotide #7904.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y. Mismatches: 99  
 Best Local Similarity: 25.60% Indels: 64  
 Query Match: 6.04%  
 RESULT 1285  
 ID ADR46580 standard; DNA; 2453 BP.  
 DE Mouse junctional adhesion molecule-1 encoding gene, SEQ ID 11.  
 PN JP2004242513-A.  
 PD 02-SEP-2004.  
 PA (DOKU-) DOKURITSU GYOSHI HOJIN KAGAKU GIJUTSU SH. Mismatches: 109  
 Best Local Similarity: 23.35% Indels: 132  
 Query Match: 6.04%  
 RESULT 1286  
 ID ADR99037 standard; DNA; 9487 BP.  
 DE Chondroitin sulfate proteoglycan 2 (versican), CSPG2, DNA SEQ ID 43.  
 PN WO2004078035-A2.  
 PD 16-SEP-2004.  
 PA (FARB ) BAYER PHARM CORP. Mismatches: 98  
 Best Local Similarity: 20.09% Indels: 48  
 Query Match: 6.04%  
 RESULT 1287  
 ID ABZ59662 standard; cDNA; 2622 BP.  
 DE Human secreted protein SECP-17 encoding cDNA SEQ ID NO:48.  
 PN WO2003004615-A2.  
 PD 16-JAN-2003.  
 PA (INCY-) INCYTE GENOMICS INC. Mismatches: 40  
 Best Local Similarity: 30.86% Indels: 3  
 Query Match: 6.00%  
 RESULT 1288

ID ABQ81849 standard; DNA; 349980 BP.  
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1105.  
PN EP1227152-A1.  
PD 31-JUL-2002.  
PA (NEST ) SOC PROD NESTLE SA.  
Best Local Similarity: 23.40% Mismatches: 103  
Query Match: 6.00% Indels: 100  
RESULT 1289  
ID AAV28137 standard; cDNA to mRNA; 1374 BP.  
DE Mouse junctional adhesion molecule gene.  
PN WO9824897-A1.  
PD 11-JUN-1998.  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
Best Local Similarity: 23.75% Mismatches: 104  
Query Match: 5.97% Indels: 121  
RESULT 1290  
ID ABL27121 standard; DNA; 4287 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32836.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 28.39% Mismatches: 59  
Query Match: 5.97% Indels: 42  
RESULT 1291  
ID ADO30240 standard; cDNA; 4488 BP.  
DE Mouse GPCR GPRC5B polynucleotide, SEQ ID NO:1343.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Best Local Similarity: 22.01% Mismatches: 96  
Query Match: 5.97% Indels: 68  
RESULT 1292  
ID AAF86431 standard; DNA; 349980 BP.  
DE Pyrococcus abyssi genomic fragment #1.  
PN FR2792651-A1.  
PD 27-OCT-2000.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
PA (IFRE-) IFREMER INST FR RECH EXPL MER.  
Best Local Similarity: 23.50% Mismatches: 51  
Query Match: 5.97% Indels: 80  
RESULT 1293  
ID AAA27366 standard; DNA; 1206 BP.  
DE Sinorhizobium meliloti ribc gene.  
PN WO200029607-A1.  
PD 25-MAY-2000.  
PA (REGC ) UNIV CALIFORNIA.  
Best Local Similarity: 27.07% Mismatches: 45  
Query Match: 5.94% Indels: 33  
RESULT 1294  
ID ABL25807 standard; DNA; 3381 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28894.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 25.00% Mismatches: 86  
Query Match: 5.94% Indels: 57  
RESULT 1295  
ID ADS48391 standard; cDNA; 3799 BP.  
DE Bacterial polynucleotide #3134.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SIAT/) SIATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Best Local Similarity: 23.61% Mismatches: 64  
Query Match: 5.94% Indels: 73  
RESULT 1296  
ID AAA27364 standard; DNA; 4248 BP.  
DE Sinorhizobium meliloti ribc/ribd gene complex.  
PN WO200029607-A1.  
PD 25-MAY-2000.

PA (REGC ) UNIV CALIFORNIA.  
Best Local Similarity: 27.07% Mismatches: 45  
Query Match: 5.94% Indels: 33  
RESULT 1297  
ID ABL25806 standard; DNA; 5381 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28891.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 25.00% Mismatches: 86  
Query Match: 5.94% Indels: 57  
RESULT 1298  
ID ADH69807 standard; DNA; 684973 BP.  
DE Human Vbeta gene.  
PN US2002150891-A1.  
PD 17-OCT-2002.  
PA (HOOD/) HOOD L E.  
PA (ROWE/) ROWEN L.  
Best Local Similarity: 26.49% Mismatches: 93  
Query Match: 5.94% Indels: 25  
RESULT 1299  
ID ABL68560 standard; DNA; 267156 BP.  
DE DE Kidney cancer related gene sequence SEQ ID NO:6897.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Best Local Similarity: 26.49% Mismatches: 93  
Query Match: 5.94% Indels: 25  
RESULT 1300  
ID ABL07173 standard; cDNA; 6353 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16001.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 25.88% Mismatches: 71  
Query Match: 5.91% Indels: 34  
RESULT 1301  
ID ABL07172 standard; cDNA; 8429 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15998.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 25.88% Mismatches: 71  
Query Match: 5.91% Indels: 34  
RESULT 1302  
ID ABQ51862 standard; DNA; 585 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38453.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 23.68% Mismatches: 50  
Query Match: 5.88% Indels: 72  
RESULT 1303  
ID ABQ51863 standard; DNA; 585 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38454.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 23.68% Mismatches: 50  
Query Match: 5.88% Indels: 72  
RESULT 1304  
ID ABQ25506 standard; DNA; 1195 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 12097.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 25.29% Mismatches: 77  
Query Match: 5.88% Indels: 31  
RESULT 1305  
ID ABQ25507 standard; DNA; 1195 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 12098.  
PN WO200218632-A2.  
PD 07-MAR-2002.

PA (EPIC-) EPIGENOMICS AG.  
 Query Match: 25.29% Mismatches: 77  
 RESULT 1306 Indels: 31  
 ID AAX22095 standard; DNA; 1767 BP.  
 DE Cellobiohydrolase CBH B coding sequence.  
 PN WO3906574-A1.  
 PD 11-FEB-1999.  
 PA (KONN ) GIST-BROCADES BV.  
 Best Local Similarity: 22.03% Mismatches: 77  
 Query Match: 5.88% Indels: 70  
 RESULT 1307  
 ID AAR81515 standard; DNA; 16978 BP.  
 DE N. meningitidis partial DNA sequence gnm\_62 SEQ ID NO:62.  
 PN WO200022430-A2.  
 PD 20-APR-2000.  
 PA (CHIR ) CHIRON CORP.  
 Best Local Similarity: 19.17% Mismatches: 113  
 Query Match: 5.88% Indels: 129  
 RESULT 1308  
 Best Local Similarity: 19.17% Mismatches: 113  
 Query Match: 5.88% Indels: 129  
 RESULT 1309  
 ID AAF21609 standard; DNA; 349980 BP.  
 DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:110.  
 PN WO200066791-A1.  
 PD 09-NOV-2000.  
 PA (CHIR ) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.  
 Best Local Similarity: 19.17% Mismatches: 113  
 Query Match: 5.88% Indels: 129  
 RESULT 1310  
 ID AAF21608 standard; DNA; 349980 BP.  
 DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.  
 PN WO200066791-A1.  
 PD 09-NOV-2000.  
 PA (CHIR ) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.  
 Best Local Similarity: 19.17% Mismatches: 113  
 Query Match: 5.88% Indels: 129  
 RESULT 1311  
 ID ACH93277 standard; DNA; 334 BP.  
 DE Human genome derived single exon probe #26472.  
 PN US2003194704-A1.  
 PD 16-OCT-2003.  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANK/) HANZEL D K.  
 Best Local Similarity: 27.27% Mismatches: 40  
 Query Match: 5.85% Indels: 8  
 RESULT 1312  
 ID ABQ33971 standard; DNA; 738 BP.  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20562.  
 PN WO200218632-A2.  
 PD 07-MAR-2002.  
 PA (EPIC-) EPIGENOMICS AG.  
 Best Local Similarity: 23.94% Mismatches: 85  
 Query Match: 5.85% Indels: 39  
 RESULT 1313  
 ID ABQ33970 standard; DNA; 738 BP.  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20561.  
 PN WO200218632-A2.  
 PD 07-MAR-2002.  
 PA (EPIC-) EPIGENOMICS AG.  
 Best Local Similarity: 23.94% Mismatches: 85  
 Query Match: 5.85% Indels: 39  
 RESULT 1314  
 ID ABQ41874 standard; DNA; 1347 BP.  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 28465.  
 PN WO200218632-A2.  
 PD 07-MAR-2002.  
 PA (EPIC-) EPIGENOMICS AG.  
 Best Local Similarity: 22.62% Mismatches: 79

Query Match: 5.85% Indels: 68  
 RESULT 1315  
 ID ABQ41875 standard; DNA; 1347 BP.  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 28466.  
 PN WO200218632-A2.  
 PD 07-MAR-2002.  
 PA (EPIC-) EPIGENOMICS AG.  
 Best Local Similarity: 22.62% Mismatches: 79  
 Query Match: 5.85% Indels: 68  
 RESULT 1316  
 ID ACA30865 standard; DNA; 2085 BP.  
 DE Prokaryotic essential gene #12522.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 21.71% Mismatches: 90  
 Query Match: 5.85% Indels: 66  
 RESULT 1317  
 ID ADA53056 standard; cDNA; 2751 BP.  
 DE Human coding sequence, SEQ ID 624.  
 PN EPI293569-A2.  
 PD 19-MAR-2003.  
 PA (HELI-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Best Local Similarity: 24.09% Mismatches: 89  
 Query Match: 5.85% Indels: 97  
 RESULT 1318  
 Best Local Similarity: 21.71% Mismatches: 90  
 Query Match: 5.85% Indels: 66  
 RESULT 1319  
 ID ABL27928 standard; DNA; 3161 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35257.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Best Local Similarity: 21.16% Mismatches: 93  
 Query Match: 5.82% Indels: 53  
 RESULT 1320  
 ID ADS63288 standard; cDNA; 3684 BP.  
 DE Bacterial polynucleotide #15275.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 23.77% Mismatches: 57  
 Query Match: 5.82% Indels: 114  
 RESULT 1321  
 ID ABX77167 standard; DNA; 125653 BP.  
 DE DNA sequence of human BAC clone RP11-8211.  
 PN WO200283897-A1.  
 PD 24-OCT-2002.  
 PA (GENE-) GENE STREAM PTY LTD.  
 Best Local Similarity: 33.68% Mismatches: 31  
 Query Match: 5.82% Indels: 21  
 RESULT 1322  
 ID ADO42013 standard; DNA; 784 BP.  
 DE Human cell adhesion and extracellular matrix protein 1 gene SeqID42.  
 PN WO2004048529-A2.  
 PD 10-JUN-2004.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 28.07% Mismatches: 48  
 Query Match: 5.79% Indels: 14  
 RESULT 1323  
 ID AAK94215 standard; cDNA; 1995 BP.  
 DE Human full-length cDNA, SEQ ID NO: 2788.  
 PN EPI130094-A2.  
 PD 05-SEP-2001.  
 PA (HELI-) HELIX RES INST.  
 Best Local Similarity: 26.32% Mismatches: 79  
 Query Match: 5.79% Indels: 55

RESULT 1324  
ID ADL30755 standard; cDNA; 1995 BP.  
DE Full length human cDNA clone SeqID 2788.  
PN EP1396543-A2.  
PA (10-MAR-2004).  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 26.32% Mismatches: 79  
Query Match: 5.79% Indels: 55  
RESULT 1325  
ID ABQ70959 standard; DNA; 4562 BP.  
DE Listeria monocytogenes 4b contig DNA sequence #901.  
PN WO200228891-A2.  
PD 11-APR-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Best Local Similarity: 19.94% Mismatches: 114  
Query Match: 5.79% Indels: 126  
RESULT 1326  
ID ABD15716 standard; DNA; 1665 BP.  
DE Pseudomonas aeruginosa polynucleotide #14320.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 25.49% Mismatches: 74  
Query Match: 5.76% Indels: 82  
RESULT 1327  
ID AAX60539 standard; DNA; 4435 BP.  
DE C. trachomatis LGV L2 HMW protein encoding DNA.  
PN WO9917741-A1.  
PD 15-APR-1999.  
PA (ANTE-) ANTEX BIOLOGICS INC.  
Best Local Similarity: 23.39% Mismatches: 70  
Query Match: 5.76% Indels: 95  
RESULT 1328  
ID AAS46385 standard; DNA; 12781 BP.  
DE Tumour suppressor gene derived chemically modified sequence #107.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 23.35% Mismatches: 51  
Query Match: 5.76% Indels: 81  
RESULT 1329  
ID ABL92228 standard; DNA; 12781 BP.  
DE Chemically treated DNA repair gene fragment#19.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 23.35% Mismatches: 51  
Query Match: 5.76% Indels: 81  
RESULT 1330  
ID ADB54127 standard; DNA; 12781 BP.  
DE Pretreated genomic DNA region 51.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 23.35% Mismatches: 51  
Query Match: 5.76% Indels: 81  
RESULT 1331  
ID AAD17184 standard; DNA; 65140 BP.  
DE Streptomyces noursei nys1 DNA of nystatin PKS gene cluster.  
PN WO200159126-A2.  
PD 16-AUG-2001.  
PA (UYN-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
PA (SNTF ) SINTEF STIFTELSEN IND TEK FORSK.  
PA (ALPH-) ALPHARMA AS.  
PA (SINV-) SINVENT AS.  
PA (DZIE/) DZIEGLEWSKA H.  
PA (ZOTC/) ZOTCHEV S B.  
PA (SEKU/) SEKUROVA O N.  
PA (FJAE/) FJAERVIK E.  
PA (BRAU/) BRAUTASET T.  
PA (STRO/) STROM A R.  
PA (VALL/) VALLA S.

Best Local Similarity: 26.39% Mismatches: 57  
Query Match: 5.76% Indels: 32  
RESULT 1332  
ID AAD17186 standard; DNA; 125401 BP.  
DE Streptomyces noursei nystatin PKS gene cluster DNA.  
PN WO200159126-A2.  
PD 16-AUG-2001.  
PA (UYN-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
PA (SNTF ) SINTEF STIFTELSEN IND TEK FORSK.  
PA (ALPH-) ALPHARMA AS.  
PA (SINV-) SINVENT AS.  
PA (DZIE/) DZIEGLEWSKA H.  
PA (ZOTC/) ZOTCHEV S B.  
PA (SEKU/) SEKUROVA O N.  
PA (FJAE/) FJAERVIK E.  
PA (BRAU/) BRAUTASET T.  
PA (STRO/) STROM A R.  
PA (VALL/) VALLA S.  
Best Local Similarity: 26.39% Mismatches: 57  
Query Match: 5.76% Indels: 32  
RESULT 1333  
ID ADE36593 standard; cDNA; 1440 BP.  
DE Human NOV1b encoding cDNA SEQ ID NO:3.  
PN WO2003080856-A2.  
PD 02-OCT-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 23.67% Mismatches: 120  
Query Match: 5.73% Indels: 72  
RESULT 1334  
ID ADN38983 standard; cDNA; 1440 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:301.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 23.67% Mismatches: 120  
Query Match: 5.73% Indels: 72  
RESULT 1335  
ID ACA30126 standard; DNA; 1455 BP.  
DE Prokaryotic essential gene #11783.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 19.69% Mismatches: 119  
Query Match: 5.73% Indels: 151  
RESULT 1336  
ID ABL12707 standard; cDNA; 2211 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32603.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 20.89% Mismatches: 127  
Query Match: 5.73% Indels: 116  
RESULT 1337  
ID ADB63598 standard; cDNA; 2304 BP.  
DE Human cDNA encoding clone THYMU20044100.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 22.90% Mismatches: 88  
Query Match: 5.73% Indels: 106  
RESULT 1338  
ID ADA53796 standard; cDNA; 2803 BP.  
DE Human coding sequence, SEQ ID 1364.  
PN EP1293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 21.93% Mismatches: 128  
Query Match: 5.73% Indels: 58  
RESULT 1339  
ID ABL12706 standard; cDNA; 4678 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32600.





Query Match: 5.70% Indels: 81  
RESULT 1358  
ID ADH12800 standard; cDNA; 2207 BP.  
DE Abalone (Haliotis discus hannai) cellulase-encoding cDNA, SEQ ID NO:1.  
PN JP2003235552-A.  
PD 26-AUG-2003.  
PA (HOKK-) HOKKAIDO TLO KK.  
Best Local Similarity: 24.09%  
Query Match: 5.70% Indels: 78  
RESULT 1359  
ID ADO64957 standard; cDNA; 2438 BP.  
DE Novel human cDNA sequence #2118.  
PN EPI440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 22.59%  
Query Match: 5.70% Indels: 66  
RESULT 1360  
ID ADA70755 standard; DNA; 2784 BP.  
DE Rice gene, SEQ ID 4078.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Best Local Similarity: 19.60%  
Query Match: 5.70% Indels: 154  
RESULT 1361  
ID ABO76313 standard; cDNA; 3401 BP.  
DE S. cerevisiae BAX-associated cDNA fragment SEQ ID 51.  
PN WO200264766-A2.  
PD 22-AUG-2002.  
PA (JANC) JANSSEN PHARM NV.  
Best Local Similarity: 20.78%  
Query Match: 5.70% Indels: 80  
RESULT 1362  
ID ACC50985 standard; cDNA; 4209 BP.  
DE Human bladder cancer associated cDNA sequence SEQ ID NO:63.  
PN WO2003003906-A2.  
PD 16-JAN-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 23.28%  
Query Match: 5.70% Indels: 77  
RESULT 1363  
ID ABD13413 standard; DNA; 1179 BP.  
DE Pseudomonas aeruginosa polynucleotide #12017.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 27.60%  
Query Match: 5.67% Indels: 59  
RESULT 1364  
ID ABO46961 standard; DNA; 1199 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 33552.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 24.49%  
Query Match: 5.67% Indels: 31  
RESULT 1365  
ID ABO46960 standard; DNA; 1199 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 33551.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 24.49%  
Query Match: 5.67% Indels: 31  
RESULT 1366  
ID ABL12433 standard; cDNA; 1946 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31781.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 23.08%  
Query Match: 5.67% Indels: 63

RESULT 1367  
ID AAS57123 standard; cDNA; 1946 BP.  
DE cDNA encoding Drosophila G-protein coupled receptor, GCPR #26.  
PN WO200170980-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 23.08%  
Query Match: 5.67% Indels: 63  
RESULT 1368  
ID ADC35825 standard; cDNA; 1946 BP.  
DE Drosophila G protein coupled receptor cDNA seq id 27.  
PN US2003092124-A1.  
PD 15-MAY-2003.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 23.08%  
Query Match: 5.67% Indels: 63  
RESULT 1369  
ID ABL12432 standard; cDNA; 3946 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31778.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 20.77%  
Query Match: 5.67% Indels: 99  
RESULT 1370  
ID AAS57122 standard; DNA; 3946 BP.  
DE DNA encoding Drosophila G-protein coupled receptor, GCPR #26.  
PN WO200170980-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 20.77%  
Query Match: 5.67% Indels: 99  
RESULT 1371  
ID ADC35824 standard; DNA; 3946 BP.  
DE Drosophila G protein coupled receptor genomic DNA seq id 26.  
PN US2003092124-A1.  
PD 15-MAY-2003.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 20.77%  
Query Match: 5.67% Indels: 99  
RESULT 1372  
ID ADP04444 standard; cDNA; 4849 BP.  
DE Sea squirt cDNA with tissue specific expression in development Seq 39.  
PN JP2004057129-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN  
Best Local Similarity: 24.06%  
Query Match: 5.67% Indels: 77  
RESULT 1373  
ID ABL33459 standard; DNA; 6047 BP.  
DE Human immune system associated gene SEQ ID NO: 1432.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 20.67%  
Query Match: 5.67% Indels: 110  
RESULT 1374  
ID ABL23194 standard; DNA; 6313 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 21055.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 20.72%  
Query Match: 5.67% Indels: 119  
RESULT 1375  
ID ABO52389 standard; DNA; 739 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38980.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 23.98%  
Query Match: 5.64% Indels: 35  
RESULT 1376

ID ABQ52388 standard; DNA; 739 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38979.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Best Local Similarity: 23.98% Mismatches: 93  
Query Match: 5.64% Indels: 35  
RESULT 1377  
ID ADE36591 standard; cDNA; 1017 BP.  
DE Human NOV1a encoding cDNA SEQ ID NO:1.  
PN WO2003080856-A2.  
PD 02-OCT-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 23.08% Mismatches: 113  
Query Match: 5.64% Indels: 71  
RESULT 1378  
ID ADE36617 standard; DNA; 1017 BP.  
DE Plasmid pCR2.1-CG57008-03-S843 15B nucleotide insert SEQ ID NO:27.  
PN WO2003080856-A2.  
PD 02-OCT-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 23.08% Mismatches: 113  
Query Match: 5.64% Indels: 71  
RESULT 1379  
ID ACC72709 standard; cDNA; 1080 BP.  
DE Human cancer related protein encoding cDNA SEQ ID NO:48.  
PN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 23.08% Mismatches: 113  
Query Match: 5.64% Indels: 71  
RESULT 1380  
ID ABZ68333 standard; DNA; 1080 BP.  
DE Nucleotide sequence of human TIM-1 allele 2.  
PN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
Best Local Similarity: 23.08% Mismatches: 113  
Query Match: 5.64% Indels: 71  
RESULT 1381  
ID ABZ68332 standard; DNA; 1080 BP.  
DE Nucleotide sequence of human TIM-1 allele 1.  
PN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
Best Local Similarity: 23.08% Mismatches: 113  
Query Match: 5.64% Indels: 71  
RESULT 1382  
ID AAS65697 standard; cDNA; 1082 BP.  
DE DNA encoding novel human diagnostic protein #1501.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 23.19% Mismatches: 73  
Query Match: 5.64% Indels: 57  
RESULT 1383  
ID ABQ52391 standard; DNA; 1185 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38982.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Best Local Similarity: 21.43% Mismatches: 84  
Query Match: 5.64% Indels: 43  
RESULT 1384  
ID ABQ52390 standard; DNA; 1185 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38981.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Best Local Similarity: 21.43% Mismatches: 84  
Query Match: 5.64% Indels: 43  
RESULT 1385  
ID ABQ44576 standard; DNA; 1190 BP.

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 31167.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Best Local Similarity: 21.43% Mismatches: 84  
Query Match: 5.64% Indels: 43  
RESULT 1386  
ID ABQ44577 standard; DNA; 1190 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 31168.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Best Local Similarity: 21.43% Mismatches: 84  
Query Match: 5.64% Indels: 43  
RESULT 1387  
ID AAS72110 standard; cDNA; 1242 BP.  
DE DNA encoding novel human diagnostic protein #7914.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 23.19% Mismatches: 73  
Query Match: 5.64% Indels: 57  
RESULT 1388  
ID ADO63160 standard; cDNA; 2176 BP.  
DE Novel human cDNA sequence #321.  
PN EPI440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 22.76% Mismatches: 84  
Query Match: 5.64% Indels: 89  
RESULT 1389  
ID ACC84451 standard; DNA; 6166 BP.  
DE Glucansucrase nucleotide sequence from strain KG15.  
PN WO2003008618-A2.  
PD 30-JAN-2003.  
PA (NEDE ) NEDERLANDSE ORG TOEGEPAST.  
Best Local Similarity: 23.28% Mismatches: 92  
Query Match: 5.64% Indels: 77  
RESULT 1390  
ID AAS46336 standard; DNA; 7348 BP.  
DE Tumour suppressor gene derived chemically modified sequence #58.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPiG-) EPIGENOMICS AG.  
Best Local Similarity: 22.65% Mismatches: 93  
Query Match: 5.64% Indels: 55  
RESULT 1391  
ID AAS60823 standard; cDNA; 7568 BP.  
DE DNA encoding novel human diagnostic protein #16627.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 5.64% Indels: 55  
RESULT 1392  
ID ADL12996 standard; cDNA; 8146 BP.  
DE Human steroid-induced C3A liver cell cDNA #725.  
PN US6673549-B1.  
PD 06-JAN-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 5.64% Indels: 55  
RESULT 1393  
ID ADL61871 standard; DNA; 9169 BP.  
DE Human ovarian cancer DNA marker #20083.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 5.64% Indels: 55  
RESULT 1394  
ID ABV24414 standard; cDNA; 9220 BP.  
DE Human prostate expression marker cDNA 24405.

PN WO200160860-A2.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 5.64% Indels: 55  
RESULT 1395  
ID ABV25265 standard; cDNA; 9220 BP.  
DE Human prostate expression marker cDNA 25256.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 5.64% Indels: 55  
RESULT 1396  
ID ASK83800 standard; cDNA; 9416 BP.  
DE Human cDNA differentially expressed in granulocytic cells #371.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 5.64% Indels: 55  
RESULT 1397  
ID ACF34559 standard; DNA; 9416 BP.  
DE Gene encoding angiogenesis protein BNO382.  
PN WO2003027285-A1.  
PD 03-APR-2003.  
PA (BION-) BIONOMICS LTD.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 5.64% Indels: 55  
RESULT 1398  
ID ADN05259 standard; cDNA; 9416 BP.  
DE Antiproliferative cDNA sequence #849.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 5.64% Indels: 55  
RESULT 1399  
ID ADR14613 standard; DNA; 9416 BP.  
DE Human NF-kappaB pathway-associated gene SeqID614.  
PN WO2004065577-A2.  
PD 05-AUG-2004.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 5.64% Indels: 55  
RESULT 1400  
ID ADI61864 standard; cDNA; 11917 BP.  
DE Human cDNA downregulated in Alzheimer's disease, INCYTE 475473.1.  
PN US6682888-B1.  
PD 27-JAN-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 5.64% Indels: 55  
RESULT 1401  
ID ADE53871 standard; cDNA; 11950 BP.  
DE Human prostate cancer cDNA #218.  
PN US2003190640-A1.  
PD 09-OCT-2003.  
PA (FARI/) FARIS M.  
PA (PEAR/) PEARSON C I.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 5.64% Indels: 55  
RESULT 1402  
ID ADF90735 standard; DNA; 11965 BP.  
DE Human hepatic-fibrosis disease marker SEQ ID 197.  
PN JP2003259877-A.  
PD 16-SEP-2003.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 5.64% Indels: 55  
RESULT 1403  
ID ADN04560 standard; cDNA; 12004 BP.  
DE Antiproliferative cDNA sequence #484.

PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 21.50% Mismatches: 77  
Query Match: 5.64% Indels: 55  
RESULT 1404  
ID ADA02891 standard; DNA; 34570 BP.  
DE Mouse Blrl carcinoma associated gene, SEQ ID NO:1409.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 25.38% Mismatches: 67  
Query Match: 5.64% Indels: 63  
RESULT 1405  
ID ADB72629 standard; DNA; 34570 BP.  
DE Mouse Blrl gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 25.38% Mismatches: 67  
Query Match: 5.64% Indels: 63  
RESULT 1406  
ID ADC85370 standard; DNA; 34570 BP.  
DE Human Blm coding sequence.  
PN WO2003045230-A2.  
PD 05-JUN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 25.38% Mismatches: 67  
Query Match: 5.64% Indels: 63  
RESULT 1407  
ID ADM74486 standard; DNA; 34570 BP.  
DE Murine carcinoma associated (CA) nucleic acid #79.  
PN US2004072154-A1.  
PD 15-APR-2004.  
PA (MORR/) MORRIS D W.  
PA (ENGE/) ENGELHARD E K.  
Best Local Similarity: 25.38% Mismatches: 67  
Query Match: 5.64% Indels: 63  
RESULT 1408  
ID ADR68967 standard; DNA; 34571 BP.  
DE Mouse cancer associated gene genomic sequence SEQ ID NO:13.  
PN WO2004074321-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Best Local Similarity: 25.38% Mismatches: 67  
Query Match: 5.64% Indels: 63  
RESULT 1409  
ID ABO81848 standard; DNA; 349980 BP.  
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1104.  
PN EP1227152-A1.  
PD 31-JUL-2002.  
PA (NEST) SOC PROD NESTLE SA.  
Best Local Similarity: 23.68% Mismatches: 62  
Query Match: 5.64% Indels: 57  
RESULT 1410  
ID ADK53470 standard; DNA; 631 BP.  
DE Plant DNA sequence which confers altered metabolic characteristic #853.  
PN WO2003020936-A1.  
PD 13-MAR-2003.  
PA (DOWC) DOW CHEM CO.  
PA (DOWC) DOW AGROSCIENCES LLC.  
Best Local Similarity: 29.37% Mismatches: 50  
Query Match: 5.61% Indels: 26  
RESULT 1411  
ID ADK56638 standard; DNA; 971 BP.  
DE Plant DNA sequence which confers altered metabolic characteristic #4021.  
PN WO2003020936-A1.  
PD 13-MAR-2003.  
PA (DOWC) DOW CHEM CO.  
PA (DOWC) DOW AGROSCIENCES LLC.  
Best Local Similarity: 29.37% Mismatches: 50  
Query Match: 5.61% Indels: 26  
RESULT 1412

ID ADQ16561 standard; DNA; 1089 BP.  
DE Dog calcitonin gene-related peptide (GGRP) receptor CGRP-R DNA.  
PN US200410170-A1.  
PD 10-JUN-2004.  
PA (REGC) UNIV CALIFORNIA.  
Best Local Similarity: 23.15% Mismatches: 72  
Query Match: 5.61% Indels: 50  
RESULT 1413  
ID ABQ17861 standard; DNA; 1128 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 4452.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 25.93% Mismatches: 80  
Query Match: 5.61% Indels: 45  
RESULT 1414  
ID ABQ17860 standard; DNA; 1128 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 4451.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 25.93% Mismatches: 80  
Query Match: 5.61% Indels: 45  
RESULT 1415  
ID AAT29035 standard; cDNA; 1321 BP.  
DE Endoglucanase (60 kDa family 5 cellulase) cDNA sequence.  
PN WO9611262-A1.  
PD 18-APR-1996.  
PA (NOVO) NOVO-NORDISK AS.  
Best Local Similarity: 30.00% Mismatches: 32  
Query Match: 5.61% Indels: 22  
RESULT 1416  
ID AAS73740 standard; cDNA; 1365 BP.  
DE DNA encoding novel human diagnostic protein #9544.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 20.49% Mismatches: 102  
Query Match: 5.61% Indels: 92  
RESULT 1417  
ID ADQ07822 standard; cDNA; 1962 BP.  
DE Mouse polynucleotide #40.  
PN US2004071700-A1.  
PD 15-APR-2004.  
PA (LIFE-) LIFE SCI DEV CORP.  
Best Local Similarity: 22.64% Mismatches: 101  
Query Match: 5.61% Indels: 96  
RESULT 1418  
ID AAT10117 standard; cDNA; 2032 BP.  
DE Drosophila scavenger receptor class CI cDNA.  
PN WO9600288-A2.  
PD 04-JAN-1996.  
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.  
Best Local Similarity: 19.92% Mismatches: 96  
Query Match: 5.61% Indels: 74  
RESULT 1419  
ID ABES3745 standard; cDNA; 2032 BP.  
DE cDNA encoding fruit fly scavenger receptor type CI (GSR-CI).  
PN US6429289-B1.  
PD 06-AUG-2002.  
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.  
Best Local Similarity: 19.92% Mismatches: 96  
Query Match: 5.61% Indels: 74  
RESULT 1420  
ID AAD33916 standard; cDNA; 2032 BP.  
DE Drosophila melanogaster scavenger receptor class CI (GSR-CI) cDNA.  
PN US6350859-B1.  
PD 26-FEB-2002.  
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.  
Best Local Similarity: 19.92% Mismatches: 96  
Query Match: 5.61% Indels: 74  
RESULT 1421  
ID ABX10897 standard; DNA; 2050 BP.

DE DNA encoding human orphan chemokine receptor RDC1.  
PN US2002166133-A1.  
PD 07-NOV-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 23.15% Mismatches: 72  
Query Match: 5.61% Indels: 50  
RESULT 1422  
ID ADK66235 standard; DNA; 2050 BP.  
DE Human NEOKINE-1 receptor RDC1 DNA.  
PN US2004019917-A1.  
PD 29-JAN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 23.15% Mismatches: 72  
Query Match: 5.61% Indels: 50  
RESULT 1423  
ID ABL16152 standard; cDNA; 3004 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 42938.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 22.32% Mismatches: 114  
Query Match: 5.61% Indels: 90  
RESULT 1424  
ID ABL25205 standard; DNA; 5931 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27088.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 32.65% Mismatches: 34  
Query Match: 5.61% Indels: 13  
RESULT 1425  
ID ADQ79681 standard; DNA; 6312 BP.  
DE Benzoate catabolic enzyme gene cluster #1.  
PN KR2003082683-A.  
PD 23-OCT-2003.  
PA (KIME/) KIM E S.  
Best Local Similarity: 24.70% Mismatches: 121  
Query Match: 5.61% Indels: 96  
RESULT 1426  
ID ABL25204 standard; DNA; 7931 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27085.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 32.65% Mismatches: 34  
Query Match: 5.61% Indels: 13  
RESULT 1427  
ID ABQ14148 standard; DNA; 647 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 739.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 27.27% Mismatches: 82  
Query Match: 5.58% Indels: 41  
RESULT 1428  
ID ABQ14149 standard; DNA; 647 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 740.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 27.27% Mismatches: 82  
Query Match: 5.58% Indels: 41  
RESULT 1429  
ID ADR60062 standard; cDNA; 907 BP.  
DE Cotton cDNA sequence, SEQ ID 843.  
PN US200418130-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Best Local Similarity: 23.58% Mismatches: 82  
Query Match: 5.58% Indels: 50  
RESULT 1430

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ID ABZ68337 standard; DNA; 1099 BP.
DE Nucleotide sequence of human TIM-1 allele 6.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
Best Local Similarity: 22.34% Mismatches: 113
Query Match: 5.58% Indels: 74
RESULT 1431
ID ABZ78250 standard; cDNA; 1185 BP.
DE A. niger aspergillopepsin I cDNA.
PN WO200268623-A2.
PD 06-SEP-2002.
PA (STAM ) DSM NV.
Best Local Similarity: 23.57% Mismatches: 106
Query Match: 5.58% Indels: 61
RESULT 1432
ID ACA42210 standard; DNA; 1275 BP.
DE Prokaryotic essential gene #23867.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 25.49% Mismatches: 74
Query Match: 5.58% Indels: 82
RESULT 1433
ID ABX94893 standard; DNA; 1275 BP.
DE P. autoginosa PAO DNA variant SEQ ID 3.
PN WO2003022881-A2.
PD 20-MAR-2003.
PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.
PA (TUEM-) TUEMMLER B.
Best Local Similarity: 25.49% Mismatches: 74
Query Match: 5.58% Indels: 82
RESULT 1434
ID AAH15685 standard; cDNA; 1709 BP.
DE Human cDNA sequence SEQ ID NO:14050.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Best Local Similarity: 22.30% Mismatches: 111
Query Match: 5.58% Indels: 57
RESULT 1435
ID ACA36388 standard; DNA; 1710 BP.
DE Prokaryotic essential gene #18045.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 21.41% Mismatches: 135
Query Match: 5.58% Indels: 67
RESULT 1436
ID AB211710 standard; cDNA; 2096 BP.
DE Human polynucleotide SEQ ID NO 592.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 22.30% Mismatches: 111
Query Match: 5.58% Indels: 57
RESULT 1437
ID ADM44228 standard; cDNA; 2096 BP.
DE Novel human arginine-rich protein cDNA #592.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
Best Local Similarity: 22.30% Mismatches: 111
Query Match: 5.58% Indels: 57
RESULT 1438
ID ADS46773 standard; cDNA; 2985 BP.
DE Bacterial polynucleotide #1516.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.

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PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 19.70% Mismatches: 139
Query Match: 5.58% Indels: 85
RESULT 1439
ID ABN79988 standard; DNA; 6113 BP.
DE Human chemically modified disease associated gene SEQ ID NO 5.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 20.45% Mismatches: 71
Query Match: 5.58% Indels: 108
RESULT 1440
ID ABA16168 standard; DNA; 6838 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8499.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 25.18% Mismatches: 99
Query Match: 5.58% Indels: 76
RESULT 1441
Best Local Similarity: 23.08% Mismatches: 79
Query Match: 5.58% Indels: 84
RESULT 1442
Best Local Similarity: 21.41% Mismatches: 135
Query Match: 5.58% Indels: 67
RESULT 1443
ID ABS77501 standard; cDNA; 736 BP.
DE Frog embryonic gene sequence Q9925909.
PN US2002081610-A1.
PD 27-JUN-2002.
PA (UYRO ) UNIV ROCKEFELLER.
Best Local Similarity: 21.83% Mismatches: 76
Query Match: 5.55% Indels: 94
RESULT 1444
ID ADK55629 standard; DNA; 747 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #3012.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC ) DOW CHEM CO.
PA (DOWC ) DOW AGROSCIENCES LLC.
Best Local Similarity: 29.60% Mismatches: 54
Query Match: 5.55% Indels: 20
RESULT 1445
ID ADK57771 standard; DNA; 747 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #5154.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC ) DOW CHEM CO.
PA (DOWC ) DOW AGROSCIENCES LLC.
Best Local Similarity: 29.60% Mismatches: 54
Query Match: 5.55% Indels: 20
RESULT 1446
ID ABZ68336 standard; DNA; 1095 BP.
DE Nucleotide sequence of human TIM-1 allele 5.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
Best Local Similarity: 21.65% Mismatches: 114
Query Match: 5.55% Indels: 76
RESULT 1447
ID ADR85331 standard; DNA; 1110 BP.
DE Aspergillus fumigatus essential gene with introns #555.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Best Local Similarity: 24.80% Mismatches: 94
Query Match: 5.55% Indels: 62
RESULT 1448
ID AAS59778 standard; DNA; 1389 BP.
DE Propionibacterium acnes immunogenic protein encoding DNA #273.

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PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 24.58% Mismatches: 89  
Query Match: 5.55% Indels: 66  
RESULT 1449  
ID AC564707 standard; DNA; 1389 BP.  
DE Propionibacterium acnes DNA contig sequence #273.  
PN WO200303315-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 24.58% Mismatches: 89  
Query Match: 5.55% Indels: 66  
RESULT 1450  
ID AA167205 standard; DNA; 1905 BP.  
DE Nucleotide sequence of GSK gene Id 239881.  
PN WO200172961-A2.  
PD 04-OCT-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
Best Local Similarity: 24.09% Mismatches: 89  
Query Match: 5.55% Indels: 97  
RESULT 1451  
ID ADR84744 standard; DNA; 3110 BP.  
DE Aspergillus fumigatus essential gene genomic sequence #555.  
PN WO2004067709-A2.  
PD 12-AUG-2004.  
PA (ELIT-) ELITRA PHARM INC.  
PA (ELIT-) ELITRA CANADA LTD.  
Best Local Similarity: 24.80% Mismatches: 94  
Query Match: 5.55% Indels: 62  
RESULT 1452  
ID ADR32198 standard; DNA; 4893 BP.  
DE Yeast FLO11 open reading frame, SEQ ID NO:3.  
PN WO2004067565-A1.  
PD 12-AUG-2004.  
PA (OSBO-) OSBORNE DISTRIBUTORA SA.  
PA (UYDO/) UNIV DE OLAVIDE PABLO.  
Best Local Similarity: 21.75% Mismatches: 114  
Query Match: 5.55% Indels: 71  
RESULT 1453  
ID ADS89638 standard; DNA; 5087 BP.  
DE Oligonucleotide of the invention SEQ ID NO:654.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 21.13% Mismatches: 69  
Query Match: 5.55% Indels: 68  
RESULT 1454  
ID ADS89578 standard; DNA; 5087 BP.  
DE Oligonucleotide of the invention SEQ ID NO:594.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 21.13% Mismatches: 69  
Query Match: 5.55% Indels: 68  
RESULT 1455  
ID ABL06739 standard; CDNA; 5269 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 14699.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 28.28% Mismatches: 55  
Query Match: 5.55% Indels: 29  
RESULT 1456  
ID ABL06738 standard; CDNA; 7740 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 14696.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 28.28% Mismatches: 55  
Query Match: 5.55% Indels: 29  
RESULT 1457

ID AAV58939 standard; DNA; 9960 BP.  
DE Mycobacterium smegmatis embCAB operon.  
PN WO9841533-A1.  
PD 24-SEP-1998.  
PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.  
Best Local Similarity: 21.62% Mismatches: 87  
Query Match: 5.55% Indels: 111  
RESULT 1458  
ID ADJ41911 standard; CDNA; 632 BP.  
DE Plant CDNA #2911.  
PN US2004016025-A1.  
PD 22-JAN-2004.  
PA (BUDW/) BUDWORTH P.  
PA (MOUG/) MOUGHAMER T.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (PROV/) PROVART N.  
PA (RICK/) RICHE D.  
PA (ZHUT/) ZHU T.  
Best Local Similarity: 23.33% Mismatches: 77  
Query Match: 5.52% Indels: 43  
RESULT 1459  
ID AAS28824 standard; CDNA; 697 BP.  
DE Human immunoglobulin encoding CDNA SEQ ID NO 70.  
PN WO200155315-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 31.71% Mismatches: 38  
Query Match: 5.52% Indels: 7  
RESULT 1460  
ID ABA06691 standard; CDNA; 697 BP.  
DE Human CDNA SEQ ID NO: 357.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 31.71% Mismatches: 38  
Query Match: 5.52% Indels: 7  
RESULT 1461  
ID ABV84028 standard; CDNA; 697 BP.  
DE Human polynucleotide SEQ ID NO 357.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Best Local Similarity: 31.71% Mismatches: 38  
Query Match: 5.52% Indels: 7  
RESULT 1462  
ID ADB31549 standard; CDNA; 697 BP.  
DE Human CDNA encoding a novel protein SEQ ID NO 70.  
PN US2003077606-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 31.71% Mismatches: 38  
Query Match: 5.52% Indels: 7  
RESULT 1463  
ID ABO67928 standard; DNA; 777 BP.  
DE Listeria monocytogenes EGD DNA sequence #52.  
PN WO200228891-A2.  
PD 11-APR-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Best Local Similarity: 21.98% Mismatches: 57  
Query Match: 5.52% Indels: 65  
RESULT 1464  
ID AAI71772 standard; DNA; 1050 BP.  
DE ActA protein fragment #2 coding sequence.  
PN WO200171356-A2.  
PD 27-SEP-2001.

PA (CNRS ) CENT NAT RECH SCI.  
 PA (CURI-) INST CURIE.  
 Best Local Similarity: 21.98% Mismatches: 57  
 Query Match: 5.52% Indels: 65  
 RESULT 1465  
 ID ABZ68334 standard; DNA; 1098 BP.  
 DE Nucleotide sequence of human TIM-1 allele 3.  
 PN WO2003002722-A2.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 Best Local Similarity: 22.60% Mismatches: 112  
 Query Match: 5.52% Indels: 77  
 RESULT 1466  
 ID AAI171771 standard; DNA; 1128 BP.  
 DE ActA protein fragment #1 coding sequence.  
 PN WO200171356-A2.  
 PA (CNRS ) CENT NAT RECH SCI.  
 PA (CURI-) INST CURIE.  
 Best Local Similarity: 21.98% Mismatches: 57  
 Query Match: 5.52% Indels: 65  
 RESULT 1467  
 ID ABL24493 standard; DNA; 1344 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 24952.  
 PN WO200171042-A2.  
 PA (PEKE ) PE CORP NY.  
 Best Local Similarity: 25.12% Mismatches: 77  
 Query Match: 5.52% Indels: 44  
 RESULT 1468  
 ID ADB58239 standard; DNA; 1548 BP.  
 DE Toxicity-related gene, SEQ ID 3265.  
 PN WO2003064624-A2.  
 PD 07-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Best Local Similarity: 21.17% Mismatches: 96  
 Query Match: 5.52% Indels: 88  
 RESULT 1469  
 ID ADB52767 standard; DNA; 1548 BP.  
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3309.  
 PN WO2003065993-A2.  
 PD 14-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Best Local Similarity: 21.17% Mismatches: 96  
 Query Match: 5.52% Indels: 88  
 RESULT 1470  
 ID ABT41946 standard; DNA; 1548 BP.  
 DE Toxicity modelling related rat gene SEQ ID No 1648.  
 PN WO200295000-A2.  
 PD 28-NOV-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Best Local Similarity: 21.17% Mismatches: 96  
 Query Match: 5.52% Indels: 88  
 RESULT 1471  
 ID AAI171770 standard; DNA; 1830 BP.  
 DE ActA protein coding sequence.  
 PN WO200171356-A2.  
 PD 27-SEP-2001.  
 PA (CNRS ) CENT NAT RECH SCI.  
 PA (CURI-) INST CURIE.  
 Best Local Similarity: 21.98% Mismatches: 57  
 Query Match: 5.52% Indels: 65  
 RESULT 1472  
 ID ABK89028 standard; DNA; 1869 BP.  
 DE Synthetic P. falciparum AMA-1 ectodomain (FVO Pf83syn) gene.  
 PN WO200252014-A2.  
 PD 04-JUL-2002.  
 PA (BIOM-) STRICHTING BIOMEDICAL PRIMATE RES CENT.  
 Best Local Similarity: 20.87% Mismatches: 107  
 Query Match: 5.52% Indels: 132  
 RESULT 1473  
 ID AAV37026 standard; DNA; 1920 BP.  
 DE Listeria monocytogenes sequence used to design primers and probes.

PN WO9820157-A2.  
 PA 14-MAY-1998.  
 PA (IDII-) IDI INFECTIO DIAGNOSTIC INC.  
 Best Local Similarity: 21.98% Mismatches: 57  
 Query Match: 5.52% Indels: 65  
 RESULT 1474  
 ID ABQ69832 standard; DNA; 1920 BP.  
 DE Listeria monocytogenes EGDe DNA sequence #44.  
 PN WO200228891-A2.  
 PD 11-APR-2002.  
 PA (INSP ) INST PASTEUR.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 Best Local Similarity: 21.98% Mismatches: 57  
 Query Match: 5.52% Indels: 65  
 RESULT 1475  
 ID ABQ67930 standard; DNA; 1920 BP.  
 DE Listeria monocytogenes EGD DNA sequence #54.  
 PN WO200228891-A2.  
 PD 11-APR-2002.  
 PA (INSP ) INST PASTEUR.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 Best Local Similarity: 21.98% Mismatches: 57  
 Query Match: 5.52% Indels: 65  
 RESULT 1476  
 ID ADS56805 standard; cDNA; 2535 BP.  
 DE Bacterial polynucleotide #8792.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 24.15% Mismatches: 115  
 Query Match: 5.52% Indels: 36  
 RESULT 1477  
 ID ACC59291 standard; DNA; 2618 BP.  
 DE P tetraurelia adenylate cyclase/ ion channel protein expression cassette.  
 PN WO2003040295-A2.  
 PD 15-MAY-2003.  
 PA (GENO-) GENOPIA BIOMEDICAL GMBH.  
 Best Local Similarity: 25.45% Mismatches: 83  
 Query Match: 5.52% Indels: 59  
 RESULT 1478  
 ID ABQ14764 standard; DNA; 3034 BP.  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1355.  
 PN WO200218632-A2.  
 PD 07-MAR-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Best Local Similarity: 31.82% Mismatches: 36  
 Query Match: 5.52% Indels: 24  
 RESULT 1479  
 ID AQ14765 standard; DNA; 3034 BP.  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1356.  
 PN WO200218632-A2.  
 PD 07-MAR-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Best Local Similarity: 31.82% Mismatches: 36  
 Query Match: 5.52% Indels: 24  
 RESULT 1480  
 ID ADS48485 standard; cDNA; 3309 BP.  
 DE Bacterial polynucleotide #3228.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 24.27% Mismatches: 59  
 Query Match: 5.52% Indels: 67  
 RESULT 1481  
 ID AAQ22986 standard; DNA; 3502 BP.



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DE Sequence of ILTV gp60 gene.
PD WO9203554-A.
PA (WEBS-) WEBSTER A PTY LTD.
Best Local Similarity: 28.49%
Query Match: 5.52%
MismatchChes: 58
Indels: 46
RESULT 1482
ID ADO67427 standard; cDNA; 3538 BP.
DE Novel human cDNA sequence #2400.
PD EP1440981-A2.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 28.29%
Query Match: 5.52%
MismatchChes: 55
Indels: 39
RESULT 1483
ID ADS49082 standard; cDNA; 3873 BP.
DE Bacterial polynucleotide #3825.
PD US200323675-A1.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 25.12%
Query Match: 5.52%
MismatchChes: 65
Indels: 66
RESULT 1484
ID ADR07198 standard; cDNA; 3932 BP.
DE Full length human cDNA useful for treating neurological disease Seq 704.
PD EP1447413-A2.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Best Local Similarity: 22.76%
Query Match: 5.52%
MismatchChes: 84
Indels: 89
RESULT 1485
ID ACC42734 standard; DNA; 6210 BP.
DE Geldanamycin PKS module 1 DNA sequence, SEQ ID 1.
PD WO2003013430-A2.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Best Local Similarity: 22.11%
Query Match: 5.52%
MismatchChes: 63
Indels: 77
RESULT 1486
ID AAD61810 standard; DNA; 6210 BP.
DE Streptomyces geldanus polyketide synthase (PKS) gene #1.
PD US2003114450-A1.
PA (SANT/) SANTI D.
PA (MYLE/) MYLES D C.
PA (TIAN/) TIAN Z.
PA (HUTC/) HUTCHINSON C R.
PA (JOHN/) JOHNSON R.
PA (ZHOU/) ZHOU Y.
PA (FENG/) FENG L.
Best Local Similarity: 22.11%
Query Match: 5.52%
MismatchChes: 63
Indels: 77
RESULT 1487
ID ACC71562 standard; DNA; 6902 BP.
DE VRC6703(pVR1012x/s Marburgdelta TM/h (codon optimised)) plasmid.
PD WO2003028632-A2.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Best Local Similarity: 19.17%
Query Match: 5.52%
MismatchChes: 120
Indels: 181
RESULT 1488
ID ABL33119 standard; DNA; 8758 BP.
DE Human immune system associated Gene SEQ ID NO: 1092.
PD WO200200928-A2.
PA (EPIG-) EPIGENOMICS AG.
Best Local Similarity: 20.59%
Query Match: 5.52%
MismatchChes: 77
Indels: 82
RESULT 1489
DE Marburg virus viral protein genomic DNA.
PD US2003215794-A1.
PA (KAWA/) KAWAKA Y.
PA (JASE/) JASENOSKY L D.
PA (NEUM/) NEUMANN G.
Best Local Similarity: 19.17%
Query Match: 5.52%
MismatchChes: 120
Indels: 181
RESULT 1490
ID ADO97577 standard; DNA; 73930 BP.
DE Human cancer associated sequence HD10-007, SEQ ID 554.
PD WO2004060304-A2.
PA (SAGR-) SAGRES DISCOVERY INC.
Best Local Similarity: 22.27%
Query Match: 5.52%
MismatchChes: 76
Indels: 71
RESULT 1491
ID ADI39159 standard; DNA; 85692 BP.
DE Streptomyces hygroscopicus geldanamycin gene cluster, SEQ ID NO:1.
PD WO2003106653-A2.
PA (KOSA-) KOSAN BIOSCIENCES INC.
PA (REID/) REID R C.
Best Local Similarity: 22.11%
Query Match: 5.52%
MismatchChes: 63
Indels: 77
RESULT 1492
DE AAD08215 standard; DNA; 114793 BP.
PD WO200142434-A1.
PA (MERI) MERCK & CO INC.
Best Local Similarity: 28.68%
Query Match: 5.52%
MismatchChes: 70
Indels: 15
RESULT 1493
ID AAF21610 standard; DNA; 349980 BP.
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:111.
PD WO2000066791-A1.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Best Local Similarity: 23.53%
Query Match: 5.52%
MismatchChes: 98
Indels: 91
RESULT 1496
ID ABO68913 standard; DNA; 1112 BP.
DE Listeria monocytogenes 4b contig DNA sequence #1679.
PD WO200228891-A2.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Best Local Similarity: 20.73%
Query Match: 5.49%
MismatchChes: 91
Indels: 76
RESULT 1497
ID ACA51121 standard; DNA; 1374 BP.
DE Prokaryotic essential gene #32778.
PD WO200277183-A2.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 26.40%
Query Match: 5.49%
MismatchChes: 44
Indels: 30
RESULT 1498
ID ABL21703 standard; DNA; 1380 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 16582.
PD WO200171042-A2.
PA (PEKE) PE CORP NY.
Best Local Similarity: 23.50%
Query Match: 5.52%
MismatchChes: 76
Indels: 82

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Query Match: 5.49% Indels: 67
RESULT 1499
ID ABK51913 standard; cDNA; 1558 BP.
DE cDNA encoding mouse Cacng2.
PN US6365337-B1.
PD 02-APR-2002.
PA (IOWA ) UNIV IOWA RES FOUND.
PA (JACK-) JACKSON LAB.
Best Local Similarity: 22.95% Mismatches: 66
Query Match: 5.49% Indels: 102
RESULT 1500
ID ADC92346 standard; DNA; 2028 BP.
DE E. faecium DNA sequence SEQ ID 1973.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 23.26% Mismatches: 96
Query Match: 5.49% Indels: 66
```



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	99	584.2	24.6	859	6	CB985681	AGENCOURT	CB985681	AGENCOURT	172	372.4	15.7	459	7	W03670
	100	583	24.6	583	5	BP291949	BP291949	BP291949		173	371.2	15.6	682	5	BP434862
	101	582	24.5	582	5	BP198472	BP198472	BP198472		174	370.6	15.6	721	7	CK976672
	102	580	24.5	580	5	BP341529	BP341529	BP341529		175	369.4	15.6	415	1	AA463325
	C 103	572.8	24.1	594	5	BM972462	UI-CF-EC1	BM972462	UI-CF-EC1	176	367.4	15.5	624	1	AV733213
	C 104	572.6	24.1	607	2	AW956729	EST368799	AW956729	EST368799	C 177	363	15.3	363	1	AA693904
	C 105	572.4	24.1	574	2	AW183039	x166b03.x	AW183039	x166b03.x	178	362.6	15.3	564	1	AL570408
	C 106	569	24.0	581	5	BP197816	BP197816	BP197816		179	361.8	15.3	696	7	CV111589
	107	568	23.9	580	5	BP339718	BP339718	BP339718		C 180	358	15.1	358	2	BF438812
	108	567.8	23.9	582	5	BP320362	BP320362	BP320362		181	357	15.1	470	7	RF76756
	109	567.2	23.9	794	4	BG566260	602585128	BG566260	602585128	C 182	356.4	15.0	358	2	BF197662
	C 110	567	23.9	584	5	BW731554	UI-E-C11-	BW731554	UI-E-C11-	C 183	355.4	15.0	370	7	W87483
	C 111	563.4	23.8	582	5	BM984915	UI-CF-EC1	BM984915	UI-CF-EC1	184	355.4	14.9	667	7	CF176921
	C 112	561.2	23.7	885	2	BP107215	601824293	BP107215	601824293	185	353.8	14.9	579	1	AI391129
	113	557.8	23.5	581	5	BP197366	BP197366	BP197366		186	349.6	14.7	670	2	BB611620
	C 114	543	22.9	543	4	BM708892	UI-E-C11-	BM708892	UI-E-C11-	C 187	347.4	14.6	349	1	AA704407
	C 115	538.2	22.7	847	1	AL544161	AL544161	AL544161		C 188	346.4	14.6	400	7	N80143
	116	535.6	22.6	709	4	BG539893	602563781	BG539893	602563781	189	346.2	14.6	540	4	BM253102
	117	531	22.4	594	5	BP345245	BP345245	BP345245		190	342	14.4	368	4	BG012717
	118	529	22.3	529	6	CD671330	f03c09.y	CD671330	f03c09.y	C 191	339	14.3	735	7	CK364727
	119	528	22.3	581	5	BP320205	BP320205	BP320205		C 192	338.2	14.3	621	7	CK949311
	120	526	22.2	586	1	AA046671	z1f2d09.x	AA046671	z1f2d09.x	193	338	14.2	361	7	H59965
	C 121	524	22.1	898	5	BP159588	BP159588	BP159588		C 194	337.4	14.2	618	7	CK957778
	C 122	521	22.0	589	5	BX391823	BX391823	BX391823		195	336.4	14.2	841	4	BI730362
	C 123	520	21.9	531	1	AI708530	as98a06.x	AI708530	as98a06.x	C 196	334	14.1	339	1	AA340162
	C 124	514.8	21.7	534	1	AA081351	zn33f09.s	AA081351	zn33f09.s	C 197	333.8	14.1	356	4	BI492332
	C 125	500.2	21.1	516	1	AA046747	z1f2d09.s	AA046747	z1f2d09.s	198	333.8	14.1	357	2	AW021291
	C 126	496.2	20.9	1023	6	BY704927	BY704927	BY704927		C 199	333.4	14.1	456	7	H93850
	C 127	492	20.7	749	1	AI453527	tj57a07.x	AI453527	tj57a07.x	C 200	333.4	14.1	374	6	CA449932
	C 128	489.6	20.6	581	5	BP344636	BP344636	BP344636		C 201	332.8	14.0	392	7	D63041
	C 129	487.4	20.5	489	1	AI151441	QC88q11.x	AI151441	QC88q11.x	C 202	329.4	13.9	392	7	R76413
	C 130	484.4	20.4	486	1	AA682494	z1l8e06.s	AA682494	z1l8e06.s	203	329.2	13.9	428	7	W87511
	C 131	479.2	20.2	974	6	CK988195	AGENCOURT	CK988195	AGENCOURT	204	328.2	13.8	333	7	D79275
	C 132	474.4	20.0	707	7	CK836545	4061500 B	CK836545	4061500 B	205	323	13.6	581	5	BP338802
	C 133	474	20.0	474	1	AI342481	qt28c08.x	AI342481	qt28c08.x	C 206	320.6	13.5	556	1	AA576601
	C 134	473.8	20.0	779	7	CK773274	961895 WA	CK773274	961895 WA	C 207	316	13.3	316	1	BE756611
	C 135	470	19.8	474	1	AI480375	tm51f03.x	AI480375	tm51f03.x	208	316	13.3	535	2	BE756611
	C 136	463	19.5	473	6	CB269023	1007930 H	CB269023	1007930 H	209	314.8	13.3	471	7	H72432
	C 137	461	19.4	461	1	AI470227	tj92d03.x	AI470227	tj92d03.x	C 210	314	13.2	556	5	BX434334
	C 138	459	19.4	798	5	BX373340	BX373340	BX373340		C 211	310.8	13.1	474	7	H02824
	C 139	453.6	19.1	751	7	CK073789	SLH03c18	CK073789	SLH03c18	212	307.8	13.0	325	6	CB054311
	C 140	452.2	19.1	751	7	CK775586	966716 WA	CK775586	966716 WA	213	306	12.9	318	7	R71437
	141	449.8	19.0	673	7	CK949504	4074881 B	CK949504	4074881 B	214	305.8	12.9	390	7	H78909
	142	448.8	18.9	675	7	CK958011	4098647 B	CK958011	4098647 B	215	305.2	12.9	499	2	BE198670
	C 143	443	18.7	443	1	AI091530	0e23d02.x	AI091530	0e23d02.x	216	305	12.8	328	1	AA397240
	C 144	442	18.6	442	7	N69434	za35e10.s1	N69434	za35e10.s1	217	304.8	12.8	392	7	R93568
	C 145	439.2	18.5	439	1	AI087965	0e20h12.x	AI087965	0e20h12.x	C 218	297.6	12.5	308	7	D63040
	C 146	437	18.4	437	6	CA406980	1003129 H	CA406980	1003129 H	C 219	290.4	12.2	307	7	H93538
	147	437	18.4	437	6	CA406980	1003129 H	CA406980	1003129 H	C 220	288.4	12.2	411	7	H02823
	148	420.6	17.7	465	7	H69328	yu19a09.r1	H69328	yu19a09.r1	C 221	288.4	12.2	398	7	H80143
	C 149	420	17.7	420	7	W69477	zd45b09.s1	W69477	zd45b09.s1	C 222	287.4	12.1	291	7	T40526
	C 150	420	17.7	420	1	AA693935	z153b05.s	AA693935	z153b05.s	C 223	284.2	11.8	453	7	T96905
	C 151	417.4	17.6	438	2	BF940071	na6c7c07.	BF940071	na6c7c07.	224	279.4	11.8	287	7	D62918
	C 152	412.4	17.4	443	3	BE439808	HTM1-670F	BE439808	HTM1-670F	225	276	11.6	288	1	AA137899
	C 153	408	17.2	793	9	AY411057	Homo sapi	AY411057	Homo sapi	C 226	272.8	11.5	289	1	AI378954
	154	398.4	16.8	433	7	W03259	za35e10.r1	W03259	za35e10.r1	C 227	271	11.4	377	7	D62168
	C 155	395.4	16.7	397	1	AI032588	ow70h11.s	AI032588	ow70h11.s	C 228	264.4	11.1	279	7	H72343
	C 156	394.8	16.6	910	6	CA786491	AGENCOURT	CA786491	AGENCOURT	C 229	263.8	11.1	776	7	CO567156
	157	393.2	16.6	1070	6	CK989089	AGENCOURT	CK989089	AGENCOURT	C 230	263.6	11.1	447	7	R71091
	C 158	392.4	16.5	403	1	AA923465	0147f01.s	AA923465	0147f01.s	231	263.4	11.1	277	7	W69476
	159	392.4	16.5	964	5	BU504417	AGENCOURT	BU504417	AGENCOURT	232	263	11.1	380	1	AA081350
	160	391.6	16.5	1298	7	CF110966	Shultzomi	CF110966	Shultzomi	233	256.4	10.8	871	4	BG173551
	C 161	389.6	16.4	642	6	CB442342	692918 WA	CB442342	692918 WA	234	255.8	10.8	474	7	CF791146
	C 162	388.6	16.4	653	5	CK373038	BX373038	CK373038	BX373038	235	255.4	10.8	437	1	AJ686473
	163	387.6	16.3	753	3	CK949012	4074228 B	CK949012	4074228 B	236	254.8	10.7	444	7	T96904
	164	387.2	16.3	409	2	AW961536	EST373608	AW961536	EST373608	237	252.6	10.6	371	2	BE684197
	165	386.6	16.3	790	9	AY411058	Pan trogl	AY411058	Pan trogl	238	251.4	10.6	455	1	AI006667
	C 166	386	16.3	391	1	AI052329	oy93h08.x	AI052329	oy93h08.x	239	251.2	10.6	301	7	T39345
	C 167	385.2	16.2	392	1	AA693582	z151f06.s	AA693582	z151f06.s	240	251	10.6	564	9	CE284850
	C 168	381.4	16.1	388	7	H57840	yr16e07.s1	H57840	yr16e07.s1	241	244.4	10.3	800	9	AY411059
	C 169	380.4	16.0	397	2	AW293109	UI-H-B12-	AW293109	UI-H-B12-	242	244	10.3	366	7	R24376
	C 170	377.4	15.9	408	1	AI470914	t191e10.x	AI470914	t191e10.x	243	243.4	10.3	337	7	R81462

244 242.8 10.2 569 2 B5622175 uu16h04.y  
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C 248 236.8 10.0 301 7 R81660 YJ02f03.s1  
C 249 234.8 9.9 540 5 B0417943 ik53a10.y  
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C 258 218.4 9.2 413 7 R24287  
C 259 216.4 9.1 424 1 AJ689190  
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C 270 202.8 8.5 321 7 CO261322 4133483.B  
C 271 200.4 8.4 385 7 W29485 mc02a12.r1  
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C 273 196 8.3 676 6 CB422955 596120.MA  
C 274 195.4 8.2 211 2 BE767809 CM3-GN004  
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C 277 185.2 7.8 634 6 CB426417 601599.MA  
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C 282 160.6 6.8 354 5 BY107653 BY107653  
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C 286 151.6 6.4 813 5 BU388030 603582582  
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C 290 147 6.2 158 7 F35420 HSPD31546.H  
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C 293 139.2 5.9 824 9 CC551496 CH240.436  
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C 348 86.2 3.6 739 7 CF110338 Shultzom1  
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C 382 66 2.8 289 2 BB570771 BB570771  
C 383 65.4 2.8 1101 9 CNS00E07 Drosophil  
C 384 65.2 2.7 567 9 CG806751 1118073E0  
C 385 65.2 2.7 661 9 CNS02QVJ AL209800 Tetraodon  
C 386 64.8 2.7 1146 9 CNS021G2 AL176843 Tetraodon  
C 387 64.5 2.7 418 1 AL835535 AL835535  
C 388 64.2 2.7 1241 9 AG448181 Mus muscu  
C 389 64.2 2.7 1489 9 AG350139 AG350139

C 390	64	2.7	576	5	BQ400750	BQ400750 NISC mp11	463	58.6	2.5	669	9	CG803177	CG803177 1118039F1
C 391	64	2.7	759	7	CF285642	AGENCOURT	C 464	58.6	2.5	1092	9	CNS020K7	AL175696 Tetraodon
C 392	64	2.7	811	7	CF285506	AGENCOURT	465	58.6	2.5	1245	9	CG747942	CG747942 P041-1-3-GO
C 393	64	2.7	833	6	CD381163	AGENCOURT	466	58.4	2.5	585	9	CG731051	CG731051 1119132H0
C 394	63.8	2.7	279	2	BB005336	BB005336	467	58.4	2.5	1101	9	CNS05AB2	AL328295 Tetraodon
C 395	63.8	2.7	592	9	CG727098	1119093B0	468	58.2	2.5	555	9	CG732401	CG732401 1119148C0
C 396	63.6	2.7	478	9	CG730972	1119131F0	469	58.2	2.5	628	8	AQ884340	HS 5510_A
C 397	63	2.7	1101	9	CNS00262	AL097301 Drosophil	470	58.2	2.5	739	8	BZ646786	OGCBS18TC
C 398	62.8	2.6	1101	9	CNS00EVL	Drosophil	C 471	58	2.4	556	9	CG730259	1119123F0
C 399	62.6	2.6	476	9	CG730975	AL069706 Drosophil	C 472	58	2.4	571	9	CG732209	1119146G0
C 400	62.6	2.6	966	9	CNS0052C	AL061991 Drosophil	C 473	58	2.4	792	1	AV399410	AV399410
C 401	62.6	2.6	1161	9	CNS0733X8	AL428118 clone BAO	474	58	2.4	975	8	BH179465	O14_P_10-
C 402	62.4	2.6	723	7	CF547545	AGENCOURT	C 475	58	2.4	1190	9	CNS020N7	AL026908 Tetraodon
C 403	62.4	2.6	906	7	CF546586	CF546586 AGENCOURT	476	57.8	2.4	490	9	CG732623	1119149G1
C 404	62.2	2.6	256	2	BB425330	BB425330	C 477	57.8	2.4	607	9	CG727346	1119094D0
C 405	62.2	2.6	539	9	CG730250	CG730250 1119123E0	478	57.8	2.4	1193	9	CG745316	CG745316 P038-1-GO
C 406	62	2.6	460	9	CG730237	AL067032 1119123D0	C 479	57.6	2.4	727	8	BH541380	BH541380 BOHGX75TR
C 407	62	2.6	1101	9	CNS001FB	AL060732 Drosophil	C 480	57.6	2.4	1055	9	CL501343	SAIL_696
C 408	62	2.6	1204	9	CNS016E2	AL106628 Drosophil	C 481	57.4	2.4	524	9	CNS01U90	AL167541 Tetraodon
C 409	61.8	2.6	596	9	CG714025	CG714025 1119034F0	C 482	57.4	2.4	603	9	CG730227	1119123C0
C 410	61.6	2.6	1101	9	CNS00EJ4	AL069257 Drosophil	C 483	57.4	2.4	952	9	CNS006V8	AL065967 Drosophil
C 411	61	2.6	598	9	CG731036	CG731036 1119132F0	C 484	57.4	2.4	992	9	CL144176	ISB1-144B
C 412	61	2.6	928	9	CNS00DKY	AL071865 Drosophil	C 485	57.4	2.4	1101	9	CNS001FB	AL060732 Drosophil
C 413	61	2.6	1225	9	CNS0161D	AL106171 Drosophil	C 486	57.4	2.4	1101	9	CNS00CVH	AL060100 Drosophil
C 414	60.8	2.6	876	9	CNS009G1	AL053529 Drosophil	C 487	57.4	2.4	1101	9	CNS0106X	AL098595 Drosophil
C 415	60.8	2.6	1101	9	CNS00EPO	AL069493 Drosophil	C 488	57.2	2.4	838	8	BH540508	BOGW81TF
C 416	60.6	2.6	360	6	C65403	C65403 C65403 Yuji	C 489	57.2	2.4	875	8	BH573211	BOGUC23TR
C 417	60.6	2.6	625	1	AU207455	AU207455 AU207455	C 490	57.2	2.4	1101	9	CNS00EB01	AL057419 Drosophil
C 418	60.4	2.5	734	9	CNS010MP	AL099163 Drosophil	C 491	57.2	2.4	1190	9	CNS020N7	AL266908 Tetraodon
C 419	60.4	2.5	1101	9	CNS0039G	AL063921 Drosophil	492	57	2.4	588	9	CG710585	CG710585 1119018A0
C 420	60.4	2.5	1101	9	CNS00E07	AL069440 Drosophil	493	57	2.4	591	9	CG807037	1118076H0
C 421	60.2	2.5	222	6	CB433605	609991 WA	494	57	2.4	598	9	CG803687	CG803687 1118045A0
C 422	60.2	2.5	606	9	CG807857	CG807857 1118087D1	C 495	57	2.4	1184	3	CR665955	CR665955 Tetraodon
C 423	60	2.5	628	9	CG721223	CG721223 1119066A0	C 496	56.8	2.4	260	6	C64070	C64070 C64070 Yuji
C 424	60	2.5	659	9	CG732143	CG732143 1119146D0	C 497	56.8	2.4	567	9	CG730248	CG730248 1119123E0
C 425	60	2.5	710	8	BH564363	BH564363 BOGHA71TF	498	56.8	2.4	600	9	CNS06G12	AL397116 T3 end of
C 426	60	2.5	1101	9	CNS00FYG	AL071206 Drosophil	499	56.6	2.4	459	9	CG723690	1119077F0
C 427	60	2.5	1101	9	CNS0145U	AL103740 Drosophil	500	56.6	2.4	476	9	CG730975	CG730975 1119131G0
C 428	59.8	2.5	194	1	AV230216	AV230216 AV230216	C 501	56.6	2.4	550	9	CG727200	1119093F1
C 429	59.8	2.5	411	4	BG657011	BG657011 dab27a03.	C 502	56.6	2.4	583	9	CG726928	CG726928 1119092C0
C 430	59.8	2.5	624	9	CG721168	CG721168 1119065G0	C 503	56.6	2.4	1101	9	CNS003BD	AL040491 Drosophil
C 431	59.8	2.5	815	9	AG471644	AG471644 Mus muscu	504	56.6	2.4	1616	3	CR734259	CR734259 Tetraodon
C 432	59.8	2.5	876	9	CNS009G1	AL053529 Drosophil	505	56.6	2.4	1626	7	CF238805	CF238805 AGENCOURT
C 433	59.8	2.5	1101	9	CNS003BD	AL064091 Drosophil	C 506	56.4	2.4	966	9	CNS001S4	AL075573 Drosophil
C 434	59.8	2.5	2077	3	CR667281	CR667281 Tetraodon	507	56.4	2.4	1019	9	AG448879	Mus muscu
C 435	59.6	2.5	330	7	D35273	D35273 CELX019C2F	C 508	56.4	2.4	1037	5	BQ648574	AGENCOURT
C 436	59.6	2.5	360	6	C63838	C63838 C63838 Yuji	C 509	56.4	2.4	1200	3	CR6660304	CR6660304 Tetraodon
C 437	59.6	2.5	636	9	CG727329	CG727329 1119094C1	C 510	56.4	2.4	1896	9	CG753083	CG753083 P048-1-CO
C 438	59.6	2.5	1061	6	CB589276	CB589276 AGENCOURT	C 511	56.2	2.4	549	9	CG806957	CG806957 1118075F0
C 439	59.6	2.5	1168	9	CL078758	CL078758 CH216-153	C 512	56.2	2.4	567	9	CG803178	CG803178 1118039F1
C 440	59.4	2.5	551	9	CG803090	CG803090 1118038D0	C 513	56.2	2.4	569	9	CG726854	1119091H0
C 441	59.4	2.5	1061	9	CNS015LM	AL105604 Drosophil	514	56.2	2.4	592	9	CG727146	CG727146 1119093D1
C 442	59.4	2.5	1092	9	CNS020K7	AL175696 Tetraodon	C 515	56.2	2.4	607	9	CG721216	CG721216 1119086A0
C 443	59	2.5	360	1	AV195161	AV195161	C 516	56.2	2.4	667	9	CG806870	CG806870 1118074H0
C 444	59	2.5	360	6	AV203653	AV203653	517	56	2.4	365	7	D37632	CELX005F3F
C 445	59	2.5	360	6	C39987	C39987 C39987 Yuji	C 518	56	2.4	499	6	CD285349	G39163.54
C 446	59	2.5	360	6	C61731	C61731 C61731 Yuji	C 519	56	2.4	526	9	CG726791	CG726791 1119091F0
C 447	59	2.5	360	6	C63572	C63572 C63572 Yuji	520	56	2.4	1069	9	CNS0107G	AL098614 Drosophil
C 448	59	2.5	360	6	C65311	C65311 C65311 Yuji	C 521	55.8	2.4	539	9	CG727303	CG727303 1119094B0
C 449	59	2.5	368	1	AV192643	AV192643	C 522	55.8	2.4	578	9	CG730231	CG730231 1119123C1
C 450	59	2.5	373	6	C69540	C69540 C69540 Yuji	C 523	55.8	2.4	637	9	CNS036CC	AL129845 Tetraodon
C 451	59	2.5	376	6	C43629	C43629 C43629 Yuji	524	55.8	2.4	987	6	CD387205	AGENCOURT
C 452	59	2.5	376	6	C44002	C44002 C44002 Yuji	525	55.6	2.3	502	9	CG727291	1119094B0
C 453	59	2.5	378	1	AV202361	AV202361	526	55.6	2.3	508	9	CG727099	1119093B0
C 454	59	2.5	804	9	AG519931	AG519931 Mus muscu	527	55.6	2.3	536	8	AQ433467	HS_5052_B
C 455	59	2.5	828	5	EX078167	EX078167 BX078167	528	55.6	2.3	539	9	CG731258	1119066B0
C 456	59	2.5	1101	9	CNS0021J	AL061936 Drosophil	529	55.6	2.3	599	9	CG732126	1119146C0
C 457	59	2.5	1101	9	CNS00LT2	AL078714 Drosophil	C 530	55.6	2.3	1001	9	CNS00JOK	CG732126 Drosophil
C 458	58.8	2.5	804	8	B12681	B12681 F27D1-SP6.1	C 531	55.6	2.3	1035	6	CD049595	AGENCOURT
C 459	58.8	2.5	975	8	BH179465	BH179465 O14_P_10-	C 532	55.6	2.3	1101	9	CNS000B8	AL076640 Drosophil
C 460	58.8	2.5	1161	9	CNS073Y8	AL428118 clone BAO	C 533	55.6	2.3	1164	8	CC218891	AL063632 AGENCOURT
C 461	58.8	2.5	1201	9	CNS0165X	AL106335 Drosophil	534	55.6	2.3	1187	8	CC218891	CH261-14M
C 462	58.6	2.5	266	2	BF710405	BF710405 MI-P-Ayl-1	535	55.4	2.3	500	6	BD1734509	B11102 F19C22-77 I

536	55.4	2.3	571	9	CG732194	1119146F0	609	54	2.3	572	6	CB016588	pgn1c.pk0
537	55.4	2.3	582	7	CG803705	1118045B1	C 610	54	2.3	867	9	CNS0758G	AL429890 clone BA0
538	55.4	2.3	575	7	CF256984	pha005_c0	C 611	54	2.3	987	9	CNS014PQ	AL104456 Drosophil
539	55.4	2.3	539	9	CG726927	1119092C0	C 612	54	2.3	1038	9	CNS01TL7	AL166660 Tetraodon
540	55.4	2.3	608	7	CF257313	pha009_f1	C 613	54	2.3	1101	9	CNS00EMH	AL069378 Drosophil
541	55.4	2.3	739	1	AJ450624	AJ450624	C 614	54	2.3	1187	9	AG381847	AG381847 Mus muscu
542	55.4	2.3	775	7	CH218866	RJA040G05	C 615	54	2.3	1193	9	CG745316	CG745316 P038-1-G0
543	55.4	2.3	811	1	AL514901	AL514901	C 616	53.8	2.3	509	9	CG721684	CG721684 1119068E0
544	55.4	2.3	855	7	CF257095	pha006_g0	C 617	53.8	2.3	530	9	CG731340	CG731340 1119139D0
545	55.4	2.3	859	7	CF257757	pha015_a1	C 618	53.8	2.3	601	9	CG727094	CG727094 1119093B0
546	55.4	2.3	885	7	CF257093	pha006_f1	C 619	53.8	2.3	609	9	CG726983	CG726983 1119092F0
547	55.4	2.3	889	7	CF251893	hdn005_f1	C 620	53.8	2.3	616	4	BJ117778	BJ117778
548	55.4	2.3	1101	9	CNS003BB	Drosophil	C 621	53.8	2.3	758	1	AV756150	AV756150
549	55.4	2.3	1388	5	BQ279227	AGENCOURT	C 622	53.8	2.3	881	7	CF251803	CF251803 hdm004_c0
550	55.4	2.3	2300	3	CR734152	Tetraodon	C 623	53.8	2.3	886	7	CF251786	CF251786 hdm004_c0
551	55.2	2.3	332	6	CD584497	RK025A2G1	C 624	53.8	2.3	961	9	CNS008HI	AL051882 Drosophil
552	55.2	2.3	478	9	CG730972	1119131F0	C 625	53.8	2.3	969	6	CD048933	CD048933 AGENCOURT
553	55.2	2.3	530	9	CG731251	1119138B0	C 626	53.8	2.3	1038	9	CNS06L7M	AL403832 T3 end of
554	55.2	2.3	958	9	CNS007AD	Drosophil	C 627	53.8	2.3	1101	9	CNS00EJ4	AL069257 Drosophil
555	55.2	2.3	1013	9	CNS06RPQ	AL412260 T7 end of	C 628	53.8	2.3	1350	9	CG744271	CG744271 P036-4-C0
556	55.2	2.3	1032	9	CL144058	ISB1-124E	C 629	53.8	2.3	1696	9	AG346840	AG346840 Mus muscu
557	55.2	2.3	1132	8	BZ695089	SP_Ba005	C 630	53.6	2.3	458	9	CG727107	CG727107 1119093C0
558	55.2	2.3	1169	9	CNS06KHO	AL402900 T3 end of	C 631	53.6	2.3	495	9	CG803905	CG803905 1118046F0
559	55.2	2.3	2142	3	CR730230	Tetraodon	C 632	53.6	2.3	636	9	CG727329	CG727329 1119094C1
560	55	2.3	407	9	CG727336	1119094D0	C 633	53.6	2.3	641	8	BZ400247	BZ400247 EINBD40TR
561	55	2.3	567	9	CL509924	SAIL_821	C 634	53.6	2.3	642	1	AV398040	AV398040 AV398040
562	55	2.3	598	9	CG727121	1119093C0	C 635	53.6	2.3	665	9	CG730213	CG730213 1119123B0
563	55	2.3	598	9	CG727121	1119093C0	C 636	53.6	2.3	687	5	BP179101	BP179101 BP179101
564	55	2.3	825	4	BM358161	GA_Ea000	C 637	53.6	2.3	799	9	AG137960	AG137960 Pan trogl
565	55	2.3	914	9	CNS002JV	Drosophil	C 638	53.6	2.3	843	9	CNS00CS1	AL059666 Drosophil
566	55	2.3	1101	9	CNS00FVE	Drosophil	C 639	53.6	2.3	850	8	BHS12733	BHS12733 BOH1K48TR
567	55	2.3	1664	3	CG721909	Tetraodon	C 640	53.6	2.3	910	9	CNS01G8P	AL142826 Anopheles
568	55	2.3	1780	9	AG320553	Mus muscu	C 641	53.6	2.3	938	9	CNS006TV	AL065906 Drosophil
569	54.8	2.3	411	9	CG731085	1119133D0	C 642	53.6	2.3	973	9	CNS071LE	AL425064 clone BA0
570	54.8	2.3	498	1	AU087066	AU087066	C 643	53.6	2.3	1038	9	CNS01TL7	AL166660 Tetraodon
571	54.8	2.3	524	9	CNS01U90	AL167541 Tetraodon	C 644	53.6	2.3	1043	9	CNS003K0	AL166660 Drosophil
572	54.8	2.3	631	9	CG731366	1119139F0	C 645	53.6	2.3	1067	6	CD386564	CD386564 AGENCOURT
573	54.8	2.3	650	9	CG807645	1118085F0	C 646	53.6	2.3	1101	9	CNS0022U	AL099152 Drosophil
574	54.8	2.3	696	8	BH484256	BOGTN39TF	C 647	53.6	2.3	1101	9	CNS0182P	AL108811 Drosophil
575	54.8	2.3	848	8	A2549808	ENTF262TF	C 648	53.6	2.3	1118	5	BX462896	BX462896 BX462896
576	54.8	2.3	945	9	CL483400	SAIL_37b	C 649	53.6	2.3	1178	8	BZ696021	BZ696021 SP_Ba007
577	54.8	2.3	961	6	CD388875	AGENCOURT	C 650	53.6	2.3	1201	9	CNS0167M	AL106396 Drosophil
578	54.8	2.3	1052	5	BUS60001	BUS60001 AGENCOURT	C 651	53.6	2.3	1306	9	CG754607	CG754607 P050-1-D0
579	54.8	2.3	1101	9	CNS00EPO	AL069493 Drosophil	C 652	53.6	2.3	1802	9	AG350317	AG350317 Mus muscu
580	54.6	2.3	443	9	CG726803	1119091F1	C 653	53.4	2.3	401	9	CG807791	CG807791 1118086H1
581	54.6	2.3	460	9	CG730210	1119123B0	C 654	53.4	2.3	482	9	CG721052	CG721052 1119065B0
582	54.6	2.3	555	9	CG727190	1119093F0	C 655	53.4	2.3	487	9	CG730305	CG730305 1119124B1
583	54.6	2.3	665	9	CG730213	1119123B0	C 656	53.4	2.3	510	9	CG731581	CG731581 1119142B0
584	54.6	2.3	897	2	B8620968	B8620968	C 657	53.4	2.3	518	9	CG732173	CG732173 1119148E1
585	54.6	2.3	928	9	CNS00DKY	AL071865 Drosophil	C 658	53.4	2.3	571	9	CG807806	CG807806 1118087B0
586	54.6	2.3	981	9	CNS02BD8	AL189701 Tetraodon	C 659	53.4	2.3	599	9	CG731383	CG731383 1119139G0
587	54.6	2.3	1043	9	CNS0145P	AL103735 Drosophil	C 660	53.4	2.3	607	9	CG727346	CG727346 1119094D0
588	54.4	2.3	508	9	CG806869	1118074H0	C 661	53.4	2.3	798	8	BZ460887	BZ460887 BONJW94TF
589	54.4	2.3	667	9	CG806870	1118074H0	C 662	53.4	2.3	837	8	ANZ669102	ANZ669102 ENTMT64TF
590	54.4	2.3	905	4	CNS00KHX	AL077798 Drosophil	C 663	53.4	2.3	847	8	AZ669102	AZ669102 ENTMT64TF
591	54.4	2.3	945	4	BM358135	GA_Ea000	C 664	53.4	2.3	918	8	BH162373	BH162373 ENTGT88TR
592	54.4	2.3	980	9	CNS00JG1	AL076232 Drosophil	C 665	53.4	2.3	945	9	CNS04D0K	AL285149 Tetraodon
593	54.4	2.3	1101	9	CNS017KE	AL108152 Drosophil	C 666	53.4	2.3	1083	9	CNS00IH6	AL074775 Drosophil
594	54.4	2.3	1200	9	CNS016CO	AL106578 Drosophil	C 667	53.4	2.3	1101	9	CNS00FYC	AL071206 Drosophil
595	54.4	2.3	1205	9	CL509381	SAIL_811	C 668	53.4	2.3	1101	9	CNS012TP	AL103207 Drosophil
596	54.2	2.3	782	7	CV484987	CV484987 AGENCOURT	C 669	53.4	2.3	1160	8	BZ579469	BZ579469 msb2_637.
597	54.2	2.3	821	9	CNS0090X	AL052985 Drosophil	C 670	53.4	2.3	1364	9	CG757970	CG757970 P053-2-C0
598	54.2	2.3	900	9	CNS03M11	AL250174 Tetraodon	C 671	53.2	2.2	437	9	CG722959	CG722959 1119074B0
599	54.2	2.3	963	9	CNS00A4L	AL054918 Drosophil	C 672	53.2	2.2	475	9	CG732245	CG732245 1119146H0
600	54.2	2.3	1027	9	CNS02T50	AL212733 Tetraodon	C 673	53.2	2.2	550	9	CG808239	CG808239 1118090F0
601	54.2	2.3	1076	9	AG477716	AG477716 Mus muscu	C 674	53.2	2.2	567	9	CG730248	CG730248 1119123E0
602	54.2	2.3	1275	9	CL033318	CH216-36F	C 675	53.2	2.2	612	9	CG803681	CG803681 1118045A0
603	54	2.3	1449	9	CG732185	1119146F0	C 676	53.2	2.2	663	9	CG807905	CG807905 1118087H0
604	54	2.3	467	8	AQ155072	HS_3039_B	C 677	53.2	2.2	860	9	CNS018BP	AL103135 Drosophil
605	54	2.3	512	9	CG727127	1119093C1	C 678	53.2	2.2	878	9	CNS0187R	AL108993 Drosophil
606	54	2.3	542	9	CG732162	1119146E0	C 679	53.2	2.2	924	9	CNS02Q6S	AL208909 Tetraodon
607	54	2.3	543	9	CG730256	1119123E1	C 680	53.2	2.2	966	6	CD388381	CD388381 AGENCOURT
608	54	2.3	556	9	CG730259	1119123F0	C 681	53.2	2.2	1013	9	CNS06RPQ	AL412260 T7 end of

682	53.2	2.2	1027	9	CNS02T50	AL212733 Tetraodon	755	52.2	2.2	639	9	CG721246
683	53.2	2.2	1038	6	CD388242	AGENCYCOURT	C 756	52.2	2.2	761	6	CD385036
684	53.2	2.2	1091	9	CL504270	SAIL_734	C 757	52.2	2.2	775	7	CK787487
685	53	2.2	417	9	CG721114	CG721114 1119065E0	C 758	52.2	2.2	795	9	AG044101
686	53	2.2	520	9	CG803697	CG803697 1118045B0	C 759	52.2	2.2	818	9	AG579058
687	53	2.2	571	8	B88488	B88488 CpG02268 Cp	C 760	52.2	2.2	887	2	BF274559
688	53	2.2	631	9	CG731287	CG731287 1119138E0	C 761	52.2	2.2	912	9	CNS006RB
689	53	2.2	669	9	CG803177	CG803177 1118039F1	C 762	52.2	2.2	962	9	CL867956
690	53	2.2	744	8	AQ050079	AQ050079 nxbx0003b	C 763	52.2	2.2	996	9	CNS000FUH
691	53	2.2	878	7	CG809521	CG809521 AGENCYCOURT	C 764	52.2	2.2	2826	3	AK084681
692	53	2.2	913	8	AZ550938	AZ550938 ENTFF44TF	C 765	52	2.2	450	9	CG721656
693	53	2.2	1017	9	CL101048	CL101048 ISB1-3604	C 766	52	2.2	462	9	CG732576
694	53	2.2	1332	9	AG429508	AG429508 Mus muscu	C 767	52	2.2	468	9	CG806831
695	53	2.2	1352	9	AG381852	AG381852 Mus muscu	C 768	52	2.2	521	9	CG808109
696	53	2.2	1974	3	CG734974	CG734974 Tetraodon	C 769	52	2.2	727	9	CG116174
697	52.8	2.2	408	9	CG721284	CG721284 1119066C0	C 770	52	2.2	759	8	CC434340
698	52.8	2.2	460	9	CG807730	CG807730 1118086D0	C 771	52	2.2	769	7	CO390209
699	52.8	2.2	555	9	CG807021	CG807021 1118076E1	C 772	52	2.2	784	8	BZ466559
700	52.8	2.2	610	9	CG806846	CG806846 1118074F0	C 773	52	2.2	786	9	CNS009A5
701	52.8	2.2	620	9	CG731250	CG731250 1119138B0	C 774	52	2.2	822	9	CNS009CW
702	52.8	2.2	806	4	BG309137	BG309137 HVSMEC000	C 775	52	2.2	826	9	AG579614
703	52.8	2.2	815	9	EX188005	EX188005 Danio rer	C 776	52	2.2	866	8	AQ258984
704	52.8	2.2	866	9	CNS006MS	AL065764 Drosophil	C 777	52	2.2	889	9	AQ258984
705	52.8	2.2	1013	9	CNS06SG4	AL413210 T7 end of	C 778	52	2.2	1101	9	CNS0021J
706	52.8	2.2	1091	7	CF934550	CF934550 T7EST-B10	C 779	52	2.2	1203	9	CNS015WU
707	52.8	2.2	1101	9	CNS00PFC	AL070972 Drosophil	C 780	52	2.2	1203	9	CNS015WU
708	52.8	2.2	1201	9	CNS0167M	AL106396 Drosophil	C 781	52	2.2	1225	8	CC238324
709	52.8	2.2	2077	3	CR667281	CR667281 Tetraodon	C 782	52	2.2	1500	8	CC286682
710	52.6	2.2	487	9	CG727008	CG727008 1119092G0	C 783	52	2.2	1527	9	CL492977
711	52.6	2.2	492	9	CG803983	CG803983 1118047B0	C 784	52	2.2	1592	9	CG750135
712	52.6	2.2	550	9	CG803095	CG803095 1118038D0	C 785	52	2.2	2466	9	CL508701
713	52.6	2.2	605	9	CG731359	CG731359 1119139E0	C 786	51.8	2.2	435	9	CG731288
714	52.6	2.2	685	8	BH471035	BH471035 BOHKJ81TR	C 787	51.8	2.2	459	9	CG721530
715	52.6	2.2	889	9	AG362888	AG362888 Mus muscu	C 788	51.8	2.2	494	9	CG732222
716	52.6	2.2	903	9	CNS02WVM	AL217579 Tetraodon	C 789	51.8	2.2	503	9	CG732172
717	52.6	2.2	915	8	BH149815	BH149815 ENTPQ52TF	C 790	51.8	2.2	512	9	CG732057
718	52.6	2.2	1234	9	AG350353	AG350353 Mus muscu	C 791	51.8	2.2	513	9	CG727073
719	52.6	2.2	1391	9	CG754863	CG754863 P050-2-G0	C 792	51.8	2.2	529	9	CG807765
720	52.6	2.2	1571	9	AG435593	AG435593 Mus muscu	C 793	51.8	2.2	576	9	CG731273
721	52.4	2.2	287	4	BJ100724	BJ100724 BJ100724	C 794	51.8	2.2	592	9	CG729361
722	52.4	2.2	426	9	CG732145	CG732145 1119146D0	C 795	51.8	2.2	599	9	CG731383
723	52.4	2.2	490	9	CG721573	CG721573 1119068A0	C 796	51.8	2.2	844	4	BM358154
724	52.4	2.2	493	9	CNS04135	CG804135 1118048A0	C 797	51.8	2.2	932	6	CD390089
725	52.4	2.2	576	9	CNS035N7	AL228940 Tetraodon	C 798	51.8	2.2	961	9	CNS008HI
726	52.4	2.2	583	9	CG726928	CG726928 1119092C0	C 799	51.8	2.2	971	9	CL120194
727	52.4	2.2	606	9	CG807857	CG807857 1118087D1	C 800	51.8	2.2	1101	9	CNS00EQL
728	52.4	2.2	681	2	BF294330	BF294330 003PBH09	C 801	51.8	2.2	1101	9	CNS00PFC
729	52.4	2.2	758	1	AV756150	AV756150 AV756150	C 802	51.8	2.2	1191	9	CL104745
730	52.4	2.2	773	8	BH186746	BH186746 032 E 23-	C 803	51.8	2.2	1205	9	CNS0165A
731	52.4	2.2	773	9	CNS07R5M	AL623692 T7 end of	C 804	51.6	2.2	371	9	CG709517
732	52.4	2.2	945	9	CNS04D0K	AL285149 Tetraodon	C 805	51.6	2.2	499	9	CG721069
733	52.4	2.2	965	6	CD384873	CD384873 AGENCYCOURT	C 806	51.6	2.2	501	9	CG807610
734	52.4	2.2	969	9	CL469446	CL469446 SAIL_1303	C 807	51.6	2.2	504	9	CG731135
735	52.4	2.2	1001	9	CNS0155H	AL105023 Drosophil	C 808	51.6	2.2	511	9	CG807598
736	52.4	2.2	1091	9	CNS007OF	AL067422 Drosophil	C 809	51.6	2.2	569	9	CG726854
737	52.4	2.2	1101	9	CNS00Z6Z	AL097301 Drosophil	C 810	51.6	2.2	574	9	CG732207
738	52.4	2.2	1225	8	CC238324	CC238324 CH261-192	C 811	51.6	2.2	575	9	CG803680
739	52.2	2.2	293	2	BE028896	BE028896 kp21c10.Y	C 812	51.6	2.2	585	9	CG807712
740	52.2	2.2	338	1	AI415305	AI415305 mc02a12.x	C 813	51.6	2.2	592	9	CG727146
741	52.2	2.2	361	7	CF582009	CF582009 AGENCYCOURT	C 814	51.6	2.2	609	9	CG726983
742	52.2	2.2	452	4	BI965863	BI965863 id48d11.Y	C 815	51.6	2.2	651	9	CG807569
743	52.2	2.2	489	9	CG803872	CG803872 1118046E0	C 816	51.6	2.2	773	4	BG854434
744	52.2	2.2	505	4	BI965801	BI965801 id47g12.Y	C 817	51.6	2.2	886	8	BH177277
745	52.2	2.2	523	9	CG731328	CG731328 1119139C0	C 818	51.6	2.2	886	9	CNS07JUX
746	52.2	2.2	550	9	CG727200	CG727200 1119093F1	C 819	51.6	2.2	1013	6	CD387611
747	52.2	2.2	556	4	BM053785	BM053785 id42d11.Y	C 820	51.6	2.2	1101	9	CNS003DQ
748	52.2	2.2	556	8	CG800480	CG800480 1118013A0	C 821	51.6	2.2	1187	9	AG337989
749	52.2	2.2	568	8	BH023448	BH023448 GH_MB5000	C 822	51.6	2.2	1303	8	BZ555610
750	52.2	2.2	574	9	CG730254	CG730254 1119123E1	C 823	51.6	2.2	2087	9	AG333887
751	52.2	2.2	578	9	CG730231	CG730231 1119123C1	C 824	51.4	2.2	475	9	CG803223
752	52.2	2.2	588	9	CG710585	CG710585 1119018A0	C 825	51.4	2.2	487	9	CG727192
753	52.2	2.2	612	9	CG803681	CG803681 1118045A0	C 826	51.4	2.2	500	9	CG732575
754	52.2	2.2	638	9	CG803213	CG803213 1118040A0	C 827	51.4	2.2	502	9	CG727387



828	51.4	2.2	581	9	CNS034DK	AL227297 Tetraodon	901	50.8	2.1	791	8	BH551361	BH551361 BOGCE09TF
829	51.4	2.2	603	9	CG730227	CG730227 1119123C0	902	50.8	2.1	821	7	CF885572	CF885572 trlc082xa
c 830	51.4	2.2	605	9	CG731359	CG731359 1119139E0	903	50.8	2.1	826	9	AG579614	AG579614 Mus muscu
c 831	51.4	2.2	646	1	AV399905	AV399905 AV399905	904	50.8	2.1	828	8	AQ739398	AQ739398 HS 5482 B
c 832	51.4	2.2	650	9	CE195951	CE195951 tigr-g8s-	905	50.8	2.1	831	9	AG477668	AG477668 Mus muscu
c 833	51.4	2.2	691	8	BH941093	BH941093 odfl6b06.	c 906	50.8	2.1	880	9	CNS009L8	AL053317 Drosophil
c 834	51.4	2.2	843	9	CNS00CS1	AL059666 Drosophil	907	50.8	2.1	921	9	CL1100769	CL1100769 ISBI-36F1
c 835	51.4	2.2	887	9	AG526041	AG526041 Mus muscu	908	50.8	2.1	939	6	CD387952	CD387952 AGENCOURT
c 836	51.4	2.2	911	9	CL478691	CL478691 SAIL_294	c 909	50.8	2.1	952	6	CD051140	CD051140 AGENCOURT
c 837	51.4	2.2	1101	9	CNS000D1	AL065414 Drosophil	910	50.8	2.1	961	7	CK230311	CK230311 ILLUMIGEN
c 838	51.4	2.2	1101	9	CNS016L1	AL106896 Drosophil	911	50.8	2.1	1012	9	CL044464	CL044464 CH216-61F
c 839	51.4	2.2	1160	8	B2579469	B2579469 msh2 637.	912	50.8	2.1	1065	9	CL040367	CL040367 CH216-49K
c 840	51.4	2.2	1200	9	CNS016CO	AL106578 Drosophil	913	50.8	2.1	1101	9	CNS00ESI	AL069797 Drosophil
c 841	51.4	2.2	1335	9	CL646802	CL646802 CH213-123	c 914	50.8	2.1	1146	9	CNS021G2	AL176843 Tetraodon
c 842	51.4	2.2	1715	9	AG288305	AG288305 Mus muscu	c 915	50.8	2.1	1196	3	CR734775	CR734775 Tetraodon
c 843	51.2	2.2	348	9	AG237623	AG237623 Lotus cor	916	50.8	2.1	1348	9	CG749499	CG749499 P043-4-A0
c 844	51.2	2.2	434	9	CG723260	CG723260 1119075E0	917	50.8	2.1	1388	9	AG278124	AG278124 Mus muscu
c 845	51.2	2.2	453	9	CG730298	CG730298 111912480	918	50.8	2.1	1392	9	CG757503	CG757503 P052-4-C0
c 846	51.2	2.2	480	9	CG721323	CG721323 1119066D0	c 919	50.8	2.1	1592	9	CG750135	CG750135 P044-3-D0
c 847	51.2	2.2	488	9	CG731260	CG731260 1119138C0	c 920	50.6	2.1	367	9	CG730984	CG730984 1119131H0
c 848	51.2	2.2	505	9	CG807903	CG807903 1118087G1	921	50.6	2.1	413	9	CG727412	CG727412 1119094G0
c 849	51.2	2.2	510	8	BH766152	BH766152 BMBAC359H	922	50.6	2.1	464	9	CG803917	CG803917 1118046G0
c 850	51.2	2.2	520	9	CG723442	CG723442 1119076D0	923	50.6	2.1	491	9	CG730328	CG730328 1119124E0
c 851	51.2	2.2	556	9	CL341275	CL341275 RPCI44_26	924	50.6	2.1	513	9	CG803105	CG803105 1118038E1
c 852	51.2	2.2	568	9	CG803931	CG803931 1118046H0	925	50.6	2.1	562	8	B68654	B68654 CIT-HSP-205
c 853	51.2	2.2	631	9	CG721223	CG721223 1119066A0	c 926	50.6	2.1	571	9	CG732209	CG732209 1119146G0
c 854	51.2	2.2	628	9	CG731287	CG731287 1119138E0	927	50.6	2.1	593	9	CG732537	CG732537 1119149B1
c 855	51.2	2.2	675	9	CG807781	CG807781 1118086H0	928	50.6	2.1	613	9	CG721572	CG721572 1119069A0
c 856	51.2	2.2	831	8	B19844	B19844 T2J23-T7 TA	929	50.6	2.1	628	9	CG807906	CG807906 1118087H0
c 857	51.2	2.2	900	8	A2678198	A2678198 ENTGV60TF	c 930	50.6	2.1	646	9	CG807859	CG807859 1118087E0
c 858	51.2	2.2	1101	9	CNS017ZQ	AL108704 Drosophil	c 931	50.6	2.1	651	9	CG807569	CG807569 1118088A0
c 859	51.2	2.2	1542	9	AG386981	AG386981 Mus muscu	c 932	50.6	2.1	656	9	CG807672	CG807672 1118085H0
c 860	51.2	2.2	2458	9	CL468223	CL468223 SAIL_1282	c 933	50.6	2.1	673	8	BH565747	BH565747 BOGWE76TF
c 861	51.2	2.2	415	9	CG731289	CG731289 1119138E0	c 934	50.6	2.1	694	9	CG807674	CG807674 1118085H0
c 862	51.2	2.2	508	9	CG728850	CG728850 1119104C0	935	50.6	2.1	704	9	BX193580	BX193580 Danio rer
c 863	51.2	2.2	523	9	CG721571	CG721571 1119068A0	c 936	50.6	2.1	806	8	B20782	B20782 T7H16-T7 TA
c 864	51.2	2.2	558	4	BM276395	BM276395 PFEST0aa8	c 937	50.6	2.1	830	8	BH248163	BH248163 BOGAV82TR
c 865	51.2	2.2	581	5	B2072818	B2072818 BP202818	c 938	50.6	2.1	939	6	BY720774	BY720774 BY720774
c 866	51.2	2.2	610	9	CG806846	CG806846 1118074F0	c 939	50.6	2.1	970	6	CB208406	CB208406 AGENCOURT
c 867	51.2	2.2	628	9	CG807906	CG807906 1118087H0	940	50.6	2.1	982	4	BM415348	BM415348 OP20422 M
c 868	51.2	2.2	631	9	CG731366	CG731366 1119139F0	941	50.6	2.1	1101	9	CNS0039R	AL063332 Drosophil
c 869	51.2	2.2	638	9	CG803213	CG803213 1118040A0	c 942	50.6	2.1	1101	9	CNS0022U	AL097152 Drosophil
c 870	51.2	2.2	659	9	CG732143	CG732143 1119146D0	c 943	50.4	2.1	1174	9	CL110860	CL110860 ISBI-54F2
c 871	51.2	2.2	698	8	B2075454	B2075454 lk86a04.	944	50.4	2.1	397	9	CG732397	CG732397 1119148B1
c 872	51.2	2.2	715	8	B2395587	B2395587 E1NBB40TF	945	50.4	2.1	436	9	CG726942	CG726942 1119092D0
c 873	51.2	2.2	826	7	CV483860	CV483860 AGENCOURT	946	50.4	2.1	442	9	CG804073	CG804073 1118047F0
c 874	51.2	2.2	828	8	A2693244	A2693244 ENTKB02TF	947	50.4	2.1	461	9	CG730244	CG730244 1119123D1
c 875	51.2	2.2	893	8	BH188563	BH188563 O36_O12-	948	50.4	2.1	481	9	CG803819	CG803819 1118048B0
c 876	51.2	2.2	893	9	CNS075JW	AL625502 T3_end of	949	50.4	2.1	567	9	CG806751	CG806751 1118073E0
c 877	51.2	2.2	920	4	BM816394	BM816394 HC114G06	950	50.4	2.1	576	9	CG807740	CG807740 1118086D0
c 878	51.2	2.2	1007	9	CNS06X9S	AL19462 T3_end of	951	50.4	2.1	685	8	B2030069	B2030069 oed82a10.
c 879	51.2	2.2	1047	9	CNS0164P	AL106291 Drosophil	952	50.4	2.1	812	8	BH178455	BH178455 O11_J_O2-
c 880	51.2	2.2	1165	3	CR677611	CR677611 Tetraodon	953	50.4	2.1	812	7	CK478557	CK478557 AGENCOURT
c 881	51.2	2.2	1178	9	CL111035	CL111035 ISBI-54K1	954	50.4	2.1	814	7	AG528710	AG528710 Mus muscu
c 882	51.2	2.2	1214	7	CK211400	CK211400 FGAS02324	955	50.4	2.1	829	9	CNS016YR	AL107373 Drosophil
c 883	51.2	2.2	1254	3	CR720510	CR720510 Tetraodon	c 956	50.4	2.1	1085	9	CNS007OF	AL067422 Drosophil
c 884	51.2	2.2	1343	9	AG333983	AG333983 Mus muscu	c 957	50.4	2.1	1091	9	CNS0039L	AL063926 Drosophil
c 885	50.8	2.1	1980	9	CG723457	CG723457 1119076E0	958	50.4	2.1	1101	9	CNS00DT7	AL075293 Drosophil
c 886	50.8	2.1	430	9	CG730971	CG730971 1119131F0	959	50.4	2.1	1101	5	BU495248	BU495248 PFEST0ab7
c 887	50.8	2.1	441	9	CG730243	CG730243 1119123D1	960	50.2	2.1	356	5	BQ451328	BQ451328 PFEST0aa9
c 888	50.8	2.1	469	9	CG731872	CG731872 1119144B1	961	50.2	2.1	367	5	BM528256	BM528256 BM528256
c 889	50.8	2.1	473	9	CG803682	CG803682 1118045A0	c 962	50.2	2.1	440	5	CG801855	CG801855 1118025C0
c 890	50.8	2.1	473	9	CG803682	CG803682 1118045A0	963	50.2	2.1	456	9	CG732472	CG732472 1119148G0
c 891	50.8	2.1	481	9	CG727147	CG727147 1119093D1	964	50.2	2.1	482	9	CG807610	CG807610 1118085C1
c 892	50.8	2.1	482	9	CG807733	CG807733 1118086D0	965	50.2	2.1	501	9	CG803873	CG803873 1118046E0
c 893	50.8	2.1	504	9	CG723258	CG723258 1119075E0	966	50.2	2.1	507	9	CNS006PU	AL065661 Drosophil
c 894	50.8	2.1	509	9	CG721196	CG721196 1119065H0	967	50.2	2.1	522	9	CNS00375	CG803757 1118045E1
c 895	50.8	2.1	523	9	CG731328	CG731328 1119139C0	c 968	50.2	2.1	519	9	CG729361	CG729361 1119111B1
c 896	50.8	2.1	550	9	CG803095	CG803095 1118038D0	c 969	50.2	2.1	592	9	CG727094	CG727094 1119093B0
c 897	50.8	2.1	593	9	CG807914	CG807914 1118087H1	c 970	50.2	2.1	601	9	CG717882	CG717882 1119050F0
c 898	50.8	2.1	609	8	CNS025K2	AL182171 Tetraodon	c 971	50.2	2.1	629	9	CB935757	CB935757 ta095f10.
c 899	50.8	2.1	627	8	BH724093	BH724093 BOHUS88TF	c 972	50.2	2.1	644	6	CB935758	CB935758 ta095f11.
c 900	50.8	2.1	714	8	BH981072	BH981072 oed66h10.	c 973	50.2	2.1	647	6	CB935758	CB935758 ta095f11.

974	50.2	2.1	719	6	CD835864	CD835864	BM45_046P	1047	49.8	2.1	991	9	CL139092	CL139092	ISB1-1110
975	50.2	2.1	770	8	AQ740708	AQ740708	HS_5507_A	1048	49.8	2.1	1101	9	CNS0042W	CNS0042W	AL055440 Drosophil
976	50.2	2.1	780	9	AG291100	AG291100	Mus muscu	C1049	49.8	2.1	1101	9	CNS0161T	CNS0161T	AL106896 Drosophil
977	50.2	2.1	793	9	AG591322	AG591322	Mus muscu	C1050	49.8	2.1	1152	9	CLA99024	CLA99024	CL499024 SAIL_662
978	50.2	2.1	836	9	CNS01100	CNS01100		1051	49.8	2.1	1201	9	CNS016E1	CNS016E1	AL106627 Drosophil
979	50.2	2.1	876	8	AZ677905	AZ677905	ENTKDS8TF	1052	49.8	2.1	1253	9	CL036722	CL036722	CH216-42D
980	50.2	2.1	889	9	AG362888	AG362888	Mus muscu	1053	49.8	2.1	1896	9	CG753083	CG753083	P048-1-CO
981	50.2	2.1	999	9	CNS06RCL	CL411787	T7 end of	1054	49.6	2.1	403	9	CG732151	CG732151	1119146D1
982	50.2	2.1	1001	9	CNS01400	AL103554	Drosophil	1055	49.6	2.1	522	9	CG730239	CG730239	1119124B0
983	50.2	2.1	1254	3	GR720510	CR720510	Tetraodon	C1056	49.6	2.1	560	5	BP179243	BP179243	BP179243
984	50.2	2.1	1294	9	AG448672	AG448672	Mus muscu	C1057	49.6	2.1	615	9	CG807731	CG807731	1118086D0
985	50.2	2.1	1313	7	CK997149	CK997149	ip15c02.b	1058	49.6	2.1	656	9	CG807672	CG807672	1118085H0
986	50.2	2.1	1616	3	CR734259	CR734259	Tetraodon	C1059	49.6	2.1	706	8	BH992021	BH992021	oen97g04.
987	50.2	2.1	1715	9	AG288305	AG288305	Mus muscu	C1060	49.6	2.1	718	7	CO720184	CO720184	ta10a11.
988	50.2	2.1	1896	3	CR722884	CR722884	Tetraodon	C1061	49.6	2.1	724	5	BP178533	BP178533	BP178533
989	50.2	2.1	416	9	CG730241	CG730241	1119123D0	1062	49.6	2.1	726	8	B18951	B18951	F611-SP6 IG
990	50.2	2.1	443	9	CG726802	CG726802	1119091F1	C1063	49.6	2.1	749	1	AV4000884	AV4000884	AV4000884
991	50.2	2.1	467	9	CG732152	CG732152	1119146D1	C1064	49.6	2.1	780	7	CK595444	CK595444	AGENCOURT
992	50.2	2.1	492	9	CG808373	CG808373	1118091G0	1065	49.6	2.1	837	9	AG480808	AG480808	Mus muscu
993	50.2	2.1	508	1	AU001161	AU001161		C1066	49.6	2.1	856	9	AG544460	AG544460	Mus muscu
994	50.2	2.1	521	1	AU001371	AU001371		1067	49.6	2.1	858	9	BX907266	BX907266	Leishmani
995	50.2	2.1	522	1	AV399582	AV399582	AV399582	C1068	49.6	2.1	867	8	AZ675186	AZ675186	ENTKU40TR
996	50.2	2.1	528	1	AU001040	AU001040		1069	49.6	2.1	945	9	CNS005W7	CNS005W7	AL062612 Drosophil
997	50.2	2.1	542	5	BP177610	BP177610		1070	49.6	2.1	1118	5	BX462896	BX462896	MX462896
998	50.2	2.1	549	5	BP178615	BP178615		1071	49.6	2.1	1233	9	AG278952	AG278952	Mus muscu
999	50.2	2.1	572	9	CG807807	CG807807	1118087B0	1072	49.6	2.1	1242	9	CL068807	CL068807	CH216-115
1000	50.2	2.1	591	9	CG807037	CG807037	1118076H0	1073	49.6	2.1	1364	9	CG757986	CG757986	P053-2-D0
1001	50.2	2.1	607	9	CG721216	CG721216	1119066A0	1074	49.6	2.1	1391	9	CG754863	CG754863	P050-2-G0
1002	50.2	2.1	628	1	AV404749	AV404749	AV404749	C1075	49.6	2.1	2201	9	AG310854	AG310854	Mus muscu
1003	50.2	2.1	639	9	CG721246	CG721246	1119066B0	1076	49.6	2.1	2736	9	AY402613	AY402613	Pan trogl
1004	50.2	2.1	647	1	AV399591	AV399591		1077	49.4	2.1	415	7	R21312	R21312	Y949G10.r1
1005	50.2	2.1	663	9	CG721115	CG721115	1119065E0	1078	49.4	2.1	462	1	AU087611	AU087611	AU087611
1006	50.2	2.1	682	8	BZ646791	BZ646791	OCGBS18TM	1079	49.4	2.1	463	9	CG805664	CG805664	1118061B0
1007	50.2	2.1	692	5	BP177891	BP177891		1080	49.4	2.1	552	9	CG732218	CG732218	1119146G0
1008	50.2	2.1	692	8	BH430772	BH430772	BOHTX76TF	C1081	49.4	2.1	556	9	CG800480	CG800480	1118013A0
1009	50.2	2.1	701	5	BP121539	BP121539		C1082	49.4	2.1	592	9	CG727098	CG727098	1119093B0
1010	50.2	2.1	704	5	BP177739	BP177739		1083	49.4	2.1	648	8	AZ527257	AZ527257	266PBD01
1011	50.2	2.1	723	3	BP178342	BP178342		C1084	49.4	2.1	656	8	BH809580	BH809580	Gm ISB001
1012	50.2	2.1	728	7	CO388065	CO388065	AGENCOURT	1085	49.4	2.1	727	5	BU384897	BU384897	603856373
1013	50.2	2.1	742	5	EX462820	EX462820	EX462820	C1086	49.4	2.1	802	8	BH681367	BH681367	BOMCI93TR
1014	50.2	2.1	759	5	BP121009	BP121009		C1087	49.4	2.1	872	5	BZ680887	BZ680887	ENTHU38TF
1015	50.2	2.1	770	1	AV399357	AV399357		C1088	49.4	2.1	917	5	BU515694	BU515694	AGENCOURT
1016	50.2	2.1	771	8	BZ438776	BZ438776	BONSBO8TR	1089	49.4	2.1	987	9	CNS014FQ	CNS014FQ	Tetraodon
1017	50.2	2.1	819	9	AG401866	AG401866	Mus muscu	C1090	49.4	2.1	994	9	CNS04NOJ	CNS04NOJ	Tetraodon
1018	50.2	2.1	849	1	AU005735	AU005735		1091	49.4	2.1	996	9	CNS00FUH	CNS00FUH	Drosophil
1019	50.2	2.1	908	7	CP257407	CP257407	pha010_g0	C1092	49.4	2.1	1032	9	CNS0201P	CNS0201P	Tetraodon
1020	50.2	2.1	935	8	B10881	B10881	F24HG-SP6.1	1093	49.4	2.1	1101	9	CNS00B01	CNS00B01	Drosophil
1021	50.2	2.1	988	9	CL087333	CL087333	ISB1-9A17	1094	49.4	2.1	1167	9	CNS07360	CNS07360	clone BA0
1022	50.2	2.1	997	6	CD049644	CD049644	AGENCOURT	1095	49.4	2.1	1272	8	CC264939	CC264939	CH261-19L
1023	50.2	2.1	1101	9	CNS00GDR	AL072060	Drosophil	1096	49.4	2.1	1352	9	CL648187	CL648187	CH213-166
1024	50.2	2.1	1101	9	CNS00YWL	AL096927	Drosophil	1097	49.2	2.1	471	9	CG732128	CG732128	1119146C0
1025	50.2	2.1	1205	9	CL509381	CL509381	SAIL_811	C1098	49.2	2.1	481	9	CG803819	CG803819	1118046B0
1026	50.2	2.1	1210	9	CG749728	CG749728	P044-1-CO	1099	49.2	2.1	489	9	CG727334	CG727334	1119094D0
1027	49.8	2.1	443	9	CG729064	CG729064	1119107C0	1100	49.2	2.1	505	9	CG730263	CG730263	1119123F0
1028	49.8	2.1	450	9	CG799178	CG799178	1118001B0	1101	49.2	2.1	507	9	CG721167	CG721167	1119065G0
1029	49.8	2.1	452	9	CG730252	CG730252	1119123E0	1102	49.2	2.1	509	9	CG721574	CG721574	1119068A0
1030	49.8	2.1	485	9	CG732429	CG732429	1119148D1	1103	49.2	2.1	521	9	CG807764	CG807764	1118086F1
1031	49.8	2.1	487	9	CG730305	CG730305	1119124B1	C1104	49.2	2.1	543	9	CG730256	CG730256	1119123E1
1032	49.8	2.1	498	9	CG721172	CG721172	1119065G0	C1105	49.2	2.1	549	9	CG807268	CG807268	1118080A0
1033	49.8	2.1	540	9	CG726775	CG726775	1119091E0	C1106	49.2	2.1	550	9	CG808239	CG808239	1118090F0
1034	49.8	2.1	558	9	CG806837	CG806837	1118074E0	C1107	49.2	2.1	559	9	CG807049	CG807049	1118077B0
1035	49.8	2.1	572	9	CG807807	CG807807	1118087B0	C1108	49.2	2.1	662	1	AV398694	AV398694	HVSMEC000
1036	49.8	2.1	576	9	CG807740	CG807740	1118086D0	C1109	49.2	2.1	762	4	BG309119	BG309119	AV398694
1037	49.8	2.1	582	5	BP229649	BP229649	BP229649	1110	49.2	2.1	768	8	BZ394392	BZ394392	EINBM19TR
1038	49.8	2.1	673	8	BH510309	BH510309	BOHJA93TF	1111	49.2	2.1	830	8	BH687659	BH687659	BOMMX94TR
1039	49.8	2.1	722	8	BH947077	BH947077	obv12e08.	C1112	49.2	2.1	907	1	AL553912	AL553912	AL553912
1040	49.8	2.1	786	9	CNS009A5	AL053317	Drosophil	1113	49.2	2.1	959	8	AZ540580	AZ540580	ENTDR43TR
1041	49.8	2.1	849	8	AZ539019	AZ539019	ENTDV05TF	C1114	49.2	2.1	965	9	CL505797	CL505797	SAIL_755
1042	49.8	2.1	914	9	CNS00ZJY	AL097768	Drosophil	C1115	49.2	2.1	999	9	CL038485	CL038485	CH216-46D
1043	49.8	2.1	952	9	CNS01016	AL098388	Drosophil	C1116	49.2	2.1	1101	9	CNS00HD9	CNS00HD9	Drosophil
1044	49.8	2.1	958	6	CB85091	CB85091	AGENCOURT	C1117	49.2	2.1	1101	9	CNS00Z82	CNS00Z82	AL073338
1045	49.8	2.1	964	9	CNS006N9	AL065781	Drosophil	1118	49.2	2.1	1101	9	CNS01525	CNS01525	Drosophil
1046	49.8	2.1	976	9	CNS04E5M	AL286627	Tetraodon	C1119	49.2	2.1	1277	8	CC253231	CC253231	CH261-180

c1120	49.2	2.1	1350	9	CL019486	CH216-5G1	1193	48.8	2.1	1206	9	CL027076	CH216-25A
c1121	49.2	2.1	1354	9	CG744717	P037-2-F0	1194	48.6	2.0	349	9	CG807125	1118078A0
c1122	49.2	2.1	1362	9	AG390999	Mus muscu	1195	48.6	2.0	409	9	CG731919	1119144E1
c1123	49	2.1	411	6	CB802631	AMGNNUC:M	1196	48.6	2.0	426	9	CG732171	1119146E0
c1124	49	2.1	415	9	CG726747	1119091D0	1197	48.6	2.0	445	9	CG721283	1119066C0
c1125	49	2.1	425	9	CG803718	1118045C0	1198	48.6	2.0	457	9	CG721709	1119068F0
c1126	49	2.1	420	9	CG727295	1119094B0	1199	48.6	2.0	468	9	CG732170	1119148E0
c1127	49	2.1	480	9	CG730265	1119123F1	1200	48.6	2.0	471	9	CG803897	1118046F0
c1128	49	2.1	507	9	CG731596	1119123F1	1201	48.6	2.0	475	9	CG807289	1118080C0
c1129	49	2.1	521	9	CG807764	1118086F1	1202	48.6	2.0	488	9	CG730332	1119124E0
c1130	49	2.1	551	9	CG803090	1118038D0	1203	48.6	2.0	499	9	CG807727	1118086C1
c1131	49	2.1	611	8	BH570603	BOGO079TR	1204	48.6	2.0	501	9	CG732556	1119149C1
c1132	49	2.1	613	9	CG721572	1119068A0	1205	48.6	2.0	503	9	CG727101	1119093B1
c1133	49	2.1	615	9	CG807731	1118086D0	1206	48.6	2.0	505	9	CG729349	1119111A0
c1134	49	2.1	624	9	CG721168	1119065G0	1207	48.6	2.0	507	9	CG731596	1119142B1
c1135	49	2.1	658	5	BH948212	1052a02.x	1208	48.6	2.0	530	9	CG803796	1118046A0
c1136	49	2.1	663	9	CG721115	1119065E0	1209	48.6	2.0	543	1	AU001085	AU001085
c1137	49	2.1	724	8	B2614777	1946e07.g	1210	48.6	2.0	553	9	CG806061	1118065A0
c1138	49	2.1	772	8	BH480795	BOHJM11TR	1211	48.6	2.0	563	9	CG807905	1118087H0
c1139	49	2.1	831	9	CNS002BX	AL097479	1212	48.6	2.0	675	8	BH969561	odh60H04.
c1140	49	2.1	897	9	CNS065QE	AL413580	1213	48.6	2.0	694	5	BP506178	BP506178
c1141	49	2.1	832	9	CNS07ABZ	AL436389	1214	48.6	2.0	736	1	AU001091	AU001091
c1142	49	2.1	938	9	CL479576	SAIL_308	1215	48.6	2.0	758	9	AG547036	Mus muscu
c1143	49	2.1	932	9	CNS011LO	AL100422	1216	48.6	2.0	793	9	CNS01GMC	AL143317
c1144	49	2.1	945	9	CL483400	SAIL_37b	1217	48.6	2.0	834	9	CNS008CK	Drosophi
c1145	49	2.1	961	9	CNS00N86	AL079258	1218	48.6	2.0	840	8	BH433039	BOHNF56TF
c1146	49	2.1	1002	9	CNS01LRP	AL100639	1219	48.6	2.0	842	8	AZ670364	ENTLN21TR
c1147	49	2.1	1010	6	CD171719	CD171719	1220	48.6	2.0	855	9	CNS04P5D	Tetraodon
c1148	49	2.1	1113	7	CF994845	CF994845	1221	48.6	2.0	865	8	AZ546251	ENTDU61TR
c1149	49	2.1	1152	4	BG309087	BG309087	1222	48.6	2.0	875	8	AZ533593	ENTCO47TF
c1150	49	2.1	1153	6	CD388959	CD388959	1223	48.6	2.0	893	5	BP507314	BP507314
c1151	49	2.1	1202	9	AG338379	AG338379	1224	48.6	2.0	919	8	AZ688396	ENTKN14TR
c1152	49	2.1	1320	9	CL103981	CL103981	1225	48.6	2.0	971	9	CNS05KU	Drosophi
c1153	49	2.1	1624	9	CL466243	CL466243	1226	48.6	2.0	991	9	CL516956	SAIL_98_C
c1154	49	2.1	1877	3	CR721531	CR721531	1227	48.6	2.0	976	9	CD248081	AGENCOURT
c1155	48.8	2.1	360	7	CN078773	CN078773	1228	48.6	2.0	991	6	CL516956	SAIL_98_C
c1156	48.8	2.1	404	9	CG713828	CG713828	1229	48.6	2.0	1017	9	CNS04URH	Tetraodon
c1157	48.8	2.1	450	9	CG799178	CG799178	1230	48.6	2.0	1101	9	CNS00240	Drosophi
c1158	48.8	2.1	462	1	AJ696357	AJ696357	1231	48.6	2.0	1101	9	CNS003B0	Drosophi
c1159	48.8	2.1	463	9	CG803217	CG803217	1232	48.6	2.0	1121	9	CL508918	SAIL_805
c1160	48.8	2.1	476	9	CG726749	CG726749	1233	48.6	2.0	1124	9	AG279040	Mus muscu
c1161	48.8	2.1	480	9	CG807661	CG807661	1234	48.6	2.0	1192	9	CNS03Y36	Tetraodon
c1162	48.8	2.1	568	9	CG803931	CG803931	1235	48.6	2.0	1205	9	CNS0165A	Drosophi
c1163	48.8	2.1	632	9	CG721033	CG721033	1236	48.6	2.0	1214	9	CL646783	CH213-123
c1164	48.8	2.1	643	4	BM159684	BM159684	1237	48.6	2.0	1242	8	BZ695766	SP_Ba006
c1165	48.8	2.1	643	4	BM160648	BM160648	1238	48.6	2.0	1263	9	AG396942	Mus muscu
c1166	48.8	2.1	646	9	CG807859	CG807859	1239	48.6	2.0	1364	9	CG757970	P053-2-C0
c1167	48.8	2.1	653	7	CN075506	CN075506	1240	48.6	2.0	1372	9	AG390627	Mus muscu
c1168	48.8	2.1	683	4	BM159163	BM159163	1241	48.6	2.0	1375	9	CL646465	CH213-116
c1169	48.8	2.1	694	9	CG807674	CG807674	1242	48.4	2.0	393	9	CG709658	1119014C0
c1170	48.8	2.1	697	8	BH989514	BH989514	1243	48.4	2.0	412	9	CG806747	1118073D1
c1171	48.8	2.1	699	8	BH929444	BH929444	1244	48.4	2.0	431	9	CG721541	1119067G1
c1172	48.8	2.1	700	4	BM170161	BM170161	1245	48.4	2.0	463	9	CG729377	111911D1
c1173	48.8	2.1	744	9	AG367833	AG367833	1246	48.4	2.0	470	6	CD979595	CD979595
c1174	48.8	2.1	784	8	BH446645	BH446645	1247	48.4	2.0	479	9	CG805662	1118061B0
c1175	48.8	2.1	790	1	AL664486	AL664486	1248	48.4	2.0	480	9	CG726949	1119092D0
c1176	48.8	2.1	800	9	CNS06PYX	AL409999	1249	48.4	2.0	508	9	CG801552	1118022D1
c1177	48.8	2.1	812	8	BH477956	BH477956	1250	48.4	2.0	519	9	CG802630	1118032F0
c1178	48.8	2.1	815	8	BZ037267	BZ037267	1251	48.4	2.0	548	1	AU001244	AU001244
c1179	48.8	2.1	872	7	CK022958	CK022958	1252	48.4	2.0	553	9	CG732166	1119145E0
c1180	48.8	2.1	872	7	CK022958	CK022958	1253	48.4	2.0	579	9	CG807571	1118085A0
c1181	48.8	2.1	886	8	AZ532704	AZ532704	1254	48.4	2.0	633	5	AU004482	AU004482
c1182	48.8	2.1	891	8	BH160327	BH160327	1255	48.4	2.0	643	1	BUS46971	BUS46971
c1183	48.8	2.1	910	9	AG526131	AG526131	1256	48.4	2.0	675	9	CG807781	1118086H0
c1184	48.8	2.1	913	9	CNS01XIW	AL171761	1257	48.4	2.0	697	9	CNS04707	Tetraodon
c1185	48.8	2.1	928	9	CNS0102F	AL098433	1258	48.4	2.0	705	8	BH461803	BH461803
c1186	48.8	2.1	949	6	CD387866	CD387866	1259	48.4	2.0	724	5	BP178072	BP178072
c1187	48.8	2.1	1042	9	CL461494	CL461494	1260	48.4	2.0	749	8	AQ361974	AQ361974
c1188	48.8	2.1	1101	9	CNS00ETW	AL069847	1261	48.4	2.0	755	9	BX150378	BX150378
c1189	48.8	2.1	1101	9	CNS00HDH	AL073338	1262	48.4	2.0	757	4	BJ130908	BJ130908
c1190	48.8	2.1	1101	9	CNS0100X	AL098379	1263	48.4	2.0	780	7	CK595444	CK595444
c1191	48.8	2.1	1131	9	CNS034FO	AL227373	1264	48.4	2.0	812	6	CA918125	CA918125
c1192	48.8	2.1	1201	9	CNS015Z2	AL106121	1265	48.4	2.0	852	8	AQ894184	AQ894184

c1266	48.4	2.0	870	9	CNS009XJ	AL054462 Drosophil	1339	48.2	2.0	943	8	AZ550749	AZ550749 ENTFO30TR
c1267	48.4	2.0	886	8	BH177277	BH177277 008 L 22-	1340	48.2	2.0	949	7	CV145129	CV145129 EST856338
c1268	48.4	2.0	886	9	CNS07JUX	AL1614235 T3 end of	1341	48.2	2.0	979	9	AL106190	AL106190 Drosophil
c1269	48.4	2.0	905	2	CNS00KHX	AL077798 Drosophil	1342	48.2	2.0	996	2	BF345477	BF345477 602019224
c1270	48.4	2.0	938	2	BF262686	BF262686 HW_CBA000	1343	48.2	2.0	1027	6	CD388470	CD388470 AGENCOURT
c1271	48.4	2.0	973	9	CNS07ILE	AL425064 clone BAO	1344	48.2	2.0	1056	9	CL492538	CL492538 SAIL_567
c1272	48.4	2.0	1011	9	CL062457	CL062457 CH216-98D	1345	48.2	2.0	1101	9	CNS000GM	AL052895 Drosophil
c1273	48.4	2.0	1014	9	CL077203	CL077203 CH216-143	1346	48.2	2.0	1184	9	CNS04P4P	AL300850 Tetraodon
c1274	48.4	2.0	1041	9	CNS015JD	AL105523 Drosophil	1347	48.2	2.0	1191	9	CL104745	CL104745 ISB1-4311
c1275	48.4	2.0	1041	6	CD387510	CD387510 AGENCOURT	1348	48.2	2.0	1214	9	CL646783	CL646783 CH213-123
c1276	48.4	2.0	1101	9	CNS003DQ	AL064580 Drosophil	1349	48.2	2.0	1221	3	CR720347	CR720347 Tetraodon
c1277	48.4	2.0	1101	9	CNS00L72	AL078714 Drosophil	1350	48.2	2.0	1315	3	CR657214	CR657214 Tetraodon
c1278	48.4	2.0	1137	5	BM917623	BM917623 AGENCOURT	1351	48.2	2.0	1456	9	CL490513	CL490513 SAIL_539
c1279	48.4	2.0	1206	8	BZ695529	BZ695529 SP_BA006	1352	48.2	2.0	1639	8	CC189230	CC189230 CH261-191
c1280	48.4	2.0	1315	3	CR657214	CR657214 Tetraodon	1353	48.2	2.0	2485	3	BC023209	BC023209 Homo sapi
c1281	48.4	2.0	1318	9	AG321035	AG321035 Mus muscu	1354	48.2	2.0	2736	9	AY402612	AY402612 Homo sapi
c1282	48.4	2.0	1348	9	AG397099	AG397099 Mus muscu	1355	48.2	2.0	2759	3	BC029313	BC029313 Homo sapi
c1283	48.4	2.0	1974	3	CR734974	CR734974 Tetraodon	1356	48.2	2.0	3270	3	BC035457	BC035457 Homo sapi
c1284	48.4	2.0	2108	9	AG390640	AG390640 Mus muscu	1357	48.2	2.0	3295	3	BC029348	BC029348 Homo sapi
c1285	48.4	2.0	328	5	BM930129	BM930129 UI-E-EJ1-	1358	48	2.0	442	9	CG803222	CG803222 1118040B1
c1286	48.2	2.0	383	9	CG709542	CG709542 1119013F0	1359	48	2.0	468	5	BU495211	BU495211 PfESToab8
c1287	48.2	2.0	423	2	BE466693	BE466693 h224C03.X	1360	48	2.0	477	9	CG806833	CG806833 1118074D1
c1288	48.2	2.0	432	9	CG726731	CG726731 1119091C1	1361	48	2.0	483	5	BU495226	BU495226 PfESToab7
c1289	48.2	2.0	437	9	CNS030FO	AL253269 Tetraodon	1362	48	2.0	509	9	CG721196	CG721196 1119065H0
c1290	48.2	2.0	452	9	CG729156	CG729156 1119108E1	1363	48	2.0	510	9	CG808131	CG808131 1118089G0
c1291	48.2	2.0	452	9	CG803919	CG803919 1118046G0	1364	48	2.0	534	4	B1815139	B1815139 PfESToaa1
c1292	48.2	2.0	452	9	CG808173	CG808173 1118090A0	1365	48	2.0	539	9	CG730250	CG730250 1119123E0
c1293	48.2	2.0	459	9	CG730232	CG730232 1119123C1	1366	48	2.0	585	9	CG807712	CG807712 1118086B0
c1294	48.2	2.0	461	9	CG730340	CG730340 1119124F1	1367	48	2.0	596	9	CG807614	CG807614 1118085D0
c1295	48.2	2.0	463	9	CG803217	CG803217 1118040B0	1368	48	2.0	642	5	BU069971	BU069971 1m1902.X
c1296	48.2	2.0	477	9	CG731889	CG731889 1119144C1	1369	48	2.0	657	9	CG803833	CG803833 1118046C0
c1297	48.2	2.0	482	9	CG732472	CG732472 1119148G0	1370	48	2.0	657	9	CG803833	CG803833 1118046C0
c1298	48.2	2.0	491	6	CB153314	CB153314 K-EST0210	1371	48	2.0	666	9	AG087640	AG087640 Pan tEogl
c1299	48.2	2.0	500	1	AU086684	AU086684 AU086684	1372	48	2.0	689	1	AV399763	AV399763 AV399763
c1300	48.2	2.0	500	1	AU087303	AU087303 AU087303	1373	48	2.0	707	4	EG770063	EG770063 602745189
c1301	48.2	2.0	507	9	CG807079	CG807079 1118077D1	1374	48	2.0	714	4	EG760615	EG760615 602717366
c1302	48.2	2.0	518	1	AV400576	AV400576 AV400576	1375	48	2.0	721	4	EG764304	EG764304 602736181
c1303	48.2	2.0	522	9	CG730299	CG730299 1119124B0	1376	48	2.0	725	8	BM162805	BM162805 EST95328
c1304	48.2	2.0	539	9	CG727303	CG727303 1119094B0	1377	48	2.0	734	4	BH487957	BH487957 BQCPK96TR
c1305	48.2	2.0	559	9	CG807049	CG807049 1118077B0	1378	48	2.0	734	9	CNS010MP	AL099163 Drosophil
c1306	48.2	2.0	560	9	CG712108	CG712108 1119024B0	1379	48	2.0	779	9	AG460770	AG460770 Mus muscu
c1307	48.2	2.0	561	2	BF527166	BF527166 602039844	1380	48	2.0	814	9	AG498052	AG498052 Mus muscu
c1308	48.2	2.0	579	9	CG807571	CG807571 1118085A0	1381	48	2.0	828	8	AQ739398	AQ739398 HS_5482_B
c1309	48.2	2.0	581	5	BP250869	BP250869 BP250869	1382	48	2.0	862	7	CNS96646	CNS96646 TTE000089
c1310	48.2	2.0	582	5	BP310145	BP310145 BP310145	1383	48	2.0	867	9	CNS00CX5	AL060052 Drosophil
c1311	48.2	2.0	582	5	BP310498	BP310498 BP310498	1384	48	2.0	868	7	CF379047	CF379047 AGENCOURT
c1312	48.2	2.0	584	5	BP217677	BP217677 BP217677	1385	48	2.0	900	9	CNS03M11	AL250174 Tetraodon
c1313	48.2	2.0	584	5	BP250707	BP250707 BP250707	1386	48	2.0	930	8	AZ541688	AZ541688 ENTEE13TR
c1314	48.2	2.0	596	9	CG807614	CG807614 1118085D0	1387	48	2.0	933	8	CC383628	CC383628 PUHQD40TD
c1315	48.2	2.0	619	5	BQ393883	BQ393883 NISC ng06	1388	48	2.0	939	7	CF935218	CF935218 TrEST-B24
c1316	48.2	2.0	620	8	BH570088	BH570088 BQGTJ80TF	1389	48	2.0	943	9	CL145947	CL145947 ISB1-1461
c1317	48.2	2.0	622	8	AQ273440	AQ273440 nbxb00301	1390	48	2.0	951	9	CL059856	CL059856 CH216-90N
c1318	48.2	2.0	696	2	BF529489	BF529489 602043246	1391	48	2.0	995	9	CNS92609	CNS92609 ZMMBBc053
c1319	48.2	2.0	697	2	BF528688	BF528688 602043443	1392	48	2.0	1029	9	CD387184	CD387184 AGENCOURT
c1320	48.2	2.0	720	6	CA447356	CA447356 UI-H-E10-	1393	48	2.0	1031	6	CNS07A2Y	AL436064 T3 end of
c1321	48.2	2.0	728	8	BH925975	BH925975 odh73e03.	1394	48	2.0	1063	9	CNS0107G	AL098614 Drosophil
c1322	48.2	2.0	738	2	BF346219	BF346219 602017695	1395	48	2.0	1069	9	CNS00YXK	AL096962 Drosophil
c1323	48.2	2.0	782	7	CV484987	CV484987 AGENCOURT	1396	48	2.0	1086	9	CNS012FZ	AL101513 Drosophil
c1324	48.2	2.0	785	4	EG911337	EG911337 602807633	1397	48	2.0	1094	9	CNS00DM8	AL076311 Drosophil
c1325	48.2	2.0	790	1	AV704163	AV704163 AV704163	1398	48	2.0	1099	9	CNS0042W	AL055440 Drosophil
c1326	48.2	2.0	800	8	AQ745095	AQ745095 HS_5501_A	1399	48	2.0	1101	9	CNS00F4X	AL1070042 Drosophil
c1327	48.2	2.0	807	9	CL1489403	CL1489403 SAIL_523	1400	48	2.0	1108	9	CNS026WQ	AL183563 Tetraodon
c1328	48.2	2.0	820	8	B11728	B11728 T8D18-Sp6.I	1401	48	2.0	1140	9	CL071552	CL071552 CH216-121
c1329	48.2	2.0	840	9	CNS010TW	AL099422 Drosophil	1402	48	2.0	1244	9	AG361248	AG361248 Mus muscu
c1330	48.2	2.0	841	2	BF528870	BF528870 602043330	1403	48	2.0	1295	9	CG757539	CG757539 P52-4-E0
c1331	48.2	2.0	875	2	BF531009	BF531009 602072338	1404	48	2.0	1489	9	AG350139	AG350139 Mus muscu
c1332	48.2	2.0	894	5	BX431647	BX431647 BX431647	1405	48	2.0	1564	9	AG382084	AG382084 Mus muscu
c1333	48.2	2.0	895	2	CNS06FSV	AL396821 T7 end of	1406	48	2.0	1780	9	AG320553	AG320553 Mus muscu
c1334	48.2	2.0	908	2	BF260452	BF260452 HVSMef002	1407	48	2.0	262	1	AA048249	AA048249 mi27b03.r
c1335	48.2	2.0	910	9	CNS01G8P	AL142826 Anopheles	1408	47.8	2.0	394	9	CG713792	CG713792 1119033D1
c1336	48.2	2.0	911	2	BF339458	BF339458 602039113	1409	47.8	2.0	396	8	AQ230058	AQ230058 HS_2025A
c1337	48.2	2.0	913	8	BH162280	BH162280 ENTDS60TR	1410	47.8	2.0	419	9	CG730365	CG730365 1119125B1
c1338	48.2	2.0	936	7	CV145318	CV145318 EST856527	1411	47.8	2.0	419	9	CG730365	CG730365 1119125B1

C1412	47.8	2.0	427	9	CG727350	CG727350	1119094D1	1485	47.6	2.0	1539	9	AG340947	AG340947 Mus_muscu
C1413	47.8	2.0	452	9	CG729156	CG729156	1119108E1	C1486	47.4	2.0	311	1	AI965701	AI965701 sc77c09.Y
C1414	47.8	2.0	461	6	BY551983	BY551983	1487	1487	47.4	2.0	413	9	CG727364	CG727364 1119094E0
C1415	47.8	2.0	466	9	CG807825	CG807825	1118087C0	1488	47.4	2.0	419	9	CG721562	CG721562 1119067H1
C1416	47.8	2.0	500	1	AU088260	AU088260	1489	1489	47.4	2.0	427	9	CG726966	CG726966 1119092E0
C1417	47.8	2.0	503	5	BU480294	BU480294	603844970	1490	47.4	2.0	452	9	CG727090	CG727090 1119093B0
C1418	47.8	2.0	503	5	CG804059	CG804059	1118047E1	C1491	47.4	2.0	453	9	CG730298	CG730298 111912480
C1419	47.8	2.0	552	9	CG724997	CG724997	1119083E0	C1492	47.4	2.0	454	9	CG804111	CG804111 11180047H0
C1420	47.8	2.0	620	8	BH068361	BH068361	RPCI-24-2	1493	47.4	2.0	464	9	CG732153	CG732153 1119146D1
C1421	47.8	2.0	661	9	CNS02QVJ	CNS02QVJ	1494	1494	47.4	2.0	468	9	CG806831	CG806831 1118074D0
C1422	47.8	2.0	702	5	BX841013	BX841013	1495	1495	47.4	2.0	475	9	CG807289	CG807289 1118080C0
C1423	47.8	2.0	759	8	BZ089333	BZ089333	1kx38e08	1496	47.4	2.0	476	9	CG727365	CG727365 1119094E0
C1424	47.8	2.0	773	9	BX236086	BX236086	Danio rer	C1497	47.4	2.0	488	9	CG731260	CG731260 1119138C0
C1425	47.8	2.0	776	8	BH711762	BH711762	BOMHG73TF	C1498	47.4	2.0	500	1	AU087594	AU087594 AU087594
C1426	47.8	2.0	810	9	CNS06G0D	CNS06G0D	1499	1499	47.4	2.0	540	5	BPI79089	BPI79089 BPI79089
C1427	47.8	2.0	821	1	AV758661	AV758661	1499	1499	47.4	2.0	544	9	BX128251	BX128251 Danio rer
C1428	47.8	2.0	834	8	AZ667977	AZ667977	1499	1499	47.4	2.0	544	9	BX128251	BX128251 Danio rer
C1429	47.8	2.0	843	7	CG389145	CG389145	1499	1499	47.4	2.0	544	9	BX128251	BX128251 Danio rer
C1430	47.8	2.0	854	9	CNS024OG	CNS024OG	1499	1499	47.4	2.0	544	9	BX128251	BX128251 Danio rer
C1431	47.8	2.0	886	8	BH153730	BH153730	1499	1499	47.4	2.0	544	9	BX128251	BX128251 Danio rer
C1432	47.8	2.0	891	5	BU484122	BU484122	603471770	1499	47.4	2.0	544	9	BX128251	BX128251 Danio rer
C1433	47.8	2.0	907	8	BH165866	BH165866	ENTTC13TF	1499	47.4	2.0	544	9	BX128251	BX128251 Danio rer
C1434	47.8	2.0	926	4	BM358145	BM358145	GA_Ea000	1499	47.4	2.0	544	9	BX128251	BX128251 Danio rer
C1435	47.8	2.0	928	7	CK406657	CK406657	AUF_Ea000	1499	47.4	2.0	544	9	BX128251	BX128251 Danio rer
C1436	47.8	2.0	1087	3	CR721616	CR721616	Tetraodon	1499	47.4	2.0	544	9	BX128251	BX128251 Danio rer
C1437	47.8	2.0	1101	9	CNS0039Q	CNS0039Q	1499	1499	47.4	2.0	544	9	BX128251	BX128251 Danio rer
C1438	47.8	2.0	1101	9	CNS00FVE	CNS00FVE	1499	1499	47.4	2.0	544	9	BX128251	BX128251 Danio rer
C1439	47.8	2.0	1101	9	CNS00KAE	CNS00KAE	1499	1499	47.4	2.0	544	9	BX128251	BX128251 Danio rer
C1440	47.8	2.0	1227	9	AG430010	AG430010	Mus muscu	1499	47.4	2.0	544	9	BX128251	BX128251 Danio rer
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C1442	47.8	2.0	1292	4	BM463105	BM463105	AGENCOURT	1499	47.4	2.0	544	9	BX128251	BX128251 Danio rer
C1443	47.8	2.0	1542	9	AG386981	AG386981	Mus muscu	1499	47.4	2.0	544	9	BX128251	BX128251 Danio rer
C1444	47.8	2.0	1837	9	AG381859	AG381859	Mus muscu	1499	47.4	2.0	544	9	BX128251	BX128251 Danio rer
C1445	47.6	2.0	300	6	C32453	C32453	Yuji	1499	47.6	2.0	300	6	C32453	Yuji
C1446	47.6	2.0	426	9	CG721421	CG721421	1499	1499	47.6	2.0	426	9	CG721421	1499
C1447	47.6	2.0	430	9	CG732195	CG732195	1499	1499	47.6	2.0	430	9	CG732195	1499
C1448	47.6	2.0	439	9	CG730281	CG730281	1499	1499	47.6	2.0	439	9	CG730281	1499
C1449	47.6	2.0	448	9	CG730282	CG730282	1499	1499	47.6	2.0	448	9	CG730282	1499
C1450	47.6	2.0	460	9	CG730210	CG730210	1499	1499	47.6	2.0	460	9	CG730210	1499
C1451	47.6	2.0	476	9	CG807890	CG807890	1499	1499	47.6	2.0	476	9	CG807890	1499
C1452	47.6	2.0	482	9	CG721052	CG721052	1499	1499	47.6	2.0	482	9	CG721052	1499
C1453	47.6	2.0	489	9	CG731039	CG731039	1499	1499	47.6	2.0	489	9	CG731039	1499
C1454	47.6	2.0	490	9	CG803859	CG803859	1499	1499	47.6	2.0	490	9	CG803859	1499
C1455	47.6	2.0	502	9	CG727077	CG727077	1499	1499	47.6	2.0	502	9	CG727077	1499
C1456	47.6	2.0	534	9	CG806296	CG806296	1499	1499	47.6	2.0	534	9	CG806296	1499
C1457	47.6	2.0	549	9	CG807268	CG807268	1499	1499	47.6	2.0	549	9	CG807268	1499
C1458	47.6	2.0	552	9	CG724997	CG724997	1499	1499	47.6	2.0	552	9	CG724997	1499
C1459	47.6	2.0	556	9	CG803777	CG803777	1499	1499	47.6	2.0	556	9	CG803777	1499
C1460	47.6	2.0	567	9	CG803178	CG803178	1499	1499	47.6	2.0	567	9	CG803178	1499
C1461	47.6	2.0	574	9	CG730254	CG730254	1499	1499	47.6	2.0	574	9	CG730254	1499
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C1468	47.6	2.0	740	7	BH513221	BH513221	1499	1499	47.6	2.0	740	7	BH513221	1499
C1469	47.6	2.0	770	7	CK478641	CK478641	1499	1499	47.6	2.0	770	7	CK478641	1499
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C1471	47.6	2.0	820	7	CG930994	CG930994	1499	1499	47.6	2.0	820	7	CG930994	1499
C1472	47.6	2.0	860	8	AZ682680	AZ682680	1499	1499	47.6	2.0	860	8	AZ682680	1499
C1473	47.6	2.0	866	7	CV482428	CV482428	1499	1499	47.6	2.0	866	7	CV482428	1499
C1474	47.6	2.0	882	8	BH167593	BH167593	1499	1499	47.6	2.0	882	8	BH167593	1499
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C1477	47.6	2.0	939	6	BY720774	BY720774	1499	1499	47.6	2.0	939	6	BY720774	1499
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C1481	47.6	2.0	1164	8	CC218891	CC218891	1499	1499	47.6	2.0	1164	8	CC218891	1499
C1482	47.6	2.0	1168	9	CL078758	CL078758	1499	1499	47.6	2.0	1168	9	CL078758	1499
C1483	47.6	2.0	1415	9	CL646438	CL646438	1499	1499	47.6	2.0	1415	9	CL646438	1499
C1484	47.6	2.0	1454	9	CL646440	CL646440	1499	1499	47.6	2.0	1454	9	CL646440	1499

1911 bp mRNA linear HTC 21-JUL-2004

full-length cDNA clone CSODI018YG12 of Placenta Cot 25-normalized

of Homo sapiens (human).

CR614790

CR614790.1 GI:50495597

HTC; CNSLUT cDNA.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Li, W.B., Gruber, C., Jesses, J., and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue

2 (bases 1 to 1911)

Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)

- Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers

1. .1911

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clones="CSODI018YG12"

/tissue="Placenta Cot 25-normalized"

/plasmid="pCMVSPORT\_6"

Query Match 80.1%; Score 1900; DB 3; Length 1911;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1900; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 12 AGCAGGAAATCCGGATGTCGTTATTAAGTGGACGAGTGGAGCTTCAACATA 71

Qy 61 GTTCCAGAACTCTCCATCCCGAGCTAGTATTATGAGCATCTGCCTTCATATCACCAGTGGC 120

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Db 72 GTTCCAGAACTCTCCATCCCGAGCTAGTATTATGAGCATCTGCCTTCATATCACCAGTGGC 131

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RESULT 2  
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of Homo sapiens (human).ACCESSION  
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HTC; CNSLT\_cDNA.SOURCE  
Homo sapiens (human)ORGANISM  
Homo sapiensREFERENCE  
1 (bases 1 to 1925)AUTHORS  
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.TITLE  
Full-length cDNA libraries and normalizationJOURNAL  
UnpublishedREMARK  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1925)REFERENCE  
2 (bases 1 to 1925)AUTHORS  
Genoscope.TITLE  
Direct SubmissionJOURNAL  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES Location/Qualifiers

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/organism="Homo sapiens"  
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/tissue\_type="Placenta Cot 25-normalized"  
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## ORIGIN

Query Match 79.9%; Score 1895; DB 3; Length 1925;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy |  
61 GTTCCAGAACTCTCCATCCGGACTAGTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120  
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91 GTTCCAGAACTCTCCATCCGGACTAGTATTGAGCATCTGCCTCTCATATCACCAGTGGC 150  
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121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGGCTG 180  
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1891 AGGAAATATCTTTTCAAGTAAACAAAAATAAAAA 1925



RESULT 3	CR605021	1945 bp	mRNA	linear	HTC 21-JUL-2004
LOCUS	CR605021	full-length cDNA clone CS0DI029YM23 of Placenta Cot 25-normalized			
DEFINITION	CR605021	of Homo sapiens (human)			
ACCESSION	CR605021	GI:50485828			
VERSION	CR605021.1	CS0DI029YM23			
KEYWORDS	HTC; CNSLUT_CDNA				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1945)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paraday Avenue				
REFERENCE	2 (bases 1 to 1945)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.				
FEATURES	Location/Qualifiers				
source	1..1945				
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	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="CS0DI029YM23"				
	/tissue_type="Placenta Cot 25-normalized"				
	/plasmid="pCMVSPORT_6"				
ORIGIN					
Query Match	79.4%;	Score 1883;	DB 3;	Length 1945;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 1883;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	AGCAGGAAATCCGGATGTCCTCGTTATCAAGTGGAGCAGTGAGTGTCAGGCTCAACATA	60		
Db	63	AGCAGGAAATCCGGATGTCCTCGTTATCAAGTGGAGCAGTGAGTGTCAGGCTCAACATA	122		
Qy	61	GTTCAGAACTCCATCCGAGTGTATTTAGCAGATGCTCTCATATCACCAGTGGC	120		
Db	123	GTTCAGAACTCCATCCGAGTGTATTTAGCAGATGCTCTCATATCACCAGTGGC	182		
Qy	121	CATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGCAGATGGCCAGGTGCTTCAGCCTG	180		
Db	183	CATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGCAGATGGCCAGGTGCTTCAGCCTG	242		
Qy	181	GTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCTCGTCCAAAGGCTCTTTGGCTGCA	240		
Db	243	GTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCTCGTCCAAAGGCTCTTTGGCTGCA	302		
Qy	241	GAGAGCTTTCCATTCAGGTGTATTCAGAAATTATGGGGATCACCTTTGTAGCAAAAAG	300		
Db	303	GAGAGCTTTCCATTCAGGTGTATTCAGAAATTATGGGGATCACCTTTGTAGCAAAAAG	362		
Qy	301	CGCAACAGCAGCTGAATTTACAGAGCTTAAGGAGGCTGTAGGCTCTGGGACTAAGT	360		
Db	363	CGCAACAGCAGCTGAATTTACAGAGCTTAAGGAGGCTGTAGGCTCTGGGACTAAGT	422		
Qy	361	TTGGCGGCAAGGACCAAGTTGAAAACAGCCTTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420		
Db	423	TTGGCGGCAAGGACCAAGTTGAAAACAGCCTTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	482		



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QY 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
Db 1563 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1622
QY 1561 GCTCTGAAGAGAAACAGTATCCACCTGACATGTCTCTTGAGCCCGGTAAAGCAAA 1620
Db 1623 GCTCTGAAGAGAAACAGTATCCACCTGACATGTCTCTTGAGCCCGGTAAAGCAAA 1682
QY 1621 AGAATGGCAGAAAAGTTTGGCCCTGAAAGCCATGGAGATTCCTATACTTTGAGACCTAA 1680
Db 1683 AGAATGGCAGAAAAGTTTGGCCCTGAAAGCCATGGAGATTCCTATACTTTGAGACCTAA 1742
QY 1681 TCTCTGTAAGCTAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA 1740
Db 1743 TCTCTGTAAGCTAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA 1802
QY 1741 GCAGGGACTGTAAACACAGACAGGCTCAAAAGTGTCTCTGTAACACATTGAGTTGGAAT 1800
Db 1803 GCAGGGACTGTAAACACAGACAGGCTCAAAAGTGTCTCTGTAACACATTGAGTTGGAAT 1862
QY 1801 CACTGTTTAGAACACACACTTACTTTTCTGCTCTCTACCACTGCTGATATTTCTCT 1860
Db 1863 CACTGTTTAGAACACACACTTACTTTTCTGCTCTCTACCACTGCTGATATTTCTCT 1922
QY 1861 AGGAATATATCTTTTACAAGTAA 1883
Db 1923 AGGAATATATCTTTTACAAGTAA 1945

RESULT 4
CR597409
LOCUS CR597409 1898 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSODI067Yg15 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR597409
VERSION CR597409.1 GI:50478216
KEYWORDS HTC; CNSLT_CDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li W.B., Gruber,C., Jessee,J. and Polayes,D.
JOURNAL Full-length cDNA libraries and normalization
REMARK Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1898)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CSODI067Yg15"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 78.8%; Score 1868; DB 3; Length 1898;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1171 TGAGGAGACACCTGAGGCTGTTTCTTTCATGCTCCCTTACCTGCCAGCTGGGAA 1230  
Qy 1201 ATCAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCCTAACTGGAATCAGC 1260  
Db 1231 ATCAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCCTAACTGGAATCAGC 1290  
Qy 1261 TCAGGACTGCCATTGGACTATGAGTGCACCAAGAGAAATGCCCTTCTCTTATTGTAAC 1320  
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Qy 1321 CTTGCTGGATCTATCTCTCTACCTCCAAAGCTTCCACGGCTCTTACGCTGGCTAT 1380  
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Qy 1381 GTCCTAATATATCCCACTGGGAGAAAGGATTTTGCAAAGTGCAGGACCTAAACATC 1440  
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Qy 1441 TCATCAGTATCCAGTGGTAAAAAGGCTCTCTGCTGTCTGAGGCTAGGTGGTTGAAAGC 1500  
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Db 1531 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1590  
Qy 1561 GCTCTGAAGAGAAACACGCTATCCCACTGACATGCTCTCTGAGCCCGTAAAGCAAA 1620  
Db 1591 GCTCTGAAGAGAAACACGCTATCCCACTGACATGCTCTCTGAGCCCGTAAAGCAAA 1650  
Qy 1621 AGAATGGCAGAAAAGTTTACGCCCTGAAAGCCATGGAGATTTCTATAACTTGAGACCTAA 1680  
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Qy 1681 TCTCTGTAAGCTAAATAAAGAAATAGACACAGGCTGAGGATACACAGTACACTGTCA 1740  
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Qy 1801 CACTGTTTGAACACACACTTACTTTTCTGCTCTCTACCACTGCTGATATTTCTCT 1860  
Db 1831 CACTGTTTGAACACACACTTACTTTTCTGCTCTCTACCACTGCTGATATTTCTCT 1890  
Qy 1861 AGGAATA 1868  
Db 1891 AGGAATA 1898

RESULT 5  
LOCUS CR612000  
DEFINITION Full-length cDNA clone CS0D1069YN02 of Placenta Cot 25-normalized of Homo sapiens (human).  
ACCESSION CR612000  
VERSION CR612000.1 GI:50492807  
KEYWORDS HTC; CNSLT\_cDNA.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1820)  
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact : Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ InvitroGen Corporation 1600  
Paraday Avenue  
2 (bases 1 to 1820)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0D1069YN02"  
/tissue type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"  
ORIGIN  
Query Match 76.7%; Score 1820; DB 3; Length 1820;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1820; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGCCCA 60  
Qy 123 TCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCAGCATGGCCAGGTGCTTCAGCCTGGT 182  
Db 61 TCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCAGCATGGCCAGGTGCTTCAGCCTGGT 120  
Qy 183 GTTGCTTCTCACTTCCATCTGGACACGAGGCTCTTGCTTCAAGGCTCTTTTGGCTGCAGA 242  
Db 121 GTTGCTTCTCACTTCCATCTGGACACGAGGCTCTTGCTTCAAGGCTCTTTTGGCTGCAGA 180  
Qy 243 AGAGCTTTCCATCCAGGTGTCATGCAAGATTTATGGGGATCACCTTGTGAGCAAAAAGGC 302  
Db 181 AGAGCTTTCCATCCAGGTGTCATGCAAGATTTATGGGGATCACCTTGTGAGCAAAAAGGC 240  
Qy 303 GAACACAGCAGCTGAATTTTACAGAACTAAGAGGCTCTGTAGGCTGCTGGGACTAAGTTT 362  
Db 241 GAACACAGCAGCTGAATTTTACAGAACTAAGAGGCTCTGTAGGCTGCTGGGACTAAGTTT 300  
Qy 363 GGCCTGCAAGGACCAAGTTTGAACAGCTTGAAGCTAGCTTTGAAACTTTGCAGCTATGG 422  
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Qy 423 CTGGGTTGGAGATGGATTCTGTGTCATCTTAGGATTAGCCCAAAACCCCAAGTGTGGAA 482  
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Qy 483 AAATGGGTGGGTGTCCTGATTTTGAAGGTTCCAGTGAGCCGACAGTTTGTGAGTACAGTAC 542  
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Qy 723 AGTTCCTACTTCTATTCCACGGGAGAAAAATTTGATTGTCTCACAGAAATTTTATGGA 782

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Qy 843 TGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGTGCTCTCTCTCTCTT 902
Db 781 TGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGTGCTCTCTCTCTCTT 840
Qy 903 TGGTCTGCAGCTGTCTTGGATTTTGTCTGTCAAAAGAGTATGTGAAGGCTTCCCTTT 962
Db 841 TGGTCTGCAGCTGTCTTGGATTTTGTCTGTCAAAAGAGTATGTGAAGGCTTCCCTTT 900
Qy 963 TACAAAACAAGATCAGCAGAGAGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAGAGGC 1022
Db 901 TACAAAACAAGATCAGCAGAGAGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAGAGGC 960
Qy 1023 CAATGATAGCAACCTTAATAGGAATCAAGAAACCTGATAAAACCCAGAGAGTCCAA 1082
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Db 1261 TGTCTGATCTATCTCTCTACCTCCAAAGCTTCCACGGCTTTCTAGCTGGCTATGT 1320
Qy 1383 CCTAATAATATCCCACTGGGAGAAAGGTTTTTGCNAAGTGCAGGACCTTAACATCTC 1442
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Db 1441 AGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTTCCGACGCTCAGACCCCTTCTTCAGC 1500
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Db 1501 TCTGAAGAGAAACACGTATCCCACTGACATGTCTTCTGAGCCGGTAAGACCAAAAG 1560
Qy 1623 AATGCGAAGAGTTTACGCCCTGAAAGCCATGAGATTTCTCATAACTTGAGACCTTAATC 1682
Db 1561 AATGCGAAGAGTTTACGCCCTGAAAGCCATGAGATTTCTCATAACTTGAGACCTTAATC 1620
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Qy 1803 CTGTTTAGAACACACACACTTACTTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCTAG 1862
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Db 1801 GAAATATACCTTTTACAAGTA 1820

RESULT 6
CR604450 1797 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSODI065YD17 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR604450
VERSION CR604450.1 GI:50495257
KEYWORDS HTC; CNSLT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1797)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1797)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
and enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
source
1. 1797
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI065YD17"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 75.8% Score 1797; DB 3; Length 1797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 GAACCTCTCCATCCGGACTAGTTATTGAGCATCTGSCCTCTCATATCACCAGTGGCATCTG 126
Db 1 GAACCTCTCCATCCGGACTAGTTATTGAGCATCTGSCCTCTCATATCACCAGTGGCATCTG 60

Qy 127 AGGTGTTTCCCTGCTCTGAAGGGGTAGGCACGATGCCAGGTCTTCAGGCTGGTGTG 186
Db 61 AGGTGTTTCCCTGCTCTGAAGGGGTAGGCACGATGCCAGGTCTTCAGGCTGGTGTG 120

Qy 187 CTTCTCACTTCCATCTCGACCCAGAGGCTCTCTGCTCCAAGGCTCTTTGCGTGCAAGAGAG 246
Db 121 CTTCTCACTTCCATCTCGACCCAGAGGCTCTCTGCTCCAAGGCTCTTTGCGTGCAAGAGAG 180

Qy 247 CTTTCCATCCAGGTGTTCATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAGCGCAAC 306
Db 181 CTTTCCATCCAGGTGTTCATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAGCGCAAC 240

Qy 307 CAGCAGCTGAATTTACAGAAAGCTAAGGAGCCCTGTAGGCTGCTGGGACTAAGTTTGCC 366
Db 241 CAGCAGCTGAATTTACAGAAAGCTAAGGAGCCCTGTAGGCTGCTGGGACTAAGTTTGCC 300

Qy 367 GGCAAGGACCAAGTTGAAACAGAGCTTGAAGAGTAGCTTTGAAACTTCAGCATATGGCTGG 426
Db 301 GGCAAGGACCAAGTTGAAACAGAGCTTGAAGAGTAGCTTTGAAACTTCAGCATATGGCTGG 360
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Db 421 GGGGTGGGTGTCCTGATTTTGGAAAGGTTCCAGTGAGCCGACAGATTTGCGAGCTATTGTTAC 480
QY 547 AACTCATCTGATCTATCTGGACTAATCTGTGATTCAGAAATTTATCACCACCAAGATCCC 606
Db 481 AACTCATCTGATCTATCTGGACTAATCTGTGATTCAGAAATTTATCACCACCAAGATCCC 540
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Db 541 ATATTCAACTCAAACTGCAACCAAAACAACAGAAATTTATTGTGTCAGTGACAGTACTAC 600
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Db 601 TCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTCTCTCTGCTCCAGCT 660
QY 727 TCCACTTCTATTCCACGGAGAAAAAATTTGATTGTGTACAGAAATTTTATGGAAGT 786
Db 661 TCCACTTCTATTCCACGGAGAAAAAATTTGATTGTGTACAGAAATTTTATGGAAGT 720
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Db 721 AGACCAATGTCTACAGAAACTGAACCAATTTGTTGAAAAATAAAGCAGCATTTCAAGAAATGAA 780
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QY 907 GCTGCAGCTGGTCTTGGAATTTGCTATGTCTAAAGGTATGTGAAGGCTTCCCTTTTACA 966
Db 841 GCTGCAGCTGGTCTTGGAATTTGCTATGTCTAAAGGTATGTGAAGGCTTCCCTTTTACA 900
QY 967 AACAAAGATCAGCAGAGGAAATGATCAACCAACCAAGTGTAAAGGAGGAGAGGCCAAT 1026
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QY 1027 GATAGCAACCTAATAGGAAATCAAGAAAACTGATAAAAACCCAGAAAGTCCAAGAGT 1086
Db 961 GATAGCAACCTAATAGGAAATCAAGAAAACTGATAAAAACCCAGAAAGTCCAAGAGT 1020
QY 1087 CCAGCAAAACTACCGTGCATGCTGGAAGCTGAACTTTAGATGACAGAAATGAGGA 1146
Db 1021 CCAGCAAAACTACCGTGCATGCTGGAAGCTGAACTTTAGATGACAGAAATGAGGA 1080
QY 1147 GACACACTGAGGCTGGTTTCTTTCATGCTCTTTACCTGCCAGCTGGGGAATCAAA 1206
Db 1081 GACACACTGAGGCTGGTTTCTTTCATGCTCTTTACCTGCCAGCTGGGGAATCAAA 1140
QY 1207 AGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCTTAATCGAATCAGCTCAGGA 1266
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QY 1267 CTGCCATTGACATATGAGTGCACCAAGAAATGCCCTTCTCTCTTATTGTAACCCGTGC 1326
Db 1201 CTGCCATTGACATATGAGTGCACCAAGAAATGCCCTTCTCTCTTATTGTAACCCGTGC 1260
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Db 1261 TGGATCTCTATCTCTTACCTTCCAAAGCTTCCACGGCTTCTAGCCTGGCTATGTCCTA 1320
QY 1387 ATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTCCAAAGGACCTAAAAATCTCATCA 1446
Db 1321 ATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTCCAAAGGACCTAAAAATCTCATCA 1380
QY 1447 GTATCCAGTGGTAAAAAGGCTCTCTGCTGCTGAGGCTAGGTGGTTGAAAGCCAGGA 1506
Db 1381 GTATCCAGTGGTAAAAAGGCTCTCTGCTGCTGAGGCTAGGTGGTTGAAAGCCAGGA 1440
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QY 1507 GTCACTGAGACCAAGGCTTTCTCTACTGATTCCGAGCTCAGACCCCTTTTTCAGTCTGT 1566
Db 1441 GTCACTGAGACCAAGGCTTTCTCTACTGATTCCGAGCTCAGACCCCTTTTTCAGTCTGT 1500
QY 1567 AAAGAGAAACACGATATCCCACTTGACATGTCTCTGAGCCCGGTAAAGACAAAGAAATG 1626
Db 1501 AAAGAGAAACACGATATCCCACTTGACATGTCTCTGAGCCCGGTAAAGACAAAGAAATG 1560
QY 1627 GCAGAAAAGTTTAGCCCTCAAGAGCCATGGAGATTCTATAACTTGAGACCTAATCTCTG 1686
Db 1561 GCAGAAAAGTTTAGCCCTCAAGAGCCATGGAGATTCTATAACTTGAGACCTAATCTCTG 1620
QY 1687 TAAAGCTAAAAATAAAGAAATAGAACCAAGGCTGAGGATACACAGTACACTGTGAGCAGGG 1746
Db 1621 TAAAGCTAAAAATAAAGAAATAGAACCAAGGCTGAGGATACACAGTACACTGTGAGCAGGG 1680
QY 1747 ACTGTAAACACACAGACAGGGTCAAAGTGTCTCTGAAACACATGAGTTGGAATCACTGT 1806
Db 1681 ACTGTAAACACACAGACAGGGTCAAAGTGTCTCTGAAACACATGAGTTGGAATCACTGT 1740
QY 1807 TTAGAAAACACACACTTACTTTTTCTGGTCTCTACCACCTGCTGATATTTTCTCTAGG 1863
Db 1741 TTAGAAAACACACACTTACTTTTTCTGGTCTCTACCACCTGCTGATATTTTCTCTAGG 1797

RESULT 7
CR614245
LOCUS CR614245 1786 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSOD1029J09 of Placentia Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR614245
VERSION CR614245.1 GI:50495052
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1786)
AUTHORS Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
Genoscope 2 (bases 1 to 1786)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source 1..1786
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1029J09"
/tissue_type="Placentia Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 75.3%; Score 1786; DB 3; Length 1786;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 TCTGCTCTCATATCACCAGTGGCCATCTGAGGTGTTTCCCTCGCTCTGAAGGGTAGGC 156
Db 1 TCTGCTCTCATATCACCAGTGGCCATCTGAGGTGTTTCCCTCGCTCTGAAGGGTAGGC 60
```

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QY 157 ACGATGGCCAGGTGCTTCAGCGCTGGTGTGCTTCTCACTTCATCTGCACACGAGGCTC 216
Db 61 ACGATGGCCAGGTGCTTCAGCGCTGGTGTGCTTCTCACTTCATCTGCACACGAGGCTC 120
QY 217 CTGGTCCAGGCTCTTTGGCGTGCAGAGAGCTTTCCATCCAGGTGTCTATGAGAAATATG 276
Db 121 CTGGTCCAGGCTCTTTGGCGTGCAGAGAGCTTTCCATCCAGGTGTCTATGAGAAATATG 180
QY 277 GGGATCACCCCTTGTGAGCAAAAGCGGAAACGAGCAGCTGAAATTTACAGAGAGCTTAAGGAG 336
Db 181 GGGATCACCCCTTGTGAGCAAAAGCGGAAACGAGCAGCTGAAATTTACAGAGAGCTTAAGGAG 240
QY 337 GCCTGTAGCTGCTGGGACTAAGTTTGGCGCGCAGGACCAAGTTGAAACAGCCTTGAA 396
Db 241 GCCTGTAGCTGCTGGGACTAAGTTTGGCGCGCAGGACCAAGTTGAAACAGCCTTGAA 300
QY 397 GCTAGCTTTGAAACTTGCAGCTATAGCTTGGGTGGAGATGGATTCGTGCTCATCTCTAGG 456
Db 301 GCTAGCTTTGAAACTTGCAGCTATAGCTTGGGTGGAGATGGATTCGTGCTCATCTCTAGG 360
QY 457 ATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTGATTTGGAAAGTTCCA 516
Db 361 ATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTGATTTGGAAAGTTCCA 420
QY 517 GTGAGCCGACAGTTTGCAGCCTATTGTTTACAACCTCATCTGATCTTGAACCTAATCTGTC 576
Db 421 GTGAGCCGACAGTTTGCAGCCTATTGTTTACAACCTCATCTGATCTTGAACCTAATCTGTC 480
QY 577 ATTCCAGAAATTTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAACA 636
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Db 541 ACAGAAATTTATGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCT 600
QY 697 GCGCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 756
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QY 817 GTTGAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGCT 876
Db 721 GTTGAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGCT 780
QY 877 CTGCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 936
Db 781 CTGCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
QY 937 AAAAGGTATGTGAAGGCTCTCCCTTTTACAACAGAAATCAGCAAGAAATGATCGAA 996
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QY 997 ACCAAAGTAGTAAAGGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAA 1056
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QY 1057 ACTGATAAAACCCGAGAGAGTCCAGAGTCCAGAGTCCAGCAAACTACCGTGGATGCTGGAA 1116
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QY 1117 GCTGAAGTTTATGAGACAGAAATGAGGAGACACACCTGAGGCTGTTCTTTCATGCT 1176
Db 1021 GCTGAAGTTTATGAGACAGAAATGAGGAGACACACCTGAGGCTGTTCTTTCATGCT 1080
QY 1177 CTTTACCCTGCCCAGCTGGGGAATCAAAAGGCGCAAAAGAACCAAGAAAGTCCAC 1236
Db 1081 CTTTACCCTGCCCAGCTGGGGAATCAAAAGGCGCAAAAGAACCAAGAAAGTCCAC 1140
QY 1237 CTTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTTGGAGTGGACCAACAAGA 1296
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Db 1141 CCTTGGTTCCTAACTGGAATCAGCTCAGGACTGCAATTTGGACTATGGAGTGCACCAAGA 1200
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Db 1201 GAATGCCCTTCTCCTTATTTGTAACCTGTCTGGATTCCTATCTCCTCTCAAGCTTC 1260
QY 1357 CCAGGGCTTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTG 1416
Db 1261 CCAGGGCTTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTG 1320
QY 1417 CAAGTCAAGGACCTAAACATCTCATCAGTATCCAGTGTGTAAGAGCCCTCTGGCTG 1476
Db 1321 CAAGTCAAGGACCTAAACATCTCATCAGTATCCAGTGTGTAAGAGCCCTCTGGCTG 1380
QY 1477 TCTGAGCTAGTGGGTGTAAGGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGAT 1536
Db 1381 TCTGAGCTAGTGGGTGTAAGGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGAT 1440
QY 1537 TCCGAGCTCAGACCCCTTTCTTCTGAGCTCTGAAAGAGAAACAGTATCCCACTGACATGT 1596
Db 1441 TCCGAGCTCAGACCCCTTTCTTCTGAGCTCTGAAAGAGAAACAGTATCCCACTGACATGT 1500
QY 1597 CCTTCTGAGCCCGTAAAGAGCAAAAGATGCGCAAAAGTTTAGCCCTGAAAGCCATGG 1656
Db 1501 CCTTCTGAGCCCGTAAAGAGCAAAAGATGCGCAAAAGTTTAGCCCTGAAAGCCATGG 1560
QY 1657 AGATTCTCATAACTTGAGACCTTAATCTCTGTGTAAGCTTAAATAAAGAAATAGAACAGGC 1716
Db 1561 AGATTCTCATAACTTGAGACCTTAATCTCTGTGTAAGCTTAAATAAAGAAATAGAACAGGC 1620
QY 1717 TGAGGATACGACATGACACTGTCTGAGCGGACTCTAAACACAGACAGGGTCAAGTGTGT 1776
Db 1621 TGAGGATACGACATGACACTGTCTGAGCGGACTCTAAACACAGACAGGGTCAAGTGTGT 1680
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Db 1681 TCTCTGAACATTTGAGTGGAACTGGAATCAGTGTGTAAGACACACACTTACTTTCTGTGTC 1740
QY 1837 TCTACCACTGCTGATATTTCTCTAGGAAATATATCTTTTACAAGTA 1882
Db 1741 TCTACCACTGCTGATATTTCTCTAGGAAATATATCTTTTACAAGTA 1786
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RESULT 8
CR598862 1781 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSODI039YJ06 of Placentia Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR598862
VERSION CR598862.1 GI:50479669
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1781)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life technologies, a
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1765)  
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Paraday Avenue  
Foster City, CA 94024  
2 (bases 1 to 1765)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
Location/Qualifiers  
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/clone="CS001079YK19"  
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Query Match 74.4%; Score 1765; DB 3; Length 1765;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 581 CAGAAATTTATCACCAACCAAGATCCATATTCACACCTCAAACTGCAACACCAACAG 640  
DB 1 CAGAAATTTATCACCAACCAAGATCCATATTCACACCTCAAACTGCAACACCAACAG 60  
QY 641 AATTTATTTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 700  
DB 61 AATTTATTTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 120  
QY 701 CTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 760  
DB 121 CTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180  
QY 761 GTGTCACAGAAAGTTTATGGAACCTAGCACCATGCTACAGAACTCAACCATTTGTTG 820  
DB 181 GTGTCACAGAAAGTTTATGGAACCTAGCACCATGCTACAGAACTCAACCATTTGTTG 240  
QY 821 AAAATAAAGCAGCATTCAGAAATGAAGCTGTGGGTTTGGAGGTGTCCTCCACGGCTCTGC 880  
DB 241 AAAATAAAGCAGCATTCAGAAATGAAGCTGTGGGTTTGGAGGTGTCCTCCACGGCTCTGC 300  
QY 881 TAGTGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 940  
DB 301 TAGTGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360  
QY 941 GGTATGTGAAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1000  
DB 361 GGTATGTGAAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
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QY 1061 ATAAAAAACCAGAGGTCAGAGTCCAGCAAACTACCGTGGATGCTGGAGCTG 1120  
DB 481 ATAAAAAACCAGAGGTCAGAGTCCAGCAAACTACCGTGGATGCTGGAGCTG 540  
QY 1121 AAGTTTATGATGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTTTCATGCTCCTT 1180  
DB 541 AAGTTTATGATGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTTTCATGCTCCTT 600

QY 1181 ACCCTGCCAGCTGGGGAAATCAAAAGGGCCAAAGAACCAAGAGAGAAAGTCCACCTT 1240  
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DB 661 GGTTCCTTAACCTGGAATCAGCTCAGGACTGCCATTGGGATATGGAGTGCCACCAAGAGAAAT 720  
QY 1301 GCCCTTCTCCTTATTTGTAACCTCTCTGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1360  
DB 721 GCCCTTCTCCTTATTTGTAACCTCTCTGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780  
QY 1361 GGCTTTCTAGCTGGCTATGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1420  
DB 781 GGCTTTCTAGCTGGCTATGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840  
QY 1421 GTCAAGGACCTAAACATCTCATCAGTATCCAGTGTGTAAGAGGCTCTCTGGCTGTCTG 1480  
DB 841 GTCAAGGACCTAAACATCTCATCAGTATCCAGTGTGTAAGAGGCTCTCTGGCTGTCTG 900  
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DB 901 AGGCTAGTGGGTTGAAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATCCG 960  
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QY 1601 CTGAGCCGGTAAAGCAAAAGATGCGAGAAAAGTTTAGCCCTGAAAGCCATGGAGAT 1660  
DB 1021 CTGAGCCGGTAAAGCAAAAGATGCGAGAAAAGTTTAGCCCTGAAAGCCATGGAGAT 1080  
QY 1661 TCTCATAACTTGAGACCTTAATCTCTGTAAGCTAAAAATAAGAAATAGAACAAAGCTGAG 1720  
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QY 1721 GATACGACGTACACTGTGACGAGGACTGTAAACACAGACAGGCTCAAGTGTCTCTC 1780  
DB 1141 GATACGACGTACACTGTGACGAGGACTGTAAACACAGACAGGCTCAAGTGTCTCTC 1200  
QY 1781 TGAACACATTTGAGTTGGAATCAGTGTGTAAGACACACACTTACTTTCTGCTCTCTA 1840  
DB 1201 TGAACACATTTGAGTTGGAATCAGTGTGTAAGACACACACTTACTTTCTGCTCTCTA 1260  
QY 1841 CCACTGCTGATATTTCTCTAGGAAATATATCTTTTACAAGTAAACAAATATAAACTCTT 1900  
DB 1261 CCACTGCTGATATTTCTCTAGGAAATATATCTTTTACAAGTAAACAAATATAAACTCTT 1320  
QY 1901 ATAAATTTCTATTTTATCTGAGTTACAGAAATGATTAAGGAGAAATTAAGTCAAGTAAAT 1960  
DB 1321 ATAAATTTCTATTTTATCTGAGTTACAGAAATGATTAAGGAGAAATTAAGTCAAGTAAAT 1380  
QY 1961 TTGTTTAAAAGTAAATAAAATTCACAAACATTTGCTGAATAGTACTATATGTCACAGTG 2020  
DB 1381 TTGTTTAAAAGTAAATAAAATTCACAAACATTTGCTGAATAGTACTATATGTCACAGTG 1440  
QY 2021 CTGTGCAAGGTATTTACACTCTGTAAATTAATTTCTCTCAAAATTTGACATAGTAG 2080  
DB 1441 CTGTGCAAGGTATTTACACTCTGTAAATTAATTTCTCTCAAAATTTGACATAGTAG 1500  
QY 2081 AACGCTATCTGGGAGCTATTTTTTTCAGTTTTTGATATTTCTAGCTTATCTACTTCCAAA 2140  
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QY 2141 CTAATTTTATTTTTCGTGAGACTAACTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2200  
DB 1561 CTAATTTTATTTTTCGTGAGACTAACTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1620  
QY 2201 AACCTTAATTTATTTTAAACATACCTAAGAGTACATTTGTTTACCTCTATATACCAAGCA 2260  
DB 1621 AACCTTAATTTATTTTAAACATACCTAAGAGTACATTTGTTTACCTCTATATACCAAGCA 1680



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Qy 2261 CATTTTAAAGTGCCATTAAACAAATGTATCACTAGCCCTCTCTTTTCCAAAGAGGGA 2320
Db 1681 CATTTTAAAGTGCCATTAAACAAATGTATCACTAGCCCTCTCTTTTCCAAAGAGGGA 1740

Qy 2321 CTGAGAGATGCAGAAATATTGTGA 2345
Db 1741 CTGAGAGATGCAGAAATATTGTGA 1765

RESULT 10
CR599107 1823 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSODI030YC09 of Placentia Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR599107 GI:50479914
VERSION HTC; CNSUT_CDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1823)
Li,W.B., Gruber,C., Jesses,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue
2 (bases 1 to 1823)
Genoscope.
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr)
REMARK - Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES Location/Qualifiers
source 1. 1823
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI030YC09"
/tissue_type="Placentia Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 67.8%; Score 1608; DB 3; Length 1823;
Best Local Similarity 92.8%; Pred. No. 0;
Matches 1741; Conservative 0; Mismatches 55; Indels 80; Gaps 2;

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Db 28 AGCAGGAAATCCGGATGTCCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCCTCAACATA 87

Qy 61 GTTCAGAACTCTCCATCCGGACTAGTATTGAGCATCTGCCTCTCATATCACCAGTGC 120
Db 88 GTTCAGAACTCTCCATCCGGACTAGTATTGAGCATCTGCCTCTCATATCACCAGTGC 147

Qy 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
Db 148 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 207

Qy 181 GTGTGCTTCTCACTTCATCTGACCAACAGGCTCTCTGGTCCAAAGCTCTTTGCGTGCA 240
Db 208 GTGTGCTTCTCACTTCATCTGACCAACAGGCTCTCTGGTCCAAAGCTCTTTGCGTGCA 267

Qy 241 GAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGATCACCTTGTGAGCAAAAAG 300
Db 268 GAAGGTAGTCTCTT----- 281
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Qy 301 GCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGAGGCCCTGTAGGCTGTGGGACTAAGT 360
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Qy 361 TTGGCCGGCAAGGACCAAGTTGAAACAGCCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420
Db 335 CTG-----TTCAACTAGTGTGTATTTCTTTTACAGCTAT 367

Qy 421 GGCTGGGTTGGAGATCGATTTCGTGGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGG 480
Db 368 GGCTGGGTTGGAGATCGATTTCGTGGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGG 427

Qy 481 AAAAAATGGGTGGGTGCTCTCGATTGGAAGTTTCCAGTGCAGCCGACAGATTGTGAGCCCTAT 540
Db 428 AAAAAATGGGTGGGTGCTCTCGATTGGAAGTTTCCAGTGCAGCCGACAGATTGTGAGCCCTAT 487

Qy 541 TGTTACAACTCATCTGATACTTGGACTAATCTGTGATTCAGAAATTTATCACCACAAA 600
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Qy 601 GATCCCATATTCAACACTCAAACTGCAACACAAACACAGAAATTTATGTCAGTGACAGT 660
Db 548 GATCCCATATTCAACACTCAAACTGCAACACAAACACAGAAATTTATGTCAGTGACAGT 607

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Db 608 ACCTACTCGGTGGCATCCCCCTTACTCTCAATAACCTGCCCTACTACTCTCTCTGCT 667

Qy 721 CAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTGTGTGTGTGTGTGTGTGTGT 780
Db 668 CAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTGTGTGTGTGTGTGTGTGTGT 727

Qy 781 GAAACTAGCACCACTGTCTACAGAAACTGAACCAATTTGTTGAAATTAAGCAGCATTTCAAG 840
Db 728 GAAACTAGCACCACTGTCTACAGAAACTGAACCAATTTGTTGAAATTAAGCAGCATTTCAAG 787

Qy 841 AATGAAGCTGCTGGGTTTGGAGGTGTCGCCACAGGCTCTGCTAGTGTGCTCTCTCTCTTC 900
Db 788 AATGAAGCTGCTGGGTTTGGAGGTGTCGCCACAGGCTCTGCTAGTGTGCTCTCTCTCTTC 847

Qy 901 TTTGGTGTGTCAGCTGCTGTTGGATTTTGTGTATGTCTAAAGGTATGTGAAGGCTTCCCT 960
Db 848 TTTGGTGTGTCAGCTGCTGTTGGATTTTGTGTATGTCTAAAGGTATGTGAAGGCTTCCCT 907

Qy 961 TTTTACAAAACAAGAAATCAGACAGAGGAAATGATCGAAACCAAACTAGTATAAGGAGGAGAAG 1020
Db 908 TTTTACAAAACAAGAAATCAGACAGAGGAAATGATCGAAACCAAACTAGTATAAGGAGGAGAAG 967

Qy 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAAACTGATAAAAAACCAGAGAGTCC 1080
Db 968 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAAACTGATAAAAAACCAGAGAGTCC 1027

Qy 1081 AAGAGTCCAAAGCAAAATACCGTGCATGCGCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140
Db 1028 AAGAGTCCAAAGCAAAATACCGTGCATGCGCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1087

Qy 1141 TGAGGAGACACACTGAGGCTGTTCTTTTCATGCTCTTTACCTTGCCCTGAGCTGGGGA 1200
Db 1088 TGAGGAGACACACTGAGGCTGTTCTTTTCATGCTCTTTACCTTGCCCTGAGCTGGGGA 1147

Qy 1201 ATCAAAAGGGCCCAAGAACCAAAAGAGAAAGTCCACCTTTGGTTCTTAATCGGAATCAGC 1260
Db 1148 ATCAAAAGGGCCCAAGAACCAAAAGAGAAAGTCCACCTTTGGTTCTTAATCGGAATCAGC 1207

Qy 1261 TCAGGACTGCAATGGACTATGAGTGCACCAAGAGAAATGCCCTTCTCTTATTTGTAAC 1320
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Qy 1321 CTTGTCTGGAATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
Db 1268 CTTGTCTGGAATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1327

Qy 1381 GTCTTAATAATATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGAAGGACCTTAAACATC 1440
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Db 1328 GTCCCTAATAATATCCACTGGGAGAAAGAGTTTTCGAAAGTGCAGGACCTAAACAATC 1387
Qy 1441 TCATCAGTATCCAGTGGTAAAAAGCCCTCTGGCTGTCTGAGGCTAGTGGTGGTGAAGAGC 1500
Db 1388 TCATCAGTATCCAGTGGTAAAAAGCCCTCTGGCTGTCTGAGGCTAGTGGTGGTGAAGAGC 1447
Qy 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGGAGCTCAGACCCCTTCTTCA 1560
Db 1448 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGGAGCTCAGACCCCTTCTTCA 1507
Qy 1561 GCTCTGAAAGAGAAAACAGCTATCCACCTGTACATGTCTCTCTGAGCCGGTAAAGAGCAA 1620
Db 1508 GCTCTGAAAGAGAAAACAGCTATCCACCTGTACATGTCTCTCTGAGCCGGTAAAGAGCAA 1567
Qy 1621 AGAATGGCAGAAAAGCTTTAGCCCTGAAAGCCATGGAGATTCTCATACTTTGAGACCTPAA 1680
Db 1568 AGAATGGCAGAAAAGCTTTAGCCCTGAAAGCCATGGAGATTCTCATACTTTGAGACCTPAA 1627
Qy 1681 TCTCTGTAAGCTAAATAAAGAAATAGAACAGGCTGAGATACGACAGTACACTGTCA 1740
Db 1628 TCTCTGTAAGCTAAATAAAGAAATAGAACAGGCTGAGATACGACAGTACACTGTCA 1687
Qy 1741 CGAGGAGTGTAAACACAGACAGGCTCAAAGTGTCTCTGAAACACATTCAGTTGGAAT 1800
Db 1688 GCAGGAGTGTAAACACAGACAGGCTCAAAGTGTCTCTGAAACACATTCAGTTGGAAT 1747
Qy 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860
Db 1748 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1807
Qy 1861 AGGAATAATACTTTTA 1876
Db 1808 AGGAATAATACTTTTA 1823
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## RESULT 11

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CR598440
LOCUS CR598440
DEFINITION full-length cDNA clone CS0DE007YF17 of Placenta of Homo sapiens
(human).
ACCESSION CR598440
VERSION CR598440.1 GI:50479247
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li.W.B., Gruber,C., Jesse,J. and Polayes,D.
JOURNAL 1 (bases 1 to 1113)
REMARK Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Paradise Avenue
REFERENCE 2 (bases 1 to 1113)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
```

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

## FEATURES

## source

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1..1113
/organism="Homo sapiens"
/mol_type="RNA"
/db_xref="taxon:9606"
/clone="CS0DE007YF17"
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## ORIGIN

Query Match 46.9%; Score 1113; DB 3; Length 1113;  
Best Local Similarity 100.0%; Pred. No. 4.2e-265;  
Matches 1113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/plasmid="pCMVSPORT\_6"

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Qy 1240 TGGTTCCTAACTGGAATCAGCTCAGGACTGCCTATGAGTGCACCAAGAGAA 1299
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Qy 1300 TGCCCTTCTCCTTATTTGAACCCCTGTCTGGATCTCTATCTCTCTCTCAAGCTTCCCA 1359
Db 61 TGCCCTTCTCCTTATTTGAACCCCTGTCTGGATCTCTATCTCTCTCAAGCTTCCCA 120
Qy 1360 CGGCTTTTCTAGCCTGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAA 1419
Db 121 CGGCTTTTCTAGCCTGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAA 180
Qy 1420 AGTCAAGGACCTAAAACATCTCATCAGTATCCAGTGGTAAAGGCTCTCGGTGTCT 1479
Db 181 AGTCAAGGACCTAAAACATCTCATCAGTATCCAGTGGTAAAGGCTCTCGGTGTCT 240
Qy 1480 GAGCTAGTGGTGTGAAAGCCAAAGGAGTCACTCAGACCAAGGCTTTCTCTACTGATTC 1539
Db 241 GAGCTAGTGGTGTGAAAGCCAAAGGAGTCACTCAGACCAAGGCTTTCTCTACTGATTC 300
Qy 1540 GCAGCTCAGACCCCTTTCTTCTGAGCTCTGAAAGAGAAACACGATATCCCACTGACATGTCT 1599
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Qy 1600 TCTGAGCCGGTAAAGAGCAAAAGAAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGA 1659
Db 361 TCTGAGCCGGTAAAGAGCAAAAGAAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGA 420
Qy 1660 TTCTCATAACTTGAGACCTAATCTCTGTAAGCTTAAATAAAGAAATAGAACAGGCTGA 1719
Db 421 TTCTCATAACTTGAGACCTAATCTCTGTAAGCTTAAATAAAGAAATAGAACAGGCTGA 480
Qy 1720 GGATACGACAGTACACTGTCTGAGGAGGACTGTAAACACAGACAGGGTCAAAAGTGTCTCT 1779
Db 481 GGATACGACAGTACACTGTCTGAGGAGGACTGTAAACACAGACAGGGTCAAAAGTGTCTCT 540
Qy 1780 CTGAACACATTTAGTGTGGAATCACTGTCTGAGACACACACACTTCTTTCTGTGTCTCT 1839
Db 541 CTGAACACATTTAGTGTGGAATCACTGTCTGAGACACACACACTTCTTTCTGTGTCTCT 600
Qy 1840 ACCACTGCTGATATTTCTCTAGGAAATATATCTTTTACAAGTAAACAAATAAAGAACTCT 1899
Db 601 ACCACTGCTGATATTTCTCTAGGAAATATATCTTTTACAAGTAAACAAATAAAGAACTCT 660
Qy 1900 TATAAATTTCTATTTTCTCTGAGTTACAGAAATGATTACTTAAGGAAGATTACTCAGTAA 1959
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Db 721 TTTGTTTAAAGAAATTAATAATTTCAACAAATTTGCTGTAAGTACTATATGTCAAGT 780
Qy 2020 GCTGTGCAAGGTATTACACTCTGTAATTTGAATATTATCTCTCAAAATAATTCACATAGTA 2079
Db 781 GCTGTGCAAGGTATTACACTCTGTAATTTGAATATTATCTCTCAAAATAATTCACATAGTA 840
Qy 2080 GAAGCTATCTGGGAAGCTATTTTTTTCAGTTTTTGATATTTCTAGCTTATCTACTTCCAA 2139
Db 841 GAAGCTATCTGGGAAGCTATTTTTTTCAGTTTTTGATATTTCTAGCTTATCTACTTCCAA 900
Qy 2140 ACTAATTTTTTATTTTCTGAGACTAATCTTATTTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 2199
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Qy 2200 TAACCTTAAATTTATTTTATACATACCTTAAGAGTACATTTGTACTCTCTATATACCAAGC 2259
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Db      961  TAACCTTAATTTATTATTAAATACATACCTAAGAGTACATGTTGTTACTCTTATATACCAAGC 1020
Qy      2260  ACATTTTTAAAGTGCCATTAAACAAATGTATCACTAGCCCTCTCTTTTCCCAACAAGAGGG 2319
Db      1021  ACATTTTAAAGTGCCATTAAACAAATGTATCACTAGCCCTCTCTTTTCCCAACAAGAGGG 1080
Qy      2320  ACTGAGAGATGCAGAAATATTTGTGACAAAAA 2352
Db      1081  ACTGAGAGATGCAGAAATATTTGTGACAAAAA 1113

RESULT 12
AL574194/c
LOCUS   AL574194 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSODI039YJ06 3-PRIME, mRNA sequence.
ACCESSION AL574194
VERSION   AL574194
KEYWORDS  AL574194.3 GI:46247285
SOURCE    EST.
ORGANISM  Homo sapiens (human)
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 1130)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On Feb 16, 2001 this sequence version replaced gi:31295529.
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen. This sequence belongs to sequence cluster
          5952.r
          For more information about this cluster, see
          http://www.genoscope.cns.fr/cdna?s=CSODI039DE03NP1&c=5952.r.

FEATURES             source
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        /note="1st strand cDNA was primed with a NotI-oligo(dT)
        primer. Five prime end enriched, double-strand cDNA was
        digested with Not I and cloned into the Not I and EcoR V
        sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match          44.4%; Score 1053.4; DB 1; Length 1130;
Best Local Similarity 97.3%; Pred. No. 2.7e-250;
Matches 1083; Conservative 8; Mismatches 20; Indels 2; Gaps 2;

Qy      746  GAAAAAAATTGATTGTGTACAGAACTTTTATGGAAACTAGCACCATGTCTACAGAAA 805
Db      1130  GAGAAAAAATTGATTGTTKTCACAGAAG-TTTTATGAAAACTAGCACCATGTCTACAGAAA 1072
Qy      806  CTGNACCATTTGTTGAAAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGAGGTG 865
Db      1071  ACTGAACCATTTGTGAAAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGG-TTGAGGTG 1013
Qy      866  TCCCCACGGCTCTGCTAGTGTCTCTCTCTCTCTCTTTTGTGTGCTGACGTGCTTCTGCAT 925
Db      1012  TCCCCACGGCTCTGCTAGTGTCTCTCTCTCTCTCTTTTGTGTGCTGACGTGCTTCTGCAT 953
Qy      926  TTTGCTATGTCAAAGGTATGTGAAGCCCTTCCCTTTTACAAAACAAGAAATCAGCAGAAG 985
Db      952  TTTGCTATGTCAAAGGTATGTGAAGCCCTTCCCTTTTACAAAACAAGAAATCAGCAGAAG 893

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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1091)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 15, 2001 this sequence version replaced gi:31272096.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
5952.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0D1039DE03QP1&c=5952.r.

FEATURES  
source

1..1091  
/organism="Homo sapiens"  
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/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/notes="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 44.0%; Score 1043.8; DB 1; Length 1091;  
Best Local Similarity 98.9%; Pred. No..6.5e-248;  
Matches 1057; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 102 CTCTCATATCACCAGTGGCCATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGCAGAT 161  
DB 1 CTCTCATATCACCAGTGGCCATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGCAGAT 60  
QY 162 GGCAGGTGTTTACAGCTGTTGTTCTTCTACATTCGATCTGACACGAGGCTCTGGT 221  
DB 61 GGCAGGTGTTTACAGCTGTTGTTCTTCTACATTCGATCTGACACGAGGCTCTGGT 120  
QY 222 CCAAGGCTCTTTCGTCGAGAAGAGCTTTCCATCCAGGTGTCTGCGAATTTATGGGGAT 281  
DB 121 CCAAGGCTCTTTCGTCGAGAAGAGCTTTCCATCCAGGTGTCTGCGAATTTATGGGGAT 180  
QY 282 CACCTTGTGAGCAAAAAGGGGACGACGAGCTGAATTTACAGAGCTAAGGAGGCTG 341  
DB 181 CACCTTGTGAGCAAAAAGGGGACGACGAGCTGAATTTACAGAGCTAAGGAGGCTG 240  
QY 342 TAGCTCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCTTGAAGCTAG 401  
DB 241 TAGCTCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCTTGAAGCTAG 300  
QY 402 CTTTGAACCTTGCAGCTATGCTGGTGGAGATGGAATTCGTGTCATCTCTAGGATTAG 461  
DB 301 CTTTGAACCTTGCAGCTATGCTGGTGGAGATGGAATTCGTGTCATCTCTAGGATTAG 360  
QY 462 CCNAAACCCCAAGTGTGGGAAAATGGGGTGGTCTGATTTGGAAGTTCCAGTGAG 521  
DB 361 CCNAAACCCCAAGTGTGGGAAAATGGGGTGGTCTGATTTGGAAGTTCCAGTGAG 420  
QY 522 CCGACAGTTTGCAGCTATTGTTACAACTCATCTGATCTTGGACTAAGCTCGTCATTCC 581  
DB 421 CCGACAGTTTGCAGCTATTGTTACAACTCATCTGATCTTGGACTAAGCTCGTCATTCC 480  
QY 582 AGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACACAGA 641  
DB 481 AGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACACAGA 540  
QY 642 ATTTATTGTGAGTACAGTACCTACTCGGTGGGACATCCCTTACTCTCAATACCTGCCCC 701

DB 541 ATTTATTGTGAGTACAGTACCTACTCGTGGCATCCCTTACTCTCAATACCTGCCCC 600  
QY 702 TACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCAGGAGAAAAAATTTGATTG 761  
DB 601 TACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCAGGAGAAAAAATTTGATTG 660  
QY 762 TGTACAGAAAGTTTATGAAACTAGCACATGTCTACAGAAACTGAACATTTGTTGA 821  
DB 661 TGTACAGAAAGTTTATGAAACTAGCACATGTCTACAGAAACTGAACATTTGTTGA 720  
QY 822 AAATAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTCTCCCGCGCTCTGCT 881  
DB 721 AAATAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTCTCCCGCGCTCTGCT 780  
QY 882 AGTCTTGTCTCTCTCTCTTGTGCTGAGCTGCTTGGATTCTGCTATGTCAAAAG 941  
DB 781 AGTCTTGTCTCTCTCTCTTGTGCTGAGCTGCTTGGATTCTGCTATGTCAAAAG 840  
QY 942 GTATGTAAGGCTTCCCTTTTACAAACAAGATCAGCAGAAAGAAATGATCGAAACCA 1001  
DB 841 GTATGTAAGGCTTCCCTTTTACAAACAAGATCAGCAGAAAGAAATGATCGAAACCA 900  
QY 1002 AGTAGTAAAGGAGAGAGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACTGA 1061  
DB 901 AGTAGTAAAGGAGAGAGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACTGA 960  
QY 1062 TAAAAACCCAGAGAGTCCCAAGAGTCCCAAGCAAACTACCGTGGATCGCTGGAAGCTGA 1121  
DB 961 TAAAAACCCAGAGAGTCCCAAGAGTCCCAAGCAAACTACCGTGGATCGCTGGAAGCTGA 1020  
QY 1122 AGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTT 1170  
DB 1021 AGTTTAGATGAGAGAAATAG--AGAAACACTGAGGCTGGTTCTTT 1067

AL541927 1101 bp mRNA linear EST 24-MAR-2004  
AL541927 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE007YF17  
5-PRIME, mRNA sequence.  
AL541927  
AL541927.3 GI:45717503  
EST.  
Homo sapiens (human)  
Homo sapiens  
Homo sapiens  
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1101)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 15, 2001 this sequence version replaced gi:30546572.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 5952.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0DE007CC09QP1&c=5952.r.

FEATURES  
source

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/organism="Homo sapiens"  
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/tissue\_type="PLACENTA"  
/clone\_lib="Homo sapiens PLACENTA"

/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 42.2%; Score 1000; DB 1; Length 1101;  
Best Local Similarity 98.1%; Pred. No. 5e-237;  
Matches 1026; Conservative 6; Mismatches 11; Indels 3; Gaps 2;

QY 1260 CTCAGGACTGCCATGAGTATGAGTGCACCAAGAGAAATGCCCTTCTCTTTATTGTAA 1319  
DB 19 CCCGGGATGCCATGAGTATGAGTGCACCAAGAGAAATGCCCTTCTCTTTATTGTAA 78

QY 1320 CCCTGTCTGATCTATCTCTCTACCTCCAAAGCTTCCACGGCTTTCTAGCCTGGCTA 1379  
DB 79 CCCTGTCTGATCTATCTCTCTACCTCCAAAGCTTCCACGGCTTTCTAGCCTGGCTA 138

QY 1380 TGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAGGACCTAAACAT 1439  
DB 139 TGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAGGACCTAAACAT 198

QY 1440 CTCATCAGTATCCAGTGGTAAAAAGGCTCTCTGCTGTCTGAGGCTAGTGGTGTGAAG 1499  
DB 199 CTCATCAGTATCCAGTGGTAAAAAGGCTCTCTGCTGTCTGAGGCTAGTGGTGTGAAG 258

QY 1500 CCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTC 1559  
DB 259 CCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTC 318

QY 1560 AGCTCTGAAAGAGAAACACGATFATCCCACTGACATGCTCTCTGAGCCGGTGAAGCAA 1619  
DB 319 AGCTCTGAAAGAGAAACACGATFATCCCACTGACATGCTCTCTGAGCCGGTGAAGCAA 378

QY 1620 AAGAATGGCGAAAGTTTAGCCCTCGAAAGCCATGGAGATTCTCATCTTGAGACCTA 1679  
DB 379 AAGAATGGCGAAAGTTTAGCCCTCGAAAGCCATGGAGATTCTCATCTTGAGACCTA 438

QY 1680 ATCTCTGTAAGCTAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTC 1739  
DB 439 ATCTCTGTAAGCTAAATAAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTC 498

QY 1740 AGCAGGAGCTGTAACACACAGAGGGTCAAGTGTCTCTCTGAAACATTTGAGTTGGAA 1799  
DB 499 AGCAGGAGCTGTAACACACAGAGGGTCAAGTGTCTCTCTGAAACATTTGAGTTGGAA 558

QY 1800 TCACCTGTTTGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATTTTCTC 1859  
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QY 1860 TAGAATATATCTTTTACAAGTACAAATAAATACTCTTAATAATTTCTATTTTATC 1919  
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QY 1920 TGAGTTACAGAAATGATTACTAGGAAGATTACTCAGTAATTTGTTTAAAGTAATAA 1979  
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QY 1980 ATTCAACAAACATTTGCTGAATAGCTACTATATGTCAAAGTCTGTGCAAGGTATTACACT 2039  
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QY 2040 CTGTAATGTAATATTATCTCAAAAATTTGCACATAGTAGAACGCTATCTGGGAAGCTA 2099  
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QY 2100 TTTTTTTTCAAGTTTGTAGCTTATCTACTTCCAACTAAATTTTATTTTCTG 2159  
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DB 919 AGACTAATCTTATTCATTTTCTCTAATATGSGAACCATTAACCTTAATTTATTATTA 978

QY 2220 CATACCTAAGAGTACATTTGTTACCTCTATATACCAAGACACATTTTAAAGTGCCATTA 2279  
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QY 2280 ACAAATGTATCACTAGCCCTCTCTTT 2305  
DB 1036 ACAAATGTATCACTAGCCCTCTTT 1061

RESULT 15  
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LOCUS 1045 bp mRNA linear EST 25-MAR-2004

DEFINITION AL550621 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0D1058YN14 5-PRIME, mRNA sequence.

ACCESSION AL550621

VERSION AL550621.3 GI:45750987

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1045)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On Feb 15, 2001 this sequence version replaced gi:31272438.

Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r

For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0D1058DG07QPl&c=5952.r.

FEATURES  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="CS0D1058YN14"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 41.8%; Score 991.6; DB 1; Length 1045;  
Best Local Similarity 98.5%; Pred. No. 6e-235;  
Matches 989; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

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DB 1 GAACCTCCATCCGAGCTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGCCATCTG 60

QY 127 AGGTGTTTCCCTGCTCTGAAGGGTAGGCACCATGCGCAGGTCTTTCAGCCTGGTCTTG 186  
DB 61 AGGTGTTTCCCTGCTCTGAAGGGTAGGCACCATGCGCAGGTCTTTCAGCCTGGTCTTG 120

QY 187 CTTCTCAGTTTCCATCTGGACACAGGCTCCTGGTCCAAGGCTCTTTGCGTCAGAGAG 246  
DB 121 CTTCTCAGTTTCCATCTGGACACAGGCTCCTGGTCCAAGGCTCTTTGCGTCAGAGAG 180

QY 247 CTTTCATCCAGTGTCTATGCAAGATTATGGGATCACCCCTTGTGAGCAAAAGGCGAAC 306  
DB 181 CTTTCATCCAGTGTCTATGCAAGATTATGGGATCACCCCTTGTGAGCAAAAGGCGAAC 240

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Qy 307 CAGCAGCTGATTTTCACAGAGCTAAGAGGCGCTGTAGGCTGCTGGGACTAAGTTTGCC 366
Db |||||
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Db |||||
Qy 367 GGCAAGGACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGAGCTATGGCTGG 426
Db |||||
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464	38.6	1.6	2384	1	US-08-258-442-10	Sequence 10, Appl	537	38.2	1.6	12313	4	US-09-949-016-13248	Sequence 13248, A
465	38.6	1.6	2384	1	US-08-328-809-5	Sequence 5, Appl	538	38.2	1.6	13607	4	US-09-949-016-11806	Sequence 11806, A
466	38.6	1.6	2384	4	US-08-866-840-5	Sequence 5, Appl	539	38.2	1.6	13609	4	US-09-949-016-12922	Sequence 12922, A
467	38.6	1.6	2384	5	PCT-US92-11107-10	Sequence 10, Appl	540	38.2	1.6	123513	4	US-09-949-016-15794	Sequence 15794, A
468	38.6	1.6	4507	2	US-08-568-459A-3	Sequence 3, Appl	541	38.2	1.6	134890	4	US-09-949-016-15602	Sequence 15602, A
469	38.6	1.6	4507	2	US-08-487-826B-3	Sequence 3, Appl	542	38.2	1.6	246240	2	US-08-724-394A-20	Sequence 20, Appl
470	38.6	1.6	4507	3	US-09-210-288-3	Sequence 3, Appl	543	38.2	1.6	246240	2	US-08-724-394A-21	Sequence 21, Appl
471	38.6	1.6	19438	4	US-09-949-016-12699	Sequence 12699, A	544	38.2	1.6	246240	2	US-08-724-394A-22	Sequence 22, Appl
472	38.6	1.6	27968	4	US-09-949-016-15191	Sequence 15191, A	545	38.2	1.6	247299	4	US-09-949-016-17590	Sequence 17590, A
473	38.6	1.6	27968	4	US-09-949-016-15192	Sequence 15192, A	546	38.2	1.6	269223	4	US-09-596-002-41	Sequence 41, Appl
474	38.6	1.6	28315	4	US-09-949-016-16916	Sequence 16916, A	547	38.2	1.6	314798	4	US-09-949-016-13539	Sequence 13539, A
475	38.6	1.6	30032	4	US-09-949-016-13933	Sequence 13933, A	548	38	1.6	399	4	US-09-621-976-8976	Sequence 8976, Ap
476	38.6	1.6	78649	4	US-09-949-016-14619	Sequence 14619, A	549	38	1.6	549	1	US-07-991-867B-28	Sequence 28, Appl
477	38.6	1.6	78649	4	US-09-949-016-14620	Sequence 14620, A	550	38	1.6	549	1	US-08-107-755A-28	Sequence 28, Appl
478	38.6	1.6	78649	4	US-09-949-016-16227	Sequence 16227, A	551	38	1.6	549	3	US-08-544-332-28	Sequence 28, Appl
479	38.6	1.6	78649	4	US-09-949-016-16228	Sequence 16228, A	552	38	1.6	549	3	US-09-370-861A-28	Sequence 28, Appl
480	38.6	1.6	80632	4	US-09-949-016-12951	Sequence 12951, A	553	38	1.6	601	4	US-09-949-016-48158	Sequence 48158, A
481	38.6	1.6	84870	4	US-09-949-016-17547	Sequence 17547, A	554	38	1.6	601	4	US-09-949-016-48160	Sequence 48160, A
482	38.6	1.6	111235	4	US-09-949-016-15328	Sequence 15328, A	555	38	1.6	601	4	US-09-949-016-96127	Sequence 96127, A
483	38.6	1.6	183790	4	US-09-949-016-15494	Sequence 15494, A	556	38	1.6	601	4	US-09-949-016-171662	Sequence 171662, A
484	38.6	1.6	421491	4	US-09-949-016-12805	Sequence 12805, A	557	38	1.6	1276	2	US-08-463-911-1	Sequence 1, Appl









c1005	36	1.5	601	4	US-09-949-016-117502	Sequence 117502,	c1078	35.8	1.5	943	3	US-09-149-476-35	Sequence 35, Appl
c1006	36	1.5	601	4	US-09-949-016-117503	Sequence 117503,	c1079	35.8	1.5	1344	4	US-09-107-433-925	Sequence 925, App
c1007	36	1.5	601	4	US-09-949-016-117504	Sequence 117504,	c1080	35.8	1.5	1555	3	US-08-669-408B-9	Sequence 9, Appli
c1008	36	1.5	601	4	US-09-949-016-117505	Sequence 117505,	c1081	35.8	1.5	1738	4	US-09-918-909A-27	Sequence 27, Appl
c1009	36	1.5	601	4	US-09-949-016-117506	Sequence 117506,	c1082	35.8	1.5	3241	4	US-09-710-279-3628	Sequence 3628, Ap
c1010	36	1.5	601	4	US-09-949-016-117507	Sequence 117507,	c1083	35.8	1.5	3451	4	US-09-710-279-3984	Sequence 3984, Ap
c1011	36	1.5	601	4	US-09-949-016-117508	Sequence 117508,	c1084	35.8	1.5	3695	4	US-09-774-528-320	Sequence 320, App
c1012	36	1.5	601	4	US-09-949-016-117509	Sequence 117509,	c1085	35.8	1.5	4383	3	US-08-397-653B-2	Sequence 2, Appli
c1013	36	1.5	601	4	US-09-949-016-169756	Sequence 169756,	c1086	35.8	1.5	4383	6	5175095-4	Patent No.5175095
c1014	36	1.5	601	4	US-09-949-016-169757	Sequence 169757,	c1087	35.8	1.5	4383	6	5177307-1	Patent No.5177307
c1015	36	1.5	601	4	US-09-949-016-171125	Sequence 171125,	c1088	35.8	1.5	4383	6	5175095-4	Patent No.5175095
c1016	36	1.5	601	4	US-09-949-016-171126	Sequence 171126,	c1089	35.8	1.5	4383	6	5177307-1	Patent No.5177307
c1017	36	1.5	601	4	US-09-949-016-171255	Sequence 171255,	c1090	35.8	1.5	9728	4	US-09-949-016-12161	Sequence 12161, A
c1018	36	1.5	601	4	US-09-949-016-171256	Sequence 171256,	c1091	35.8	1.5	9729	4	US-09-949-016-13612	Sequence 13612, A
c1019	36	1.5	601	4	US-09-949-016-171451	Sequence 171451,	c1092	35.8	1.5	19157	4	US-09-949-016-13142	Sequence 13142, A
c1020	36	1.5	737	4	US-09-270-767-11417	Sequence 11417, A	c1093	35.8	1.5	20303	1	US-08-370-975B-6	Sequence 6, Appli
c1021	36	1.5	746	4	US-09-270-767-3259	Sequence 3259, Ap	c1094	35.8	1.5	24221	4	US-09-949-016-14964	Sequence 14964, A
c1022	36	1.5	746	4	US-09-270-767-18541	Sequence 18541, A	c1095	35.8	1.5	25067	4	US-09-949-016-11794	Sequence 11794, A
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c1027	36	1.5	2839	3	US-09-160-496-3	Sequence 3, Appli	c1100	35.8	1.5	50263	4	US-09-949-016-13563	Sequence 13563, A
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c1029	36	1.5	2839	4	US-09-197-503-5	Sequence 5, Appli	c1102	35.8	1.5	63588	4	US-10-243-735-3	Sequence 3, Appli
c1030	36	1.5	3504	1	US-08-485-568A-5	Sequence 5, Appli	c1103	35.8	1.5	66804	4	US-09-740-041-3	Sequence 3, Appli
c1031	36	1.5	3504	1	US-08-620-717A-8	Sequence 8, Appli	c1104	35.8	1.5	76985	4	US-09-949-016-12416	Sequence 12416, A
c1032	36	1.5	3504	2	US-08-590-554A-5	Sequence 5, Appli	c1105	35.8	1.5	76986	4	US-09-949-016-13120	Sequence 13120, A
c1033	36	1.5	3504	2	US-09-184-223-5	Sequence 5, Appli	c1106	35.8	1.5	77586	4	US-09-949-016-13220	Sequence 13220, A
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c1035	36	1.5	3805	4	US-09-627-122-21	Sequence 1443, Ap	c1108	35.8	1.5	79350	4	US-09-949-016-12467	Sequence 12467, A
c1036	36	1.5	5340	4	US-09-627-122-21-53	Sequence 21, Appl	c1109	35.8	1.5	79351	4	US-09-949-016-16275	Sequence 16275, A
c1037	36	1.5	16592	4	US-08-556-171B-53	Sequence 53, Appl	c1110	35.8	1.5	82178	4	US-09-949-016-13394	Sequence 13394, A
c1038	36	1.5	16592	4	US-08-781-986A-53	Sequence 53, Appl	c1111	35.8	1.5	93778	4	US-09-949-016-15096	Sequence 15096, A
c1039	36	1.5	23975	4	US-09-949-016-17126	Sequence 17126, A	c1112	35.8	1.5	101011	4	US-09-949-016-16933	Sequence 16933, A
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c1041	36	1.5	33411	4	US-09-949-016-15201	Sequence 15201, A	c1114	35.8	1.5	137743	4	US-09-949-016-12172	Sequence 12172, A
c1042	36	1.5	37940	4	US-09-949-016-15550	Sequence 15550, A	c1115	35.8	1.5	160018	4	US-09-949-016-12617	Sequence 12617, A
c1043	36	1.5	42075	4	US-09-949-016-14995	Sequence 14995, A	c1116	35.8	1.5	160018	4	US-09-949-016-15994	Sequence 15994, A
c1044	36	1.5	58407	4	US-08-916-421B-2	Sequence 2, Appli	c1117	35.8	1.5	168104	4	US-09-949-016-12026	Sequence 12026, A
c1045	36	1.5	58407	4	US-09-692-570-2	Sequence 2, Appli	c1118	35.8	1.5	168105	4	US-09-949-016-16554	Sequence 16554, A
c1046	36	1.5	60141	4	US-09-949-016-15874	Sequence 15874, A	c1119	35.8	1.5	176006	4	US-09-949-016-16804	Sequence 16804, A
c1047	36	1.5	92304	4	US-09-949-016-15943	Sequence 15943, A	c1120	35.8	1.5	193303	4	US-09-497-855A-37	Sequence 37, Appl
c1048	36	1.5	112507	4	US-09-949-016-12420	Sequence 12420, A	c1121	35.8	1.5	193303	4	US-09-497-855A-44	Sequence 44, Appl
c1049	36	1.5	112507	4	US-09-949-016-12794	Sequence 12794, A	c1122	35.8	1.5	200663	4	US-09-949-016-12569	Sequence 12569, A
c1050	36	1.5	112508	4	US-09-949-016-16589	Sequence 16589, A	c1123	35.8	1.5	203093	4	US-09-949-016-14445	Sequence 14445, A
c1051	36	1.5	112508	4	US-09-949-016-16590	Sequence 16590, A	c1124	35.8	1.5	203163	4	US-09-949-016-17009	Sequence 17009, A
c1052	36	1.5	114842	4	US-09-949-016-14993	Sequence 14993, A	c1125	35.8	1.5	236474	4	US-09-949-016-13418	Sequence 13418, A
c1053	36	1.5	126176	4	US-09-949-016-16137	Sequence 16137, A	c1126	35.8	1.5	253375	4	US-09-949-016-12849	Sequence 12849, A
c1054	36	1.5	126176	4	US-09-949-016-16138	Sequence 16138, A	c1127	35.8	1.5	278866	4	US-09-949-016-13922	Sequence 13922, A
c1055	36	1.5	126982	4	US-09-949-016-16597	Sequence 16597, A	c1128	35.8	1.5	278866	4	US-09-949-016-13923	Sequence 13923, A
c1056	36	1.5	145241	4	US-09-949-016-17394	Sequence 17394, A	c1129	35.8	1.5	278866	4	US-09-949-016-13924	Sequence 13924, A
c1057	36	1.5	145241	4	US-09-949-016-17395	Sequence 17395, A	c1130	35.8	1.5	278866	4	US-09-949-016-13925	Sequence 13925, A
c1058	36	1.5	256171	4	US-09-949-016-12822	Sequence 12822, A	c1131	35.8	1.5	278866	4	US-09-949-016-13926	Sequence 13926, A
c1059	36	1.5	256176	4	US-09-949-016-15524	Sequence 15524, A	c1132	35.8	1.5	278866	4	US-09-949-016-14699	Sequence 14699, A
c1060	36	1.5	363032	4	US-09-949-016-12415	Sequence 12415, A	c1133	35.8	1.5	278866	4	US-09-949-016-14700	Sequence 14700, A
c1061	36	1.5	363033	4	US-09-949-016-15754	Sequence 15754, A	c1134	35.8	1.5	278866	4	US-09-949-016-14701	Sequence 14701, A
c1062	36	1.5	1830121	4	US-09-557-884-1	Sequence 1, Appli	c1135	35.8	1.5	278866	4	US-09-949-016-14702	Sequence 14702, A
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c1065	35.8	1.5	601	4	US-09-949-016-50946	Sequence 50946, A	c1138	35.8	1.5	670690	4	US-09-949-016-14207	Sequence 14207, A
c1066	35.8	1.5	601	4	US-09-949-016-51000	Sequence 51000, A	c1139	35.6	1.5	189	4	US-09-513-999C-21756	Sequence 21756, A
c1067	35.8	1.5	601	4	US-09-949-016-57131	Sequence 57131, A	c1140	35.6	1.5	417	4	US-09-248-796A-2849	Sequence 2849, Ap
c1068	35.8	1.5	601	4	US-09-949-016-72668	Sequence 72668, A	c1141	35.6	1.5	601	4	US-09-949-016-28524	Sequence 28524, A
c1069	35.8	1.5	601	4	US-09-949-016-103973	Sequence 103973, A	c1142	35.6	1.5	601	4	US-09-949-016-60957	Sequence 60957, A
c1070	35.8	1.5	601	4	US-09-949-016-120884	Sequence 120884, A	c1143	35.6	1.5	601	4	US-09-949-016-113260	Sequence 113260, A
c1071	35.8	1.5	601	4	US-09-949-016-120886	Sequence 120886, A	c1144	35.6	1.5	601	4	US-09-949-016-133630	Sequence 133630, A
c1072	35.8	1.5	601	4	US-09-949-016-151246	Sequence 151246, A	c1145	35.6	1.5	601	4	US-09-949-016-159300	Sequence 159300, A
c1073	35.8	1.5	601	4	US-09-949-016-180548	Sequence 180548, A	c1146	35.6	1.5	601	4	US-09-949-016-164036	Sequence 164036, A
c1074	35.8	1.5	601	4	US-09-949-016-195406	Sequence 195406, A	c1147	35.6	1.5	601	4	US-09-949-016-171504	Sequence 171504, A
c1075	35.8	1.5	665	3	US-08-998-416-937	Sequence 937, App	c1148	35.6	1.5	658	3	US-08-998-416-595	Sequence 595, App
c1076	35.8	1.5	711	3	US-08-998-416-786	Sequence 786, App	c1149	35.6	1.5	740	3	US-08-998-416-971	Sequence 971, App
c1077	35.8	1.5	840	4	US-09-248-796A-1930	Sequence 1930, Ap	c1150	35.6	1.5	966	4	US-09-248-796A-9577	Sequence 9577, Ap



c1151	35.6	1.5	1441	4	US-08-956-171E-1000	Sequence 1000, Ap	c1224	35.4	1.5	1041	3	US-09-033-055A-4	Sequence 4, Appli
c1152	35.6	1.5	1441	4	US-08-781-986A-1000	Sequence 1000, Ap	1225	35.4	1.5	1712	3	US-09-144-776B-5	Sequence 5, Appli
c1153	35.6	1.5	1485	4	US-09-248-796A-2443	Sequence 2443, Ap	1226	35.4	1.5	1712	3	US-09-144-776B-5	Sequence 5, Appli
c1154	35.6	1.5	2349	4	US-09-601-198-46	Sequence 46, Appl	1227	35.4	1.5	1712	4	US-08-882-431B-5	Sequence 7, Appli
c1155	35.6	1.5	2481	2	US-08-630-118A-1	Sequence 1, Appli	1228	35.4	1.5	1712	4	US-08-882-431B-5	Sequence 7, Appli
c1156	35.6	1.5	2481	2	US-08-838-399-1	Sequence 1, Appli	1229	35.4	1.5	2049	3	US-09-134-001C-2413	Sequence 2413, Ap
c1157	35.6	1.5	2481	3	US-09-235-839-1	Sequence 1, Appli	1230	35.4	1.5	2529	4	US-09-270-767-118	Sequence 118, Ap
c1158	35.6	1.5	2481	3	US-09-327-035-1	Sequence 1, Appli	1231	35.4	1.5	2529	4	US-09-270-767-118	Sequence 118, Ap
c1159	35.6	1.5	2604	2	US-08-630-118A-3	Sequence 3, Appli	c1232	35.4	1.5	2646	1	US-08-539-304A-5	Sequence 5, Appli
c1160	35.6	1.5	2604	3	US-09-235-839-3	Sequence 3, Appli	1233	35.4	1.5	2998	4	US-09-710-279-3506	Sequence 3506, Ap
c1161	35.6	1.5	2604	3	US-09-327-035-3	Sequence 3, Appli	1234	35.4	1.5	3001	4	US-09-539-333D-188	Sequence 188, Ap
c1162	35.6	1.5	2604	3	US-09-327-035-3	Sequence 3, Appli	1235	35.4	1.5	3088	3	US-09-937-610-3	Sequence 3, Appli
c1163	35.6	1.5	2960	3	US-08-913-842-3	Sequence 3, Appli	1236	35.4	1.5	3173	4	US-09-710-279-3554	Sequence 3554, Ap
c1164	35.6	1.5	3129	4	US-09-897-425-40	Sequence 40, Appl	1237	35.4	1.5	3527	4	US-09-710-279-3890	Sequence 3890, Ap
c1165	35.6	1.5	3440	1	US-08-471-791-27	Sequence 27, Appl	1238	35.4	1.5	3941	4	US-09-710-279-3755	Sequence 3755, Ap
c1166	35.6	1.5	3440	5	PCT-US91-0174E-27	Sequence 27, Appl	1239	35.4	1.5	4126	4	US-09-710-279-4154	Sequence 4154, Ap
c1167	35.6	1.5	3787	4	US-09-897-425-48	Sequence 48, Appl	c1240	35.4	1.5	4185	4	US-09-417-485D-7	Sequence 7, Appli
c1168	35.6	1.5	3888	4	US-09-897-425-42	Sequence 42, Appl	1241	35.4	1.5	4291	2	US-08-417-210A-80	Sequence 80, Appl
c1169	35.6	1.5	3888	4	US-09-897-425-45	Sequence 45, Appl	1242	35.4	1.5	4291	2	US-08-417-210A-80	Sequence 80, Appl
c1170	35.6	1.5	4545	4	US-09-897-425-53	Sequence 53, Appl	1243	35.4	1.5	4857	2	US-08-566-398-16	Sequence 16, Appl
c1171	35.6	1.5	4546	4	US-09-897-425-50	Sequence 50, Appl	c1244	35.4	1.5	6243	2	US-09-056-075-1	Sequence 1, Appli
c1172	35.6	1.5	4652	4	US-09-893-525-36	Sequence 36, Appl	1245	35.4	1.5	6628	3	US-08-815-809-3	Sequence 3, Appli
c1173	35.6	1.5	4910	4	US-09-023-655-1125	Sequence 1125, Ap	1246	35.4	1.5	6649	2	US-08-816-155B-5	Sequence 5, Appli
c1174	35.6	1.5	4910	4	US-09-814-915A-75	Sequence 75, Appl	1247	35.4	1.5	6649	2	US-09-079-587-5	Sequence 5, Appli
c1175	35.6	1.5	4910	4	US-09-949-016-129	Sequence 129, App	1248	35.4	1.5	7091	2	US-08-658-665-40	Sequence 40, Appl
c1176	35.6	1.5	5390	4	US-09-893-525-41	Sequence 41, Appl	1249	35.4	1.5	7091	3	US-08-796-101-4	Sequence 40, Appl
c1177	35.6	1.5	5418	4	US-09-893-525-38	Sequence 38, Appl	1250	35.4	1.5	7091	3	US-09-085-273-40	Sequence 40, Appl
c1178	35.6	1.5	6768	1	US-08-107-755A-1	Sequence 1, Appli	1251	35.4	1.5	7351	1	US-09-916-963-40	Sequence 40, Appl
c1179	35.6	1.5	12658	4	US-08-956-171E-127	Sequence 127, App	1252	35.4	1.5	7351	1	US-08-224-391-83	Sequence 83, Appl
c1180	35.6	1.5	12658	4	US-08-781-986A-127	Sequence 127, App	1253	35.4	1.5	7351	1	US-08-484-304-83	Sequence 83, Appl
c1181	35.6	1.5	2205	4	US-09-949-016-16199	Sequence 16199, A	1254	35.4	1.5	7351	2	US-08-184-009-127	Sequence 127, App
c1182	35.6	1.5	2717	4	US-09-949-016-16284	Sequence 16284, A	1255	35.4	1.5	7351	2	US-08-566-398-39	Sequence 39, Appl
c1183	35.6	1.5	29335	4	US-09-949-016-11871	Sequence 11871, A	1256	35.4	1.5	7351	2	US-08-458-356-127	Sequence 127, App
c1184	35.6	1.5	29336	4	US-09-949-016-14443	Sequence 14443, A	1257	35.4	1.5	7351	2	US-08-658-665-39	Sequence 39, Appl
c1185	35.6	1.5	43250	4	US-09-949-016-17171	Sequence 17171, A	1258	35.4	1.5	7351	3	US-08-796-101-3	Sequence 3, Appli
c1186	35.6	1.5	43253	4	US-09-949-016-15302	Sequence 15302, A	1259	35.4	1.5	7351	3	US-08-460-736-127	Sequence 127, App
c1187	35.6	1.5	51161	4	US-09-949-016-17416	Sequence 17416, A	1260	35.4	1.5	7351	3	US-09-085-273-39	Sequence 39, Appl
c1188	35.6	1.5	60376	4	US-09-949-016-12423	Sequence 12423, A	1261	35.4	1.5	7351	4	US-09-535-370-127	Sequence 127, App
c1189	35.6	1.5	82000	4	US-09-949-016-15595	Sequence 15595, A	1262	35.4	1.5	7351	4	US-09-916-963-39	Sequence 39, Appl
c1190	35.6	1.5	82612	4	US-09-949-016-16823	Sequence 16823, A	1263	35.4	1.5	7351	4	US-09-663-667-127	Sequence 127, App
c1191	35.6	1.5	84171	4	US-09-949-016-16356	Sequence 16356, A	c1264	35.4	1.5	9636	1	US-08-323-170B-1	Sequence 1, Appli
c1192	35.6	1.5	94830	4	US-09-949-016-12414	Sequence 12414, A	c1265	35.4	1.5	9636	3	US-08-954-441-1	Sequence 1, Appli
c1193	35.6	1.5	94847	4	US-09-949-016-16336	Sequence 16336, A	1266	35.4	1.5	27916	4	US-09-949-016-15202	Sequence 15202, A
c1194	35.6	1.5	108877	4	US-09-949-016-13276	Sequence 13276, A	1267	35.4	1.5	33529	4	US-09-949-016-12865	Sequence 12865, A
c1195	35.6	1.5	113060	4	US-09-949-016-14773	Sequence 14773, A	1268	35.4	1.5	33529	4	US-09-949-016-17364	Sequence 17364, A
c1196	35.6	1.5	113060	4	US-09-949-016-14774	Sequence 14774, A	c1269	35.4	1.5	36242	4	US-09-949-016-12996	Sequence 12996, A
c1197	35.6	1.5	137046	4	US-09-949-016-12427	Sequence 12427, A	c1270	35.4	1.5	36242	4	US-09-949-016-12997	Sequence 12997, A
c1198	35.6	1.5	137046	4	US-09-949-016-13438	Sequence 13438, A	c1271	35.4	1.5	36242	4	US-09-949-016-12998	Sequence 12998, A
c1199	35.6	1.5	142504	4	US-09-949-016-13693	Sequence 13693, A	c1272	35.4	1.5	36242	4	US-09-949-016-12999	Sequence 12999, A
c1200	35.6	1.5	142506	4	US-09-949-016-12474	Sequence 12474, A	c1273	35.4	1.5	36242	4	US-09-949-016-13000	Sequence 13000, A
c1201	35.6	1.5	145287	4	US-09-949-016-13530	Sequence 13530, A	c1274	35.4	1.5	38371	4	US-09-949-016-12061	Sequence 12061, A
c1202	35.6	1.5	145287	4	US-09-949-016-13531	Sequence 13531, A	c1275	35.4	1.5	38371	4	US-09-949-016-12488	Sequence 12488, A
c1203	35.6	1.5	148567	4	US-09-801-876B-3	Sequence 3, Appli	c1276	35.4	1.5	38371	4	US-09-949-016-15596	Sequence 15596, A
c1204	35.6	1.5	148567	4	US-10-254-869-3	Sequence 3, Appli	c1277	35.4	1.5	38371	4	US-09-949-016-15597	Sequence 15597, A
c1205	35.6	1.5	148567	4	US-10-667-442-3	Sequence 3, Appli	c1278	35.4	1.5	39937	4	US-09-949-016-16147	Sequence 16147, A
c1206	35.6	1.5	193169	4	US-09-949-016-15091	Sequence 15091, A	c1279	35.4	1.5	44439	4	US-09-949-016-17102	Sequence 17102, A
c1207	35.6	1.5	24286	4	US-09-949-016-15497	Sequence 15497, A	1280	35.4	1.5	45840	4	US-09-949-016-13903	Sequence 13903, A
c1208	35.6	1.5	254405	4	US-09-949-016-14381	Sequence 14381, A	1281	35.4	1.5	45840	4	US-09-949-016-15042	Sequence 15042, A
c1209	35.6	1.5	294836	4	US-09-949-016-15974	Sequence 15974, A	1282	35.4	1.5	46559	4	US-09-949-016-15043	Sequence 15043, A
c1210	35.6	1.5	385136	4	US-09-949-016-16073	Sequence 16073, A	c1283	35.4	1.5	54245	4	US-09-949-016-13499	Sequence 13499, A
c1211	35.6	1.5	670689	4	US-09-949-016-12505	Sequence 12505, A	1284	35.4	1.5	60002	4	US-09-949-016-12464	Sequence 12464, A
c1212	35.6	1.5	670690	4	US-09-949-016-14207	Sequence 14207, A	1285	35.4	1.5	60003	4	US-09-949-016-13843	Sequence 13843, A
c1213	35.4	1.5	601	4	US-09-949-016-65915	Sequence 65915, A	c1286	35.4	1.5	60003	4	US-09-949-016-15849	Sequence 15849, A
c1214	35.4	1.5	601	4	US-09-949-016-105996	Sequence 105996, A	c1287	35.4	1.5	68490	4	US-09-949-016-13313	Sequence 13313, A
c1215	35.4	1.5	601	4	US-09-949-016-145592	Sequence 145592, A	1288	35.4	1.5	75212	4	US-09-949-016-13314	Sequence 13314, A
c1216	35.4	1.5	601	4	US-09-949-016-145593	Sequence 145593, A	c1289	35.4	1.5	75212	4	US-09-949-016-13315	Sequence 13315, A
c1217	35.4	1.5	601	4	US-09-949-016-145594	Sequence 145594, A	c1290	35.4	1.5	84571	4	US-09-949-016-17420	Sequence 17420, A
c1218	35.4	1.5	601	4	US-09-949-016-157975	Sequence 157975, A	1291	35.4	1.5	85122	4	US-09-949-016-14693	Sequence 14693, A
c1219	35.4	1.5	601	4	US-09-949-016-179398	Sequence 179398, A	c1292	35.4	1.5	87523	4	US-09-949-016-12670	Sequence 12670, A
c1220	35.4	1.5	601	4	US-09-949-016-206449	Sequence 206449, A	1293	35.4	1.5	87523	4	US-09-949-016-15047	Sequence 15047, A
c1221	35.4	1.5	615	3	US-08-998-416-186	Sequence 186, App	c1294	35.4	1.5	87523	4	US-09-949-016-15048	Sequence 15048, A
c1222	35.4	1.5	724	3	US-08-998-416-683	Sequence 683, App	1295	35.4	1.5	87523	4	US-09-949-016-15049	Sequence 15049, A
c1223	35.4	1.5	940	1	US-08-448-600-2	Sequence 2, Appli	c1296	35.4	1.5	87869	4	US-09-949-016-11744	Sequence 11744, A

c1297	35.4	1.5	87869	4	US-09-949-016-15044	Sequence 15044, A	c1370	35.2	1.5	18788	4	US-09-949-016-17090	Sequence 17090, A
c1298	35.4	1.5	87869	4	US-09-949-016-15045	Sequence 15045, A	c1371	35.2	1.5	20935	4	US-09-949-016-15383	Sequence 15383, A
c1299	35.4	1.5	87869	4	US-09-949-016-15046	Sequence 15046, A	c1372	35.2	1.5	24508	4	US-09-949-016-16005	Sequence 16005, A
c1300	35.4	1.5	94879	4	US-09-949-016-12101	Sequence 12101, A	c1373	35.2	1.5	24519	4	US-09-949-016-11864	Sequence 11864, A
c1301	35.4	1.5	94880	4	US-09-949-016-13393	Sequence 13393, A	c1374	35.2	1.5	25512	4	US-09-949-016-15886	Sequence 15886, A
c1302	35.4	1.5	95890	4	US-09-949-016-16412	Sequence 16412, A	c1375	35.2	1.5	25512	4	US-09-949-016-15887	Sequence 15887, A
c1303	35.4	1.5	100836	4	US-09-949-016-12871	Sequence 12871, A	c1376	35.2	1.5	35380	4	US-09-949-016-11994	Sequence 11994, A
c1304	35.4	1.5	100837	4	US-09-949-016-12871	Sequence 12871, A	c1377	35.2	1.5	35380	4	US-09-949-016-13788	Sequence 13788, A
c1305	35.4	1.5	101894	4	US-09-949-016-12005	Sequence 12005, A	c1378	35.2	1.5	38702	4	US-09-949-016-13788	Sequence 13788, A
c1306	35.4	1.5	103894	4	US-09-949-016-14450	Sequence 14450, A	c1379	35.2	1.5	47883	4	US-09-949-016-11886	Sequence 11886, A
c1307	35.4	1.5	119214	4	US-09-949-016-12507	Sequence 12507, A	c1380	35.2	1.5	47883	4	US-09-949-016-17213	Sequence 17213, A
c1308	35.4	1.5	125192	4	US-09-949-016-14120	Sequence 14120, A	c1381	35.2	1.5	54161	4	US-09-949-016-11905	Sequence 11905, A
c1309	35.4	1.5	126254	4	US-09-949-016-15341	Sequence 15341, A	c1382	35.2	1.5	57392	4	US-09-949-016-12070	Sequence 12070, A
c1310	35.4	1.5	134434	4	US-09-949-016-17362	Sequence 17362, A	c1383	35.2	1.5	57402	4	US-09-949-016-13293	Sequence 13293, A
c1311	35.4	1.5	162450	3	US-09-945-882-1	Sequence 1, Appli	c1384	35.2	1.5	59948	4	US-09-949-016-15594	Sequence 15594, A
c1312	35.4	1.5	174493	4	US-09-804-471A-3	Sequence 3, Appli	c1385	35.2	1.5	67899	4	US-09-949-016-15432	Sequence 15432, A
c1313	35.4	1.5	174493	4	US-10-238-709-3	Sequence 3, Appli	c1386	35.2	1.5	67902	4	US-09-949-016-11870	Sequence 11870, A
c1314	35.4	1.5	174956	4	US-09-949-016-14382	Sequence 14382, A	c1387	35.2	1.5	95318	4	US-09-949-016-11784	Sequence 11784, A
c1315	35.4	1.5	192956	4	US-09-949-016-13675	Sequence 13675, A	c1388	35.2	1.5	95318	4	US-09-949-016-13998	Sequence 13998, A
c1316	35.4	1.5	235452	4	US-09-949-016-13675	Sequence 13675, A	c1389	35.2	1.5	103447	4	US-09-949-016-16320	Sequence 16320, A
c1317	35.4	1.5	237241	4	US-09-949-016-16101	Sequence 16101, A	c1390	35.2	1.5	103447	4	US-09-949-016-16320	Sequence 16320, A
c1318	35.4	1.5	312957	4	US-09-949-001-31	Sequence 31, Appl	c1391	35.2	1.5	129415	4	US-09-949-016-16369	Sequence 16369, A
c1319	35.4	1.5	312972	4	US-09-949-001-34	Sequence 34, Appl	c1392	35.2	1.5	136917	4	US-09-949-016-17030	Sequence 17030, A
c1320	35.4	1.5	1830121	4	US-09-557-884-1	Sequence 1, Appli	c1393	35.2	1.5	139049	4	US-09-949-016-16476	Sequence 16476, A
c1321	35.2	1.5	504	4	US-09-248-796A-3317	Sequence 3317, Ap	c1394	35.2	1.5	141560	4	US-09-949-016-15127	Sequence 15127, A
c1322	35.2	1.5	573	4	US-09-270-767-11606	Sequence 11606, A	c1395	35.2	1.5	145812	4	US-09-949-016-15698	Sequence 15698, A
c1323	35.2	1.5	601	4	US-09-949-016-18853	Sequence 18853, A	c1396	35.2	1.5	168575	3	US-09-426-290-1	Sequence 1, Appli
c1324	35.2	1.5	601	4	US-09-949-016-23163	Sequence 23163, A	c1397	35.2	1.5	190078	4	US-09-949-016-12707	Sequence 12707, A
c1325	35.2	1.5	601	4	US-09-949-016-39049	Sequence 39049, A	c1398	35.2	1.5	190078	4	US-09-949-016-17026	Sequence 17026, A
c1326	35.2	1.5	601	4	US-09-949-016-48180	Sequence 48180, A	c1399	35.2	1.5	202001	4	US-09-822-871-3	Sequence 3, Appli
c1327	35.2	1.5	601	4	US-09-949-016-48181	Sequence 48181, A	c1400	35.2	1.5	254366	4	US-09-949-016-12822	Sequence 12822, A
c1328	35.2	1.5	601	4	US-09-949-016-53598	Sequence 53598, A	c1401	35.2	1.5	256176	4	US-09-949-016-15524	Sequence 15524, A
c1329	35.2	1.5	601	4	US-09-949-016-56718	Sequence 56718, A	c1402	35.2	1.5	256176	4	US-09-949-016-13165	Sequence 13165, A
c1330	35.2	1.5	601	4	US-09-949-016-77239	Sequence 77239, A	c1403	35	1.5	346112	4	US-09-621-976-14088	Sequence 14088, A
c1331	35.2	1.5	601	4	US-09-949-016-77371	Sequence 77371, A	c1404	35	1.5	503	4	US-09-949-016-62003	Sequence 62003, A
c1332	35.2	1.5	601	4	US-09-949-016-87593	Sequence 87593, A	c1405	35	1.5	601	4	US-09-949-016-15524	Sequence 15524, A
c1333	35.2	1.5	601	4	US-09-949-016-93907	Sequence 93907, A	c1406	35	1.5	601	4	US-09-949-016-67921	Sequence 67921, A
c1334	35.2	1.5	601	4	US-09-949-016-12853	Sequence 12853, A	c1407	35	1.5	601	4	US-09-949-016-67922	Sequence 67922, A
c1335	35.2	1.5	601	4	US-09-949-016-134924	Sequence 134924, A	c1408	35	1.5	601	4	US-09-949-016-70250	Sequence 70250, A
c1336	35.2	1.5	601	4	US-09-949-016-162837	Sequence 162837, A	c1409	35	1.5	601	4	US-09-949-016-171661	Sequence 171661, A
c1337	35.2	1.5	601	4	US-09-949-016-162838	Sequence 162838, A	c1410	35	1.5	601	4	US-09-949-016-180665	Sequence 180665, A
c1338	35.2	1.5	601	4	US-09-949-016-168053	Sequence 168053, A	c1411	35	1.5	601	4	US-09-949-016-198587	Sequence 198587, A
c1339	35.2	1.5	601	4	US-09-949-016-168054	Sequence 168054, A	c1412	35	1.5	601	4	US-09-949-016-198588	Sequence 198588, A
c1340	35.2	1.5	601	4	US-09-949-016-168055	Sequence 168055, A	c1413	35	1.5	606	4	US-09-601-198-166	Sequence 166, App
c1341	35.2	1.5	601	4	US-09-949-016-168056	Sequence 168056, A	c1414	35	1.5	612	4	US-09-902-540-1357	Sequence 1357, Ap
c1342	35.2	1.5	601	4	US-09-949-016-187216	Sequence 187216, A	c1415	35	1.5	612	4	US-09-621-976-17640	Sequence 17640, A
c1343	35.2	1.5	601	4	US-09-949-001-304	Sequence 304, App	c1416	35	1.5	667	4	US-09-621-976-17640	Sequence 2499, Ap
c1344	35.2	1.5	601	4	US-09-949-001-742	Sequence 742, App	c1417	35	1.5	680	4	US-09-248-796A-2499	Sequence 4201, Ap
c1345	35.2	1.5	782	3	US-08-998-416-224	Sequence 224, App	c1418	35	1.5	807	4	US-09-248-796A-4201	Sequence 4201, Ap
c1346	35.2	1.5	1209	4	US-09-601-198-158	Sequence 158, App	c1419	35	1.5	1026	4	US-09-543-681A-3283	Sequence 3283, Ap
c1347	35.2	1.5	1374	4	US-09-601-198-158	Sequence 158, App	c1420	35	1.5	1314	4	US-09-248-796A-1709	Sequence 1709, Ap
c1348	35.2	1.5	1381	4	US-09-270-767-3258	Sequence 3258, Ap	c1421	35	1.5	1446	4	US-09-601-198-8	Sequence 8, Appli
c1349	35.2	1.5	1381	4	US-09-270-767-18540	Sequence 18540, A	c1422	35	1.5	1737	3	US-09-270-542-129	Sequence 129, App
c1350	35.2	1.5	1844	3	US-09-002-361-1	Sequence 1, Appli	c1423	35	1.5	1820	3	US-09-023-655-1031	Sequence 1031, Ap
c1351	35.2	1.5	1947	3	US-08-604-991-1	Sequence 1, Appli	c1424	35	1.5	1820	3	US-09-476-124-9	Sequence 9, Appli
c1352	35.2	1.5	1947	3	US-09-363-639-1	Sequence 1, Appli	c1425	35	1.5	1870	3	US-09-270-542-128	Sequence 128, App
c1353	35.2	1.5	2230	3	US-08-844-188-34	Sequence 34, Appl	c1426	35	1.5	1870	3	US-09-270-542-128	Sequence 5, Appli
c1354	35.2	1.5	2230	3	US-08-844-188-34	Sequence 34, Appl	c1427	35	1.5	2317	3	US-08-749-522-5	Sequence 5, Appli
c1355	35.2	1.5	2230	3	US-09-548-334A-34	Sequence 34, Appl	c1428	35	1.5	2454	1	US-08-359-696-3	Sequence 3, Appli
c1356	35.2	1.5	2230	4	US-09-547-621-34	Sequence 34, Appl	c1429	35	1.5	2718	4	US-09-667-135-1	Sequence 1, Appli
c1357	35.2	1.5	2230	4	US-09-643-596B-34	Sequence 34, Appl	c1430	35	1.5	2718	4	US-09-710-279-4239	Sequence 4239, Ap
c1358	35.2	1.5	2251	3	US-08-991-677-11	Sequence 11, Appl	c1431	35	1.5	3161	4	US-09-601-198-102	Sequence 102, App
c1359	35.2	1.5	2358	4	US-09-248-796A-10389	Sequence 10389, A	c1432	35	1.5	3168	4	US-09-710-279-1211	Sequence 1211, Ap
c1360	35.2	1.5	3095	6	5231168-1	Patent No. 5231168	c1433	35	1.5	3198	4	US-09-134-001C-963	Sequence 963, App
c1361	35.2	1.5	3095	6	5231168-1	Patent No. 5231168	c1434	35	1.5	3204	3	US-09-620-312D-658	Sequence 658, App
c1362	35.2	1.5	3307	4	US-09-949-016-5348	Sequence 5348, Ap	c1435	35	1.5	3483	4	US-09-620-312D-658	Sequence 3647, Ap
c1363	35.2	1.5	4117	4	US-09-949-016-252	Sequence 252, App	c1436	35	1.5	3647	4	US-09-710-279-3775	Sequence 3775, Ap
c1364	35.2	1.5	5555	1	US-08-494-438-3	Sequence 3, Appli	c1437	35	1.5	3714	3	US-08-467-504-3	Sequence 3, Appli
c1365	35.2	1.5	7480	4	US-09-949-016-11999	Sequence 11999, A	c1438	35	1.5	3974	3	US-09-949-016-14008	Sequence 14008, A
c1366	35.2	1.5	7567	4	US-09-949-016-16486	Sequence 16486, A	c1439	35	1.5	5650	4	US-09-213-053-1	Sequence 1, Appli
c1367	35.2	1.5	9636	1	US-08-323-170B-1	Sequence 1, Appli	c1440	35	1.5	6216	3	US-09-895-917A-2	Sequence 2, Appli
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ALIGNMENTS

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; Sequence 200, Application US/09907794A  
; Patent No. 6635468  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Deanoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; Sequence Match 100.0%; Score 2372; DB 4; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Math, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/907,794A  
; PRIOR FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 200  
; LENGTH: 2372  
; TYPE: DNA  
; ORGANISM: Homo sapiens

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RESULT 2

; Sequence 200, Application US/09905125A  
; Patent No. 6664376  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/905,125A  
; PRIORITY FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
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; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
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; PRIOR FILING DATE: 1999-12-02  
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; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20  
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; PRIOR FILING DATE: 1999-12-20  
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; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 200  
; LENGTH: 2372  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
  
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Best Local Similarity 100.0%; Pred. No. 0;  
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Qy 2041 TGTAATTTGAATATTTATTCCTCAAAAAATTCACATAGTAGAACGCTATCTGGGAAGCTAT 2100  
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Qy 2101 TTTTTCAGTTTGGATATTTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTCTGCTGA 2160  
Db 2101 TTTTTCAGTTTGGATATTTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTCTGCTGA 2160  
Qy 2161 GACTAATCTTATTCATTTCTCTAAATATGCAACCACTTATAAACCCTTAATTTATTTTAAAC 2220  
Db 2161 GACTAATCTTATTCATTTCTCTAAATATGCAACCACTTATAAACCCTTAATTTATTTTAAAC 2220  
Qy 2221 ATACCTAAGAAGTACATTTGTTTACCTCTATATACCAAGCACATTTTAAAAAGTCCCATTA 2280  
Db 2221 ATACCTAAGAAGTACATTTGTTTACCTCTATATACCAAGCACATTTTAAAAAGTCCCATTA 2280  
Qy 2281 CAAATGTATCAGTACGCTCTCTTTTCCCAACAAGAGGACTGAGAGATGCGAGAAATATT 2340  
Db 2281 CAAATGTATCAGTACGCTCTCTTTTCCCAACAAGAGGACTGAGAGATGCGAGAAATATT 2340  
Qy 2341 TGTGACAAAAAATTTAAAGCAATTTAGAAAACTT 2372  
Db 2341 TGTGACAAAAAATTTAAAGCAATTTAGAAAACTT 2372

RESULT 3

; Sequence 200, Application US/09902775A  
; Patent No. 6686451  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/902,775A  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594





Qy 1681 TCTCTGTAAGCTAAATAAAGAAATAGAACAGGCTGAGATACGACGTACACTGTCA 1740  
Db 1681 TCTCTGTAAGCTAAATAAAGAAATAGAACAGGCTGAGATACGACGTACACTGTCA 1740  
Qy 1741 GCAGGAGCTGTAACACAGACAGGCTCAAAAGTGTCTCTCTGAACACATTGAGTTGGAAT 1800  
Db 1741 GCAGGAGCTGTAACACAGACAGGCTCAAAAGTGTCTCTCTGAACACATTGAGTTGGAAT 1800  
Qy 1801 CACTGTTTAGAACACACACACTTACTTTTCTGCTCTCTACCACTGCTGATATTTCTCT 1860  
Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGCTCTCTACCACTGCTGATATTTCTCT 1860  
Qy 1861 AGGAATATATCTTTTCAAGTAACAAATAAATAAATCTTATAAATTTCTATTTTATCT 1920  
Db 1861 AGGAATATATCTTTTCAAGTAACAAATAAATAAATCTTATAAATTTCTATTTTATCT 1920  
Qy 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAAATTTGTTAAAAAGTAATAAAA 1980  
Db 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAAATTTGTTAAAAAGTAATAAAA 1980  
Qy 1981 TTCAACAAACATTGCTGTAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTTACACTC 2040  
Db 1981 TTCAACAAACATTGCTGTAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTTACACTC 2040  
Qy 2041 TGTAAATGAAATATTATTTCTCAAAAAATTTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100  
Db 2041 TGTAAATGAAATATTATTTCTCAAAAAATTTGCACATAGTAGAACGCTATCTGGGAAGCTAT 2100  
Qy 2101 TTTTTCAGTCTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTTTTTGTCTGA 2160  
Db 2101 TTTTTCAGTCTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTTTTTGTCTGA 2160  
Qy 2161 GACTAATCTTATTCATTTTCTCTAATATGGCAACATTATAACCTTAATTTATTTAATAC 2220  
Db 2161 GACTAATCTTATTCATTTTCTCTAATATGGCAACATTATAACCTTAATTTATTTAATAC 2220  
Qy 2221 ATACCTAAGAGTACATTGTTTACCTCTATATACAAAGACATTTTAAAAAGTGCCATTAA 2280  
Db 2221 ATACCTAAGAGTACATTGTTTACCTCTATATACAAAGACATTTTAAAAAGTGCCATTAA 2280  
Qy 2281 CAAATGTATCACTAGCCCTCTCTTTTCCAAAGAGGAGCTGAGAGATGAGAGAAATATT 2340  
Db 2281 CAAATGTATCACTAGCCCTCTCTTTTCCAAAGAGGAGCTGAGAGATGAGAGAAATATT 2340  
Qy 2341 TGTGACAAAAAATTAAGCATTTAGAAAACTT 2372  
Db 2341 TGTGACAAAAAATTAAGCATTTAGAAAACTT 2372

RESULT 4

; Sequence 200, Application US/09906700  
; Patent No. 6723535  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Borstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/906,700  
; CURRENT FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,598  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 200  
; LENGTH: 2372  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
Query Match 100.0%; Score 2372; DB 4; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AGCAGGGAATCCGGATGTCTCGGTTATGAAGTGGACGAGTGTGAGCTCAACATA 60  
Db 1 AGCAGGGAATCCGGATGTCTCGGTTATGAAGTGGACGAGTGTGAGCTCAACATA 60  
Qy 61 GTTCCAGAACTCTCCATCCCGACTAGTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120  
Db 61 GTTCCAGAACTCTCCATCCCGACTAGTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120  
Qy 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTCTTCAGGCTG 180  
Db 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTCTTCAGGCTG 180  
Qy 181 GTGTTGCTTCTCACTTCCATCTGGACCAACGAGGCTCTGTGTCACCAAGGCTCTTTCCGTGCA 240  
Db 181 GTGTTGCTTCTCACTTCCATCTGGACCAACGAGGCTCTGTGTCACCAAGGCTCTTTCCGTGCA 240  
Qy 241 GAAGAGCTTTCCATCCAGGTGTCTATGAGAAATTATGGGATCACCTTTGTGAGCAAAAAG 300  
Db 241 GAAGAGCTTTCCATCCAGGTGTCTATGAGAAATTATGGGATCACCTTTGTGAGCAAAAAG 300



Db 241 GAAGAGCTTTCCATCCAGGTGTCAGCAGAAATTATGGGGATCACCCCTGTGAGCAAAAAG 300  
Qy 301 GCGAACCCAGAGCTGAATTTTACAGAAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGT 360  
Db 301 GCGAACCCAGAGCTGAATTTTACAGAAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGT 360  
Qy 361 TTGGCCGCGCAGGACCAAGTTGAAACAGCCCTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420  
Db 361 TTGGCCGCGCAGGACCAAGTTGAAACAGCCCTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420  
Qy 421 GGCTGGGTGGAGATGGATTCGTGTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGG 480  
Db 421 GGCTGGGTGGAGATGGATTCGTGTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGG 480  
Qy 481 AAAAAATGGGTGGGTGTCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCCTAT 540  
Db 481 AAAAAATGGGTGGGTGTCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCCTAT 540  
Qy 541 TGTGTACAACTCATCTGTACTTGGACTAACTCGTGCATTTCCAGAAATTTATCACCACCAAA 600  
Db 541 TGTGTACAACTCATCTGTACTTGGACTAACTCGTGCATTTCCAGAAATTTATCACCACCAAA 600  
Qy 601 GATCCCATATTTCAACACTCAAACTGCAACACAAACACAGAAATTTATTTGTCAGTGACAGT 660  
Db 601 GATCCCATATTTCAACACTCAAACTGCAACACAAACACAGAAATTTATTTGTCAGTGACAGT 660  
Qy 661 ACCTACTCGGTGGATCCCTTTACTCTACAATACCTGCCCTACTACTCTCTCTCTCTCT 720  
Db 661 ACCTACTCGGTGGATCCCTTTACTCTACAATACCTGCCCTACTACTCTCTCTCTCTCTCT 720  
Qy 721 CCAGCTTCCACTTCTATTTCCAGGAGAAAAAATTTGATTGTGTACAGAAATTTTATG 780  
Db 721 CCAGCTTCCACTTCTATTTCCAGGAGAAAAAATTTGATTGTGTACAGAAATTTTATG 780  
Qy 781 GAAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAATTAAGCAGCATTTCAAG 840  
Db 781 GAAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAATTAAGCAGCATTTCAAG 840  
Qy 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGTCTCTCTCTCTCT 900  
Db 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGTCTCTCTCTCTCT 900  
Qy 901 TTTGGTGTGAGCTGGTCTTGGATTTTGTCTATGTCAAAAGGTATGTGAAGGCTTCCCT 960  
Db 901 TTTGGTGTGAGCTGGTCTTGGATTTTGTCTATGTCAAAAGGTATGTGAAGGCTTCCCT 960  
Qy 961 TTTTCAAAACAGAAATCAGCAGAGGAAATGATGCAAAACCAAGTAGTAAAGGAGGAGAG 1020  
Db 961 TTTTCAAAACAGAAATCAGCAGAGGAAATGATGCAAAACCAAGTAGTAAAGGAGGAGAG 1020  
Qy 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAAACTGATAAAAAACCCAGAGAGTCC 1080  
Db 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAAACTGATAAAAAACCCAGAGAGTCC 1080  
Qy 1081 AAGAGTCAAGCAAAACTACCGTGGATGCTGGAAGCTGGAAGCTGGAAGCTTGAAGAGAGAA 1140  
Db 1081 AAGAGTCAAGCAAAACTACCGTGGATGCTGGAAGCTGGAAGCTGGAAGCTTGAAGAGAGAA 1140  
Qy 1141 TGAGGAGACACCTGAGGCTGGTTCTTTCATGCTCCTTACCTGCTCCCGCCAGCTGGGGAA 1200  
Db 1141 TGAGGAGACACCTGAGGCTGGTTCTTTCATGCTCCTTACCTGCTCCCGCCAGCTGGGGAA 1200  
Qy 1201 ATCAAAAGGGCAAGAACCAAGAGAAAGTCCACCCCTGGTTCCCTAACTGGAATCAGC 1260  
Db 1201 ATCAAAAGGGCAAGAACCAAGAGAAAGTCCACCCCTGGTTCCCTAACTGGAATCAGC 1260  
Qy 1261 TCAGGACTGCGCATTTGGACTATGGAGTGCAACAAAGAGATGCGCCTTCTCTTTATGTAAAC 1320  
Db 1261 TCAGGACTGCGCATTTGGACTATGGAGTGCAACAAAGAGATGCGCCTTCTCTTTATGTAAAC 1320  
Qy 1321 CCTGCTGGATCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380  
Db 1321 CCTGCTGGATCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380

RESULT 5  
; Sequence 200, Application US/09903603A  
; Patent No. 6767995

Qy 1381 GTCCCTAATAATATCCCACTGGGAGAAAAGGAGTTTTCGAAAGTGCAGAGACCTTAAACATC 1440  
Db 1381 GTCCCTAATAATATCCCACTGGGAGAAAAGGAGTTTTCGAAAGTGCAGAGACCTTAAACATC 1440  
Qy 1441 TCATCAGTATCCAGTGGTAAAGAGCCCTCTGGGTGCTGTAGGCTAGGTGGTTCGAAAGC 1500  
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Db 1501 CAAGGAGTCACTGAGAGCAACAGGCTTTCTCTACTGATTTCCGAGAGCTCAGACCCCTTCTTCA 1560  
Qy 1561 GCTCTGAAGAGAAACACGATATCCACCTGACATGTCTTCTGAGCCCGGTAAAGACAAA 1620  
Db 1561 GCTCTGAAGAGAAACACGATATCCACCTGACATGTCTTCTGAGCCCGGTAAAGACAAA 1620  
Qy 1621 AGAATGCGAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680  
Db 1621 AGAATGCGAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA 1680  
Qy 1681 TCTCTGTAAGAGTAAAAATAGAAATAGAAACAAAGGCTGAGGATACGACAGTACACTGTCA 1740  
Db 1681 TCTCTGTAAGAGTAAAAATAGAAATAGAAACAAAGGCTGAGGATACGACAGTACACTGTCA 1740  
Qy 1741 GCAGGAGTGTAAACACAGACAGGGTCAAAAGTGTCTTCTGAAACACATTCAGTTGGAAT 1800  
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Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGCTCTACCACTGCTGATATTTCTCTCT 1860  
Qy 1861 AGGAAATATACCTTTTCAAGTAACAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1920  
Db 1861 AGGAAATATACCTTTTCAAGTAACAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1920  
Qy 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAAATAAAA 1980  
Db 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAAATAAAA 1980  
Qy 1981 TTCAGCAAACTTTGCTGTAATAGTACTATATGTCAAGTGTGTCGCAAGGTATTACACTC 2040  
Db 1981 TTCAGCAAACTTTGCTGTAATAGTACTATATGTCAAGTGTGTCGCAAGGTATTACACTC 2040  
Qy 2041 TGTAATTTGAATATTTATTTCTCAAAATAAGTACATAGTAGAACGCTATCTGGGAAGCTAT 2100  
Db 2041 TGTAATTTGAATATTTATTTCTCAAAATAAGTACATAGTAGAACGCTATCTGGGAAGCTAT 2100  
Qy 2101 TTTTCTCAGTTTGTGATATTTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTGTCTGA 2160  
Db 2101 TTTTCTCAGTTTGTGATATTTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTGTCTGA 2160  
Qy 2161 GACTAATCTTATTTCTTCTTAATATGGCAACATTATTAACCTTAAATTTATTTATTAAC 2220  
Db 2161 GACTAATCTTATTTCTTCTTAATATGGCAACATTATTAACCTTAAATTTATTTATTAAC 2220  
Qy 2221 ATACCTAAGAGTACATTTGTTTACCTCTATATACCAAGACACATTTTAAAGTGGCATTAA 2280  
Db 2221 ATACCTAAGAGTACATTTGTTTACCTCTATATACCAAGACACATTTTAAAGTGGCATTAA 2280  
Qy 2281 CAAATGTATCAGTACCCCTCTTTTCCAAAGAGGAGCTGAGAGATGAGAGATGAGAGATTT 2340  
Db 2281 CAAATGTATCAGTACCCCTCTTTTCCAAAGAGGAGCTGAGAGATGAGAGATGAGAGATTT 2340  
Qy 2341 TGTGACAAAAAATTAAGCATTTAGAAAACTT 2372  
Db 2341 TGTGACAAAAAATTAAGCATTTAGAAAACTT 2372

GENERAL INFORMATION:		Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
; APPLICANT: Genentech, Inc.		Qy	1	AGCAGGAAATCCGGATGTCCTCGTTATGAAGTGGAGCAGTGAAGTGGAGCCTCAACATA	60
; APPLICANT: Ashkenazi, Avi		Db	1	AGCAGGAAATCCGGATGTCCTCGTTATGAAGTGGAGCAGTGAAGTGGAGCCTCAACATA	60
; APPLICANT: Botstein, David		Qy	61	GTTCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTCCCTCTCATATCACCAGTGGC	120
; APPLICANT: Desnoyers, Luc		Db	61	GTTCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTCCCTCTCATATCACCAGTGGC	120
; APPLICANT: Eaton, Dan L.		Qy	121	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGACGATGCCAGGTCTTCAGCCTG	180
; APPLICANT: Ferrara, Napoleone		Db	121	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGACGATGCCAGGTCTTCAGCCTG	180
; APPLICANT: Fillaroff, Ellen		Qy	181	GTGTTGCTTCTCACTTCCATCTGGACACAGAGCTCTGTCCTCAAGGCTCTTTCGCTGCA	240
; APPLICANT: Fong, Sherman		Db	181	GTGTTGCTTCTCACTTCCATCTGGACACAGAGCTCTGTCCTCAAGGCTCTTTCGCTGCA	240
; APPLICANT: Gao, Wei-Qiang		Qy	241	GAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTTATGGGATCACCTTTGTGAGCAAAAG	300
; APPLICANT: Gerber, Hanspeter		Db	241	GAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTTATGGGATCACCTTTGTGAGCAAAAG	300
; APPLICANT: Gerritsen, Mary E.		Qy	301	GCAGACAGCAGCTGAATTTACAGAACTAAGAGGCTGTAGGCTGGGACTAAGT	360
; APPLICANT: Goddard, A.		Db	301	GCAGACAGCAGCTGAATTTACAGAACTAAGAGGCTGTAGGCTGGGACTAAGT	360
; APPLICANT: Godowski, Paul J.		Qy	361	TTGGCCGGCAAGCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTCGAGCTAT	420
; APPLICANT: Grimaldi, Christopher J.		Db	361	TTGGCCGGCAAGCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTCGAGCTAT	420
; APPLICANT: Gurney, Austin L.		Qy	421	GGCTGGTTGGAGATGGATTCGTGGTCACTCTAGGATTAGCCCAACCCCAAGTGTGGG	480
; APPLICANT: Hillan, Kenneth, J.		Db	421	GGCTGGTTGGAGATGGATTCGTGGTCACTCTAGGATTAGCCCAACCCCAAGTGTGGG	480
; APPLICANT: KJavin, Ivar J.		Qy	481	AAAAATGGGTGGGTGTCTGTGATTTGGAGGTTCCAGTGGCGACAGATTTGAGCCTAT	540
; APPLICANT: Mather, Jennie P.		Db	481	AAAAATGGGTGGGTGTCTGTGATTTGGAGGTTCCAGTGGCGACAGATTTGAGCCTAT	540
; APPLICANT: Pan, James		Qy	541	TGTTACAACTCATCTGATCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT	600
; APPLICANT: Paoni, Nicholas F.		Db	541	TGTTACAACTCATCTGATCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT	600
; APPLICANT: Roy, Margaret Ann		Qy	601	GATCCCATATTTCAACACTCAAACTGCAACAAACAAACAGAAATTTATGTCAGTGACAGT	660
; APPLICANT: Stewart, Timothy A.		Db	601	GATCCCATATTTCAACACTCAAACTGCAACAAACAAACAGAAATTTATGTCAGTGACAGT	660
; APPLICANT: Tumas, Daniel		Qy	661	ACCTACTCGGTGGATCCCTTACTCTAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	720
; APPLICANT: Williams, P. Mickey		Db	661	ACCTACTCGGTGGATCCCTTACTCTAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	720
; APPLICANT: Wood, William, I.		Qy	721	CCAGCTTCCACTTCTATTTCCACGGAGAAAAATTTGATTTGTCACAGAAATTTTATG	780
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic		Db	721	CCAGCTTCCACTTCTATTTCCACGGAGAAAAATTTGATTTGTCACAGAAATTTTATG	780
; TITLE OF INVENTION: Acids Encoding the Same		Qy	781	GAACCTAGCACCATGTCTACAGAAACTGAACTGTTGTTGAAATAAAGCAGCATTTCAAG	840
; FILE REFERENCE: GNE.1618P2C12		Db	781	GAACCTAGCACCATGTCTACAGAAACTGAACTGTTGTTGAAATAAAGCAGCATTTCAAG	840
; CURRENT APPLICATION NUMBER: US/09/903,603A		Qy	841	AATGAAGCTGCTGGGTTTGAGGTGCTCCACGGCTCTGCTAGTGTGCTGCTGCTGCTGCT	900
; CURRENT FILING DATE: 2001-07-11		Db	841	AATGAAGCTGCTGGGTTTGAGGTGCTCCACGGCTCTGCTAGTGTGCTGCTGCTGCTGCT	900
; PRIOR APPLICATION NUMBER: PCT/US00/04414		Qy	901	TTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	960
; PRIOR FILING DATE: 2000-02-22		Db	901	TTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	960
; PRIOR APPLICATION NUMBER: US 60/143,048		Qy	961	TTTACAAAACAGAAATCAGCAGAGAGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAAG	1020
; PRIOR FILING DATE: 1999-07-07		Db	961	TTTACAAAACAGAAATCAGCAGAGAGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAAG	1020
; PRIOR APPLICATION NUMBER: US 60/145,698		Qy	1021	GCCAAATGATAGCAACCTTAATAGGAAATCAAGAAACTGATATAAAACCCAGAGAGTCC	1080
; PRIOR FILING DATE: 1999-07-26		Db	1021	GCCAAATGATAGCAACCTTAATAGGAAATCAAGAAACTGATATAAAACCCAGAGAGTCC	1080
; PRIOR APPLICATION NUMBER: US 60/146,222					
; PRIOR FILING DATE: 1999-07-28					
; PRIOR APPLICATION NUMBER: PCT/US99/20594					
; PRIOR FILING DATE: 1999-09-08					
; PRIOR APPLICATION NUMBER: PCT/US99/20944					
; PRIOR FILING DATE: 1999-09-13					
; PRIOR APPLICATION NUMBER: PCT/US99/21090					
; PRIOR FILING DATE: 1999-09-15					
; PRIOR APPLICATION NUMBER: PCT/US99/21547					
; PRIOR FILING DATE: 1999-09-15					
; PRIOR APPLICATION NUMBER: PCT/US99/23089					
; PRIOR FILING DATE: 1999-10-05					
; PRIOR APPLICATION NUMBER: PCT/US99/28214					
; PRIOR FILING DATE: 1999-11-29					
; PRIOR APPLICATION NUMBER: PCT/US99/28313					
; PRIOR FILING DATE: 1999-11-30					
; PRIOR APPLICATION NUMBER: PCT/US99/28564					
; PRIOR FILING DATE: 1999-12-02					
; PRIOR APPLICATION NUMBER: PCT/US99/28565					
; PRIOR FILING DATE: 1999-12-02					
; PRIOR APPLICATION NUMBER: PCT/US99/30095					
; PRIOR FILING DATE: 1999-12-16					
; PRIOR APPLICATION NUMBER: PCT/US99/30911					
; PRIOR FILING DATE: 1999-12-20					
; PRIOR APPLICATION NUMBER: PCT/US99/30999					
; PRIOR FILING DATE: 1999-12-20					
; PRIOR APPLICATION NUMBER: PCT/US00/00219					
; PRIOR FILING DATE: 2000-01-05					
; NUMBER OF SEQ ID NOS: 423					
; SEQ ID NO 200					
; LENGTH: 2372					
; TYPE: DNA					
; ORGANISM: Homo sapiens					
Query Match		100.0%;		Score 2372; DB 4; Length 2372;	
Best Local Similarity		100.0%;		Pred. No. 0;	

Qy 1081 AAGAGTCAAGCAAAACTACCGTGGATGCTCTGAGCTGAAGTTTAGATGAGACAGAAA 1140  
Db 1081 AAGAGTCAAGCAAAACTACCGTGGATGCTCTGAGCTGAAGTTTAGATGAGACAGAAA 1140  
Qy 1141 TGAGGAGACACACCTGAGGCTGGTTCTTTTCATGCTCCTTACCTGCCCCAGCTGGGGAA 1200  
Db 1141 TGAGGAGACACACCTGAGGCTGGTTCTTTTCATGCTCCTTACCTGCCCCAGCTGGGGAA 1200  
Qy 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCCTGGTTCTTAACTGGGAATCAGC 1260  
Db 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCCTGGTTCTTAACTGGGAATCAGC 1260  
Qy 1261 TCAGGACTGCCATTTGGACTATGAGGTGCACCAAGAGAAATGCCCTTCTCCTTTATGTAAAC 1320  
Db 1261 TCAGGACTGCCATTTGGACTATGAGGTGCACCAAGAGAAATGCCCTTCTCCTTTATGTAAAC 1320  
Qy 1321 CCTGTCTGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380  
Db 1321 CCTGTCTGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380  
Qy 1381 GTCTCTAATAATATCCACTGGGAGAAAGGAGTTTTCGAAAGTGAAGGACCTAAACATC 1440  
Db 1381 GTCTCTAATAATATCCACTGGGAGAAAGGAGTTTTCGAAAGTGAAGGACCTAAACATC 1440  
Qy 1441 TCATCAGTATCCAGTGTAAAAGGCCCTCTGGCTGTCTGAGGCTAGTGGTGTGAAGC 1500  
Db 1441 TCATCAGTATCCAGTGTAAAAGGCCCTCTGGCTGTCTGAGGCTAGTGGTGTGAAGC 1500  
Qy 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATCTCCGAGCTCAGACCTTCTTCA 1560  
Db 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATCTCCGAGCTCAGACCTTCTTCA 1560  
Qy 1561 GCTCTGAAGAGAAACACGTATCCACCTGACATGTCTCTCTGAGCCGGTAAAGCAAA 1620  
Db 1561 GCTCTGAAGAGAAACACGTATCCACCTGACATGTCTCTCTGAGCCGGTAAAGCAAA 1620  
Qy 1621 AGAATGGCAGAAAAGTTTGGCCCTGAAGCCATGGAGATTTCTCATACCTTGAGACCTAA 1680  
Db 1621 AGAATGGCAGAAAAGTTTGGCCCTGAAGCCATGGAGATTTCTCATACCTTGAGACCTAA 1680  
Qy 1681 TCTCTGTAAGCTTAAATAAAGAAATAGAACAAGCTGAGGATACGACAGTACACTGTCA 1740  
Db 1681 TCTCTGTAAGCTTAAATAAAGAAATAGAACAAGCTGAGGATACGACAGTACACTGTCA 1740  
Qy 1741 GCAGGAGCTGTAAACACAGACAGGCTCAAAGTGTCTCTCTGAACACATTTGAGTTGGAAT 1800  
Db 1741 GCAGGAGCTGTAAACACAGACAGGCTCAAAGTGTCTCTCTGAACACATTTGAGTTGGAAT 1800  
Qy 1801 CACTGTTTAGAACACACACACTTACTTTTCTGCTCTCTACCACTGCTGTATTTTCTCT 1860  
Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGCTCTCTACCACTGCTGTATTTTCTCT 1860  
Qy 1861 AGGAAATATCTTTTACAGTAACAAAATAAAGTCTTATAATTTCTATTTTCTATCT 1920  
Db 1861 AGGAAATATCTTTTACAGTAACAAAATAAAGTCTTATAATTTCTATTTTCTATCT 1920  
Qy 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAAATAAA 1980  
Db 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAAATAAA 1980  
Qy 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTAATTTACACTC 2040  
Db 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTAATTTACACTC 2040  
Qy 2041 TGTAAATGAATATTTCTCTCAAAAATTTGACATAGTAGAACCTATCTGGGAGCTAT 2100  
Db 2041 TGTAAATGAATATTTCTCTCAAAAATTTGACATAGTAGAACCTATCTGGGAGCTAT 2100  
Qy 2101 TTTTTCAGTTTTCATATTTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTGTCTGA 2160  
Db 2101 TTTTTCAGTTTTCATATTTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTGTCTGA 2160

RESULT 6

; Sequence 200, Application US/09904920A  
; Patent No. 6806352  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas P.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/904,920A  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30

Qy 2161 GACTAATCTTATTCAATTTTCTCTAATATGCAACCATTAACCTTAATTTATTATTAAAC 2220  
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Qy 2221 ATACCTAAGAAGTACATTTGTTTACCTCTATATACCAAGGACATTTTAAAAAGTGCCATTAA 2280  
Db 2221 ATACCTAAGAAGTACATTTGTTTACCTCTATATACCAAGGACATTTTAAAAAGTGCCATTAA 2280  
Qy 2281 CAAATGTATCACTAGCCCTCTCTTTTCCAAAGGAGGACTGAGAGATGCAGAAATATT 2340  
Db 2281 CAAATGTATCACTAGCCCTCTCTTTTCCAAAGGAGGACTGAGAGATGCAGAAATATT 2340  
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Db 2341 TGTGACAAAAAATTAAGCATTTAGAAAACTT 2372

; PRIOR APPLICATION NUMBER: PCT/US99/28564									
; PRIOR FILING DATE: 1999-12-02									
; PRIOR APPLICATION NUMBER: PCT/US99/28565									
; PRIOR FILING DATE: 1999-12-02									
; PRIOR APPLICATION NUMBER: PCT/US99/30095									
; PRIOR FILING DATE: 1999-12-16									
; PRIOR APPLICATION NUMBER: PCT/US99/30911									
; PRIOR FILING DATE: 1999-12-20									
; PRIOR APPLICATION NUMBER: PCT/US99/30999									
; PRIOR FILING DATE: 1999-12-20									
; PRIOR APPLICATION NUMBER: PCT/US00/00219									
; PRIOR FILING DATE: 2000-01-05									
; NUMBER OF SEQ ID NOS: 423									
; SEQ ID NO 200									
; LENGTH: 2372									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
Query Match 100.0%; Score 2372; DB 4; Length 2372;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	AGCAGGAAATCCGATGTCTCGGTATGAAGTGGACGAGTGAGTGGACCTCAACATA	60						
Db	1	AGCAGGAAATCCGATGTCTCGGTATGAAGTGGACGAGTGAGTGGACCTCAACATA	60						
Qy	61	GTTCAGAACTCTCCATCCGACTAGTATTGAGCATCTGCCCTCATATCACCAGTGGC	120						
Db	61	GTTCAGAACTCTCCATCCGAGCTAGTATTGAGCATCTGCCCTCATATCACCAGTGGC	120						
Qy	121	CATCTGAGGTGTTTCCCTCGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGGCTG	180						
Db	121	CATCTGAGGTGTTTCCCTCGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGGCTG	180						
Qy	181	GTGTGCTTCTCACTTCCATCTGACCAACGAGGCTCTGGTCAAAGGCTCTTTGCGTGCA	240						
Db	181	GTGTGCTTCTCACTTCCATCTGACCAACGAGGCTCTGGTCAAAGGCTCTTTGCGTGCA	240						
Qy	241	GAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGGATCACCTTGTGACCAAAAG	300						
Db	241	GAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGGATCACCTTGTGACCAAAAG	300						
Qy	301	GCGAACCAAGCAGCTGAATTTACAGAAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGT	360						
Db	301	GCGAACCAAGCAGCTGAATTTACAGAAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGT	360						
Qy	361	TTGCCGGCAAGGACCAAGCTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420						
Db	361	TTGCCGGCAAGGACCAAGCTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTAT	420						
Qy	421	GGCTGGGTGGAGATGGAATCGTGGTCACTCTAGGATTAGCCAAACCCCAAGTGTGGG	480						
Db	421	GGCTGGGTGGAGATGGAATCGTGGTCACTCTAGGATTAGCCAAACCCCAAGTGTGGG	480						
Qy	481	AAAAATGGGTGGGTGCTGCTGATTGGAAGGTTCCAGTGAGCCGACAGATTTGACGCCCTAT	540						
Db	481	AAAAATGGGTGGGTGCTGCTGATTGGAAGGTTCCAGTGAGCCGACAGATTTGACGCCCTAT	540						
Qy	541	TGTTAACACTCATCTGATACCTTACTCTACAACTGCAATTCGTCGATTTCCAGAAATATCACCAAAA	600						
Db	541	TGTTAACACTCATCTGATACCTTACTCTACAACTGCAATTCGTCGATTTCCAGAAATATCACCAAAA	600						
Qy	601	GATCCCAATTTCAACACTCAAACTGCAACCAACACAGAAATTTATTGTGTCAGTGACAGT	660						
Db	601	GATCCCAATTTCAACACTCAAACTGCAACCAACACAGAAATTTATTGTGTCAGTGACAGT	660						
Qy	661	ACCTACTCGGTGGCATCCCTTACTCTACAACTGCAATTCGTCGATTTCCAGAAATATCACCAAAA	720						
Db	661	ACCTACTCGGTGGCATCCCTTACTCTACAACTGCAATTCGTCGATTTCCAGAAATATCACCAAAA	720						
Qy	721	CCAGCTTCCACTTCTATTTCCACGAGAAAAAATTTGATTTGTGTACAGAAATTTTATG	780						
Db	721	CCAGCTTCCACTTCTATTTCCACGAGAAAAAATTTGATTTGTGTACAGAAATTTTATG	780						

Qy	781	GAAACTAGCACCATGTCTACAGAAACTGAACCAATTTGTTGAAATAAAGCAGCATTC	840
Db	781	GAAACTAGCACCATGTCTACAGAAACTGAACCAATTTGTTGAAATAAAGCAGCATTC	840
Qy	841	AATGAAGCTGCTGGGTTTGAGAGTGTCCCCACACGGCTCTGCTAGTGTCTCTCTTC	900
Db	841	AATGAAGCTGCTGGGTTTGAGAGTGTCCCCACACGGCTCTGCTAGTGTCTCTCTTC	900
Qy	901	TTTGGTGTGACGCTGGTCTTGGAATTTTGCTATGTCAAAGGATGTGAAGGCTTC	960
Db	901	TTTGGTGTGACGCTGGTCTTGGAATTTTGCTATGTCAAAGGATGTGAAGGCTTC	960
Qy	961	TTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACCAAAGTGTAAAGGAGGAGA	1020
Db	961	TTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACCAAAGTGTAAAGGAGGAGA	1020
Qy	1021	GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACCTGATAAAACCCAGAGAGTCC	1080
Db	1021	GCCAATGATAGCAACCCCTAATGAGGAATCAAAGAAACCTGATAAAACCCAGAGAGTCC	1080
Qy	1081	AGAGTCCAAAGCAAAACCTACCGTGCATGCTCGAAGCTGAAAGTTAGATGACACAGAAA	1140
Db	1081	AGAGTCCAAAGCAAAACCTACCGTGCATGCTCGAAGCTGAAAGTTAGATGACACAGAAA	1140
Qy	1141	TGAGGAGACACACTCGAGGCTGGTCTTTTCATGCTCTTACCTGCCCCAGCTGGGGAA	1200
Db	1141	TGAGGAGACACACTCGAGGCTGGTCTTTTCATGCTCTTACCTGCCCCAGCTGGGGAA	1200
Qy	1201	ATCAAAGGGSCCAAGAACCAAAAGAAAGTAGTCACCTTTGGTTCCTAACTGGAATCAGC	1260
Db	1201	ATCAAAGGGSCCAAGAACCAAAAGAAAGTAGTCACCTTTGGTTCCTAACTGGAATCAGC	1260
Qy	1261	TCAGGACTGCCATTTGAACTATGAGTGCACCAAGAGATGCCCTTCTCTTATTTGTAAC	1320
Db	1261	TCAGGACTGCCATTTGAACTATGAGTGCACCAAGAGATGCCCTTCTCTTATTTGTAAC	1320
Qy	1321	CCTGTCTGGATCCTATCTCTACCTCCAAAGCTTCCACGGCTTTCTAGACCTGGGTAT	1380
Db	1321	CCTGTCTGGATCCTATCTCTACCTCCAAAGCTTCCACGGCTTTCTAGACCTGGGTAT	1380
Qy	1381	GTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGGAAAGTCAAGGACCTAAACATC	1440
Db	1381	GTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGGAAAGTCAAGGACCTAAACATC	1440
Qy	1441	TCATCAGTATCCAGTGGTAAAAAGGCTCTCTGCTGTCTCAGGCTAGGTGGTTGAAAGC	1500
Db	1441	TCATCAGTATCCAGTGGTAAAAAGGCTCTCTGCTGTCTCAGGCTAGGTGGTTGAAAGC	1500
Qy	1501	CAAGGAGTCACTCAGACCAAGGCTTTCTCTACTGATTCCGAGCTCAGACCTTCTTCA	1560
Db	1501	CAAGGAGTCACTCAGACCAAGGCTTTCTCTACTGATTCCGAGCTCAGACCTTCTTCA	1560
Qy	1561	GCTCTGAAGAGAAACACGATCCCACTGACATGTCCTTTCTGAGCCGGTAAAGCAAA	1620
Db	1561	GCTCTGAAGAGAAACACGATCCCACTGACATGTCCTTTCTGAGCCGGTAAAGCAAA	1620
Qy	1621	AGATGCGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1680
Db	1621	AGATGCGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1680
Qy	1681	TCTCTGTAAAGCTTAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGCA	1740
Db	1681	TCTCTGTAAAGCTTAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGCA	1740
Qy	1741	GCAGGAGCTGTAAACACAGACAGGCTCAAAAGTGTCTCTGAACACATTTAGTTGGAAT	1800
Db	1741	GCAGGAGCTGTAAACACAGACAGGCTCAAAAGTGTCTCTGAACACATTTAGTTGGAAT	1800
Qy	1801	CACGTGTTAGAACACACACTTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1860
Db	1801	CACGTGTTAGAACACACACTTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1860

Qy	1861	AGGAAATATAC	TTTTTAC	AGGTAA	CAAAAAA	TAAAAA	CTCTTAT	AAAAAT	TTCTTAT	TTTTTAT	CT	1920	
Db	1861	AGGAAATATAC	TTTTTAC	AGGTAA	CAAAAAA	TAAAAA	CTCTTAT	AAAAAT	TTCTTAT	TTTTTAT	CT	1920	
Qy	1921	GAGTTACAGAAA	TGATTTACT	AAAGGAAG	TACTCAG	TAAATTTG	TTTTAAAA	AGTAATA	AAAA			1980	
Db	1921	GAGTTACAGAAA	TGATTTACT	AAAGGAAG	TACTCAG	TAAATTTG	TTTTAAAA	AGTAATA	AAAA			1980	
Qy	1981	TTCAACAAAA	CATTTGCTG	GAATAG	CTACTATAT	GTCAAG	TGCTGTG	CAAGGTAT	TACACTC			2040	
Db	1981	TTCAACAAAA	CATTTGCTG	GAATAG	CTACTATAT	GTCAAG	TGCTGTG	CAAGGTAT	TACACTC			2040	
Qy	2041	TGTAATTTGAAT	TATTTATTTCC	TCAAAAAA	TTGCACAT	AGTAAAG	CGCTATCT	TGGGAAG	CGTAT			2100	
Db	2041	TGTAATTTGAAT	TATTTATTTCC	TCAAAAAA	TTGCACAT	AGTAAAG	CGCTATCT	TGGGAAG	CGTAT			2100	
Qy	2101	TTTTTT	CAGTTTTG	ATATTTCT	AGTCTAT	CTATCTT	TCCAAAC	CTAATTTT	TATTTT	TGCTGA		2160	
Db	2101	TTTTTT	CAGTTTTG	ATATTTCT	AGTCTAT	CTATCTT	TCCAAAC	CTAATTTT	TATTTT	TGCTGA		2160	
Qy	2161	GACTAA	TCTTTAT	CATTTTCT	TAAATG	CCAAC	CAATTA	TAAAC	CTTAATTT	TATTTAT	TAAAC	2220	
Db	2161	GACTAA	TCTTTAT	CATTTTCT	TAAATG	CCAAC	CAATTA	TAAAC	CTTAATTT	TATTTAT	TAAAC	2220	
Qy	2221	ATACCT	TAAGAAG	TACATTTG	TTTAC	CTCTAT	ATATAC	CAAAAG	CACTTTT	AAAAAG	TGCCATTAA	2280	
Db	2221	ATACCT	TAAGAAG	TACATTTG	TTTAC	CTCTAT	ATATAC	CAAAAG	CACTTTT	AAAAAG	TGCCATTAA	2280	
Qy	2281	CAAA	TGAT	CACAT	AGCCCTC	CTTTTT	TCCAC	AGAAG	GGGACT	GAGAG	TGCAGAA	TATT	2340
Db	2281	CAAA	TGAT	CACAT	AGCCCTC	CTTTTT	TCCAC	AGAAG	GGGACT	GAGAG	TGCAGAA	TATT	2340
Qy	2341	TGTGAC	AAAAA	TTTAA	AGCATTT	TAGAAAA	CTTT					2372	
Db	2341	TGTGAC	AAAAA	TTTAA	AGCATTT	TAGAAAA	CTTT					2372	

## RESULT 7

Sequence 200, Application US/09909064  
Patent No. 6818449  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/909,064  
CURRENT FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22

:	PRIOR APPLICATION NUMBER:	US 60/143,048
:	PRIOR FILING DATE:	1999-07-07
:	PRIOR APPLICATION NUMBER:	US 60/145,698
:	PRIOR FILING DATE:	1999-07-26
:	PRIOR APPLICATION NUMBER:	US 60/146,222
:	PRIOR FILING DATE:	1999-07-28
:	PRIOR APPLICATION NUMBER:	PCT/US99/20594
:	PRIOR FILING DATE:	1999-09-08
:	PRIOR APPLICATION NUMBER:	PCT/US99/20944
:	PRIOR FILING DATE:	1999-09-13
:	PRIOR APPLICATION NUMBER:	PCT/US99/21090
:	PRIOR FILING DATE:	1999-09-15
:	PRIOR APPLICATION NUMBER:	PCT/US99/21547
:	PRIOR FILING DATE:	1999-09-15
:	PRIOR APPLICATION NUMBER:	PCT/US99/23089
:	PRIOR FILING DATE:	1999-10-05
:	PRIOR APPLICATION NUMBER:	PCT/US99/28214
:	PRIOR FILING DATE:	1999-11-29
:	PRIOR APPLICATION NUMBER:	PCT/US99/28313
:	PRIOR FILING DATE:	1999-11-30
:	PRIOR APPLICATION NUMBER:	PCT/US99/28564
:	PRIOR FILING DATE:	1999-12-02
:	PRIOR APPLICATION NUMBER:	PCT/US99/28565
:	PRIOR FILING DATE:	1999-12-02
:	PRIOR APPLICATION NUMBER:	PCT/US99/30095
:	PRIOR FILING DATE:	1999-12-16
:	PRIOR APPLICATION NUMBER:	PCT/US99/30911
:	PRIOR FILING DATE:	1999-12-20
:	PRIOR APPLICATION NUMBER:	PCT/US99/30999
:	PRIOR FILING DATE:	1999-12-20
:	PRIOR APPLICATION NUMBER:	PCT/US00/00219
:	PRIOR FILING DATE:	2000-01-05
:	NUMBER OF SEQ ID NOS:	423
:	SEQ ID NO 200	
:	LENGTH:	2372
:	TYPE:	DNA
:	ORGANISM:	Homo sapiens
Query Match                  100.0%;      Score 2372;      DB 4;      Length 2372;		
Best Local Similarity       100.0%;      Pred No. 0;		
Matches 2372; Conservative     0; Mismatches     0; Indels     0; Gaps     0;		
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DB	1	AGCAGGGAAATCCGGATGTC TCGGTTTATGAAGTGAGCAGTAGTGAGCCTCAACATA 60
QY	61	GTTCCAGAAGCTCCCATCCGAGTAGTTATTGAGCATCTGCCTCTCATATCACAGTGGC 120
DB	61	GTTCCAGAAGCTCCCATCCGAGTAGTTATTGAGCATCTGCCTCTCATATCACAGTGGC 120
QY	121	CATCTCAGGTGTTTTCCCTCGCTCTGAAGGGTAGGCCACCATGSCCAGGTGCTTTCAGCCTG 180
DB	121	CATCTCAGGTGTTTTCCCTCGCTCTGAAGGGTAGGCCACCATGSCCAGGTGCTTTCAGCCTG 180
QY	181	GTGTTGCTTCTCACTTCCATCTGGACCAGCAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
DB	181	GTGTTGCTTCTCACTTCCATCTGGACCAGCAGGCTCCTGGTCCAAGGCTCTTTGCGTGCA 240
QY	241	GAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGGATCACCCCTGTGAGCAAAAAG 300
DB	241	GAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGGATCACCCCTGTGAGCAAAAAG 300
QY	301	GGCAACCCAGCAGTGAATTTACAGAAAGCTAAGGAGGCTGTAGGCTCTGGGACTTAAGT 360
DB	301	GGCAACCCAGCAGTGAATTTACAGAAAGCTAAGGAGGCTGTAGGCTCTGGGACTTAAGT 360
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DB	361	TTGGCCGGCAAGGACCAAAGTTGAAAACAGCCTTGAAAGCTAGCTTTGAAACTTTGCAGCTAT 420
QY	421	GGCTGGGTTGGAGATGGATTTCTGTGGTFCATCTCTAGGATTAGCCCCAACCCCAAGTGTGGG 480
DB	421	GGCTGGGTTGGAGATGGATTTCTGTGGTFCATCTCTAGGATTAGCCCCAACCCCAAGTGTGGG 480

Qy 481 AAAAAATGGGTGGGTGCTGATTTGGAAGGTTCCAGTGAGCGGACAGTTTGGAGCCTAT 540  
Db 481 AAAAAATGGGTGGGTGCTGATTTGGAAGGTTCCAGTGAGCGGACAGTTTGGAGCCTAT 540  
Qy 541 TGTTCACAACTCATCTGATACCTTGACCTAACTCGTGCAATTCAGAAAATATCACCACCAAA 600  
Db 541 TGTTCACAACTCATCTGATACCTTGACCTAACTCGTGCAATTCAGAAAATATCACCACCAAA 600  
Qy 601 GATCCCATATTCACAACTCAAACTGCAACACAAACAAAGAAATTTATGTCAGTGACAGT 660  
Db 601 GATCCCATATTCACAACTCAAACTGCAACACAAACAAAGAAATTTATGTCAGTGACAGT 660  
Qy 661 ACCTACTCGGTGGGCATCCCTTACTCTACAACTACCTGCCCTACTACTCTCCCTGCT 720  
Db 661 ACCTACTCGGTGGGCATCCCTTACTCTACAACTACCTGCCCTACTACTCTCCCTGCT 720  
Qy 721 CCAGCTTCCACTTCTATTTCCACGGAGAAAATTTGATTTGTGTCACAGAAATTTTATG 780  
Db 721 CCAGCTTCCACTTCTATTTCCACGGAGAAAATTTGATTTGTGTCACAGAAATTTTATG 780  
Qy 781 GAAACTAGCACCATGCTACAGAACTGAACCATTTGTTGAAATTAAGCAGCATTCGAG 840  
Db 781 GAAACTAGCACCATGCTACAGAACTGAACCATTTGTTGAAATTAAGCAGCATTCGAG 840  
Qy 841 AATGAAGCTGCTGGTGGTGGAGGTGTCGCCACGGCTCTGCTAGTGCTTCTCCTCTTC 900  
Db 841 AATGAAGCTGCTGGTGGTGGAGGTGTCGCCACGGCTCTGCTAGTGCTTCTCCTCTTC 900  
Qy 901 TTTGGTGTGCTGAGCTGGTCTTGGATTTTGGCTATGTCACAAAGGTATGTGAAGGCTTCCCT 960  
Db 901 TTTGGTGTGCTGAGCTGGTCTTGGATTTTGGCTATGTCACAAAGGTATGTGAAGGCTTCCCT 960  
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Db 961 TTTACAAACAGAAATACAGAGAGAAATGATCGAAACCAAAGTAGTAAAGGAGGAAG 1020  
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Db 1021 GCCAATGATAGCAACCTAATGAGGAATCAAGAAAATGATAAACCAGAGAGGTCC 1080  
Qy 1081 AAGAGTCCAAGCAAACTACCGTGGATGCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140  
Db 1081 AAGAGTCCAAGCAAACTACCGTGGATGCTGGAAGCTGAAGTTTAGATGAGACAGAAA 1140  
Qy 1141 TGAGGAGACACCTGAGGCTGGTTCTTCATGCTCTTACCTGCCCGCCAGCTGGGGAA 1200  
Db 1141 TGAGGAGACACCTGAGGCTGGTTCTTCATGCTCTTACCTGCCCGCCAGCTGGGGAA 1200  
Qy 1201 ATCAAAAGGGCCAAAGAACCAAGAAAGTCCACACCTTGGTTCTTAACCTGGAATCAGC 1260  
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Qy 1381 GTCTCTAATATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGAAGGACCTAAACATC 1440  
Db 1381 GTCTCTAATATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGAAGGACCTAAACATC 1440  
Qy 1441 TCATCAGTATCCAGTGGTAAAAAGGCTTCTCGCTGTCTGAGGCTAGTGGGTTGAAAGC 1500  
Db 1441 TCATCAGTATCCAGTGGTAAAAAGGCTTCTCGCTGTCTGAGGCTAGTGGGTTGAAAGC 1500  
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Db 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGGAGCTCAGACCTTCTTCA 1560

Qy 1561 GCTCTGAAAGAGAAAAACACGTATCCACCTGACATGCTCTCTGAGCCCGGTGAAGACAAA 1620  
Db 1561 GCTCTGAAAGAGAAAAACACGTATCCACCTGACATGCTCTCTGAGCCCGGTGAAGACAAA 1620  
Qy 1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTTGAGACCTAA 1680  
Db 1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTTGAGACCTAA 1680  
Qy 1681 TCTCTGTAAAGCTAAATTAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA 1740  
Db 1681 TCTCTGTAAAGCTAAATTAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA 1740  
Qy 1741 GCAGGAGCTCTAAACACAGACAGGCTCAAAAGTGTCTCTGAAACACATTTGAGTTGGAAT 1800  
Db 1741 GCAGGAGCTCTAAACACAGACAGGCTCAAAAGTGTCTCTGAAACACATTTGAGTTGGAAT 1800  
Qy 1801 CACTGTTTAGAACACACACTTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860  
Db 1801 CACTGTTTAGAACACACACTTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT 1860  
Qy 1861 AGGAAATATACCTTTTACAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920  
Db 1861 AGGAAATATACCTTTTACAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920  
Qy 1921 GAGTTACAGAAATGATTTACTTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980  
Db 1921 GAGTTACAGAAATGATTTACTTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980  
Qy 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCGAAGTCTGTGCAAGGTATTACACTC 2040  
Db 1981 TTCAACAAACATTTGCTGAATAGCTACTATATGTCGAAGTCTGTGCAAGGTATTACACTC 2040  
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Db 2041 TGTAAATGAATATTTCTTCAAAAATTTGCACATAGTAGAAACGCTATCTGGGAAGCTAT 2100  
Qy 2101 TTTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTGTCTGA 2160  
Db 2101 TTTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAAACTAAATTTTATTTTGTCTGA 2160  
Qy 2161 GACTAATCTTATTTCTTCTTAATATGGAACCAATATTAACCTTTAATTTTATTTAAAC 2220  
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Qy 2221 ATACCTAAGAGTACATTTGTTACCTCTATATACCAAGACATTTTAAAAAGTGCCATTAA 2280  
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Qy 2281 CAAATGTATCACTAGCCCTCTTTTTTCCAAACAAAGAGGGACTGAGAGATCGAGAAATATT 2340  
Db 2281 CAAATGTATCACTAGCCCTCTTTTTTCCAAACAAAGAGGGACTGAGAGATCGAGAAATATT 2340  
Qy 2341 TGTGACAAAAAATTAAGCAATTTAGAAAACTT 2372  
Db 2341 TGTGACAAAAAATTAAGCAATTTAGAAAACTT 2372

RESULT 8  
; Sequence 200, Application US/09905381A  
; Patent No. 6818746  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.		181	GTGTTGCTTCTCACTTCCATCTGGACCAACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGA	240
; APPLICANT: Grimaldi, Christopher J.		Qy		
; APPLICANT: Gurney, Austin L.		181	GTGTTGCTTCTCACTTCCATCTGGACCAACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGA	240
; APPLICANT: Hillan, Kenneth J.		Db		
; APPLICANT: Kljavin, Ivar J.		241	GAAGAGCTTTCCATCCAGGCTGTCATGAGAGCTTATGGGATCACCCTTGTGAGCAAAAAG	300
; APPLICANT: Math, Jennie P.		Qy		
; APPLICANT: Pan, James		241	GAAGAGCTTTCCATCCAGGCTGTCATGAGAGCTTATGGGATCACCCTTGTGAGCAAAAAG	300
; APPLICANT: Paoni, Nicholas F.		Qy		
; APPLICANT: Roy, Margaret Ann		301	CGGAAACAGAGCTGAAATTTTACAGAGAGCTTAAAGAGGCTCTAGGCTCTGGGACTAAGT	360
; APPLICANT: Stewart, Timothy A.		Qy		
; APPLICANT: Tumas, Daniel		301	CGGAAACAGAGCTGAAATTTTACAGAGAGCTTAAAGAGGCTCTAGGCTCTGGGACTAAGT	360
; APPLICANT: Williams, P. Mickey		361	TTGCGCGGCAAGGACCAAGTTGAAACAGCTTGAAGAGCTAGCTTTGAAACTTGCAGCTAT	420
; APPLICANT: Wood, William, I.		Qy		
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic		361	TTGCGCGGCAAGGACCAAGTTGAAACAGCTTGAAGAGCTAGCTTTGAAACTTGCAGCTAT	420
; TITLE OF INVENTION: Acids Encoding the Same		Qy		
; FILE REFERENCE: 10466-14		421	GGCTGGCTTGGAGATGGAATTCGCTGATCTCTAGGATTTAGCCCAAAACCCCAAGTGTGG	480
; CURRENT APPLICATION NUMBER: US/09/905,381A		421	GGCTGGCTTGGAGATGGAATTCGCTGATCTCTAGGATTTAGCCCAAAACCCCAAGTGTGG	480
; PRIOR FILING DATE: 2001-07-13		Qy		
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; PRIOR FILING DATE: 1999-07-07		Qy		
; PRIOR APPLICATION NUMBER: US 60/145,698		541	TGTTTCAACTCATCTGATACCTTGGACTAAGTTCGTCGATTTCCAGAAATTTATCACCACCAA	600
; PRIOR FILING DATE: 1999-07-26		Qy		
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; PRIOR APPLICATION NUMBER: PCT/US99/28214		721	CCAGCTTCCACTTCTATTCCACGGAGAAAAATTTGATTTGTGTGTCACAGAAAGTTTATG	780
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; PRIOR APPLICATION NUMBER: PCT/US99/28313		781	GAACTAGCACCATCTCTACAGAACTGAAACCTTTGTTGAAAAATTAAGCAGCATTCAAG	840
; PRIOR FILING DATE: 1999-11-30		Qy		
; PRIOR APPLICATION NUMBER: PCT/US99/28564		781	GAACTAGCACCATCTCTACAGAACTGAAACCTTTGTTGAAAAATTAAGCAGCATTCAAG	840
; PRIOR FILING DATE: 1999-12-02		Qy		
; PRIOR APPLICATION NUMBER: PCT/US99/28565		841	AATGAAGCTGCTGGGTTTGGAGGTGTCACACGGCTCTGCTAGTGTGCTCTCTCTCTCTTC	900
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; PRIOR APPLICATION NUMBER: PCT/US99/30095		841	AATGAAGCTGCTGGGTTTGGAGGTGTCACACGGCTCTGCTAGTGTGCTCTCTCTCTCTTC	900
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; PRIOR APPLICATION NUMBER: PCT/US99/30911		901	TTTGGTCTGCTGAGCTGCTTTGGATTTTGTCTATGTCAAAAAGGTTATGTAAGGCTTCCCT	960
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; PRIOR APPLICATION NUMBER: PCT/US99/30999		901	TTTGGTCTGCTGAGCTGCTTTGGATTTTGTCTATGTCAAAAAGGTTATGTAAGGCTTCCCT	960
; PRIOR FILING DATE: 1999-12-20		Qy		
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; PRIOR FILING DATE: 2000-01-05		Qy		
; NUMBER OF SEQ ID NOS: 423		961	TTTACAAAACAGATCAGCAGAGGAAATGATGAAAACCAAGTAGTAAAGGAGGAGAG	1020
; SEQ ID NO 200		1021	GCCATCATAGCAACCTTAATAGGAATCAAGAAAACTGATAAAAAACCCAGAGAGTCC	1080
; LENGTH: 2372		1021	GCCATCATAGCAACCTTAATAGGAATCAAGAAAACTGATAAAAAACCCAGAGAGTCC	1080
; TYPE: DNA		1081	AAGAGTCCAAAGCAAACTACCGTGCATGCTGGAAGCTGAAAGTTTATGATGAGACAGAAA	1140
; ORGANISM: Homo sapiens		1081	AAGAGTCCAAAGCAAACTACCGTGCATGCTGGAAGCTGAAAGTTTATGATGAGACAGAAA	1140
Query Match		1141	AGAGTCCAAAGCAAACTACCGTGCATGCTGGAAGCTGAAAGTTTATGATGAGACAGAAA	1200
Best Local Similarity		1141	AGAGTCCAAAGCAAACTACCGTGCATGCTGGAAGCTGAAAGTTTATGATGAGACAGAAA	1200
Matches 2372; Conservative		1201	ATCAAAAGGGCCAAAGAAACCAAGAAAGTCCACCTTGGTTTCTTAACCTGGAATCAGC	1260
Query		1201	ATCAAAAGGGCCAAAGAAACCAAGAAAGTCCACCTTGGTTTCTTAACCTGGAATCAGC	1260
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Qy		121	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGGCTG	180
Db		121	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGGCTG	180

Query Match		100.0%	Score 2372;	DB 4;	Length 2372;
Best Local Similarity		100.0%	Pred. No. 0;		
Matches 2372; Conservative		0;	Mismatches	0;	Gaps 0;
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Qy		61	GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGC	120	
Db		61	GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGC	120	
Qy		121	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGGCTG	180	
Db		121	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGGCTG	180	



Qy 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAATGCCCTTCTCCTTATTGTAAAC 1320  
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Qy 1261 TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAATGCCCTTCTCCTTATTGTAAAC 1320  
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Qy 1321 CTTGCTGGATCTTATCTCTCTACCTCAAAGCTTCCACGGCCCTTTCTAGCCCTGGCTAT 1380  
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Qy 1381 GTCTTAATATATATCCCACTGGAGAAAAGGATTTTGCAAGTGCACGAGCTAAACATC 1440  
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Qy 1381 GTCTTAATATATATCCCACTGGAGAAAAGGATTTTGCAAGTGCACGAGCTAAACATC 1440  
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Qy 1441 TCATCAGTATCCAGTGGTGAAGAGCCCTCTCGGCTGTCTGAGGCTAGGTGGTGAAGC 1500  
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Qy 1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTTCCGAGCTCAGACCTTCTTCA 1560  
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Qy 1801 CACTGTTTAGAACACACACACTTACTTTTCTGCTCTCTACCACTGCTGATATTTCTCT 1860  
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Qy 1861 AGGAAATATATCTTTTACAAGTAAACAAATAAACTCTTATAAAATTTCTATTTTATCT 1920  
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Qy 1921 GAGTTACAGAATGATTACTAAGGAGATTAAGTAAATTTGTTTAAAGTAAATAAAA 1980  
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Qy 2161 GACTAATCTTATTTCTTAATATGGCAACATTAATACCTTAATTTATTTATTAAC 2220  
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Qy 2281 CAAATGTATCACTAGCCCTCTTTTCCAAAGAGGACTGAGAGATGCGAGAAATATT 2340  
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RESULT 9  
; Sequence 200, Application US/09906618  
; Patent No. 6828146  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/906,618  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423



				Query Match				100.0%; Score 2372; DB 4; Length 2372;			
				Best Local Similarity 100.0%; Pred. No. 0;							
				Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
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Db	1	AGCAGGGAATCCGGATGTC	60	Db	961	TTTACAAACAAGATCAGCAGAGGAATGATCGAAACCAAGTAGTAAAGGAGGAGAG	1020				
Qy	61	GTTCAGAACTCTCCATCCGACTAGTTATTTAGAGCATCTGCCTCTCATATCACAGTGGC	120	Qy	1021	GCCAATGATAGCAACCTTAATGAGGAATCAAGAAACTGATATAAAACCCAGAAAGTCC	1080				
Db	61	GTTCAGAACTCTCCATCCGACTAGTTATTTAGAGCATCTGCCTCTCATATCACAGTGGC	120	Db	1021	GCCAATGATAGCAACCTTAATGAGGAATCAAGAAACTGATATAAAACCCAGAAAGTCC	1080				
Qy	121	CATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGCAGATGGCCAGGTGCTTCAGCCTG	180	Qy	1081	AAGAGTCCAAGCAAAACTACCGTGCATGCTGGAAGCTGAAGTTTAGATGAGACAGAAA	1140				
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Db	241	GAAGAGCTTTCCATCAGGTGTCAGAGAAATTTATGGGGATCACCTTTGTGAGCAAAAAG	300	Db	1201	ATCAAAAGGGCCAAAGAACCAAGAAAGTCCACCTTGGTTCTTAACTGGGAATCAGC	1260				
Qy	301	GGGAACACGACCTGAATTTACAGAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGT	360	Qy	1261	TCAGGACTGCCAATTTGGACTATGGAGTGCAACAAAGAGAAATGCCCTTCTCTTATTGTAAC	1320				
Db	301	GGGAACACGACCTGAATTTACAGAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGT	360	Db	1261	TCAGGACTGCCAATTTGGACTATGGAGTGCAACAAAGAGAAATGCCCTTCTCTTATTGTAAC	1320				
Qy	361	TTGGCGGCAAGGACCAAGTTGAAACAGCTTTGAAAGCTAGCTTTGAAACTTTGACAGCTAT	420	Qy	1321	CCTGTCTGGATCTTATCCTCTACTCTCCAAAGCTTCCACGGCTTTCTTAGCCTGGCTAT	1380				
Db	361	TTGGCGGCAAGGACCAAGTTGAAACAGCTTTGAAAGCTAGCTTTGAAACTTTGACAGCTAT	420	Db	1321	CCTGTCTGGATCTTATCCTCTACTCTCCAAAGCTTCCACGGCTTTCTTAGCCTGGCTAT	1380				
Qy	421	GGCTGGTGGAGATGGATTCGTGTCTATCTTAGGATTTAGCCCAAAACCCCAAGTGTGGG	480	Qy	1381	GTCTCTAATAATATCCCACTGGGAGAAAGGAGTGTTCGAAAGTGCNAGGCTTAAACAATC	1440				
Db	421	GGCTGGTGGAGATGGATTCGTGTCTATCTTAGGATTTAGCCCAAAACCCCAAGTGTGGG	480	Db	1381	GTCTCTAATAATATCCCACTGGGAGAAAGGAGTGTTCGAAAGTGCNAGGCTTAAACAATC	1440				
Qy	481	AAAAATGGGGTGGTCTGATTTTGAAGGTTCCAGTGAGCGGACAGTTTGCAGCCTAT	540	Qy	1441	TCATCAGTATCCAGTGGTAAAGAGCCCTCTCGGCTGTCTGAGGCTAGTGGTGTGAAAGC	1500				
Db	481	AAAAATGGGGTGGTCTGATTTTGAAGGTTCCAGTGAGCGGACAGTTTGCAGCCTAT	540	Db	1441	TCATCAGTATCCAGTGGTAAAGAGCCCTCTCGGCTGTCTGAGGCTAGTGGTGTGAAAGC	1500				
Qy	541	TGTTACAACTCATCTGATCTTGGACTAACTCGTGCAATTCAGAAATTTATCACCAACAA	600	Qy	1501	CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCTTTCTTCA	1560				
Db	541	TGTTACAACTCATCTGATCTTGGACTAACTCGTGCAATTCAGAAATTTATCACCAACAA	600	Db	1501	CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCTTTCTTCA	1560				
Qy	601	GATCCCATATTCAACACTCAAACTGCAACACAAACAGAAATTTATGTCAGTGACAGT	660	Qy	1561	GCTCTGAAAGAGAAACAGTATCCACCTGACATGCTCTTCTGAGCCCGGTAAAGAGCAAA	1620				
Db	601	GATCCCATATTCAACACTCAAACTGCAACACAAACAGAAATTTATGTCAGTGACAGT	660	Db	1561	GCTCTGAAAGAGAAACAGTATCCACCTGACATGCTCTTCTGAGCCCGGTAAAGAGCAAA	1620				
Qy	661	ACCTACTCGGTGGCATCCCTTACTCTCAATATACCTGCGCCCTACTACTCTCTCTGCT	720	Qy	1621	AGAAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTTCTCATAACTTGAGACCTAA	1680				
Db	661	ACCTACTCGGTGGCATCCCTTACTCTCAATATACCTGCGCCCTACTACTCTCTCTGCT	720	Db	1621	AGAAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTTCTCATAACTTGAGACCTAA	1680				
Qy	721	CCAGCTTCCACTTCTATTCCAGGAGAAAAATTTGATTTGTGTCACAGAAATTTTATG	780	Qy	1681	TCTCTGTAAGCTAAAAATAGAAATAGAAACAGGCTGAGGATACGACAGTACACTGTCA	1740				
Db	721	CCAGCTTCCACTTCTATTCCAGGAGAAAAATTTGATTTGTGTCACAGAAATTTTATG	780	Db	1681	TCTCTGTAAGCTAAAAATAGAAATAGAAACAGGCTGAGGATACGACAGTACACTGTCA	1740				
Qy	781	GAACCTAGCAATGCTGTACAGAACTGAACCAATTTGTTGAAATTAAGAGCAGATTCAG	840	Qy	1741	GCAGGAGCTGTAACACAGACAGGCTCAAGTGTCTCTGAAACACATTTGAGTTGGAAT	1800				
Db	781	GAACCTAGCAATGCTGTACAGAACTGAACCAATTTGTTGAAATTAAGAGCAGATTCAG	840	Db	1741	GCAGGAGCTGTAACACAGACAGGCTCAAGTGTCTCTGAAACACATTTGAGTTGGAAT	1800				
Qy	841	AATGAAGCTGCTGGGTTGGAGGTGTCACAGGCTGCTGCTGCTGCTGCTGCTGCTGCT	900	Qy	1801	CAGTGTTAGAACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT	1860				
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Qy	901	TTTGTGCTGACGCTGGTCTTGGATTTTGTATGTCAAAAGGTAATGTAAGGCTTCCCT	960	Qy	1861	AGGAAATATCTTTTACAAGTAACAAAAATTAATAAATTTCTATTTTATCT	1920				
Db	901	TTTGTGCTGACGCTGGTCTTGGATTTTGTATGTCAAAAGGTAATGTAAGGCTTCCCT	960	Db	1861	AGGAAATATCTTTTACAAGTAACAAAAATTAATAAATTTCTATTTTATCT	1920				



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Qy 1809 AGAACACACACACTTACTTTTCTGCTCTCTACCACTGCTGATATTTTCTTAGGAATA 1868
Db 1741 AGAACACACACACTTACTTTTCTGCTCTCTACCACTGCTGATATTTTCTTAGGAATA 1800
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Db 1801 TACTTTTCAAGTAAACAAATAAATAAATCTTTATAAATTTCTATTTTATCTGAGTTACA 1860
Qy 1929 GAAATGATTAAGAGAGATTAATCACTAGTAATTTGTTTAAAGTAATAAATAAATCAACAA 1988
Db 1861 GAAATGATTAAGAGAGATTAATCACTAGTAATTTGTTTAAAGTAATAAATAAATCAACAA 1920
Qy 1989 ACATTTGCTGAATAGTACTATATCTCAAGTCTGCAAGTATTAACACTCTGTAATTG 2048
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Qy 2049 AATATTATTTCTCAAAAAATGACATAGTAGAAGCTATCTGGGAAGCTATTTTTTTTCA 2108
Db 1981 AATATTATTTCTCAAAAAATGACATAGTAGAAGCTATCTGGGAAGCTATTTTTTTTCA 2040
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Db 2281 AAAATTAAGCATTTAGAAA 2301
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## RESULT 11

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US-08-892-880-1
; Sequence 1, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
```

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; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNES, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HERewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2113 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..1056
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 154..1056
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 91..153
; US-08-892-880-1
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Query Match 96.6%; Score 2290.2; DB 2; Length 2313;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2292; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 6 CATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGTGTTT 65
Qy 135 CCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGTGGCTTACGCTGGTGTGCTTCTCAC 194
Db 66 CCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGTGGCTTACGCTGGTGTGCTTCTCAC 125
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Db 246 GAATTTACAGAGACCTTAAGAGGCTCTAGGCTCTGGGACTAAGTTTGGCCGCAAGGA 305
Qy 375 CCAAGTTGAAACAGCCTTTGAAAGCTAGCTTTGAAACTTTGCAAGCTATGCTGGTGGGAGA 434
Db 306 CCAAGTTGAAACAGCCTTTGAAAGCTAGCTTTGCAAGCTATGCTGGTGGGTTGGCGA 365
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Qy 435 TGGATTGCTGTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGG 494  
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Qy 495 TGTCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACATCATC 554  
Db 426 TGTCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACATCATC 485  
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Db 486 TGATACCTTGGACTAACTCGTCATTTCCAGAAATTTATCACCAACCAAGATCCCATATTCAA 545  
Qy 615 CACTCAAACTGCAACACAAACAAAGATTTATTGTGTCAGTGACAGTACTACTCGGTGGC 674  
Db 546 CACTCAAACTGCAACACAAACAAAGATTTATTGTGTCAGTGACAGTACTACTCGGTGGC 605  
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Db 606 ATCCCTTACTCTACATACCTGCGCTTACTACTCTCTCTGTCAGCTTCCACTTC 665  
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Db 726 GTCTACAGAACTGAACCATTTGTTGAAAAATAAAGCAGCATTTCAAGAAATGAAGCTGTGG 785  
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Qy 1155 TGAGGCTGGTTTCTTTTCATGCTCCTTACCCTGCCCCAGCTGGGAAATCAAAAGGGCCAA 1214  
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Db 1146 AGAACCAAGAGAAAGTCCACCTTGTTCCTTAACCTGGAATCAGCTCAGGACTGCCATTT 1205  
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Db 1266 ATCTCTCTACCTCCAAAGCTTCCACGGCCCTTTCTAGCCTGGCTATGTCCTTAATAATATC 1325  
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Db 1446 GACCAAGGCTTTCTTACTGATTTCCGAGCTCAGACCTTTCTTTCAGCTCTGAAAGAGAA 1505  
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Db 1506 ACAGGTATCCACCTGACATGTCTTCTGAGCCCGGTAAAGAGCAAAAAGATGCGAGAAA 1565  
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Db 1566 GTTTAGCCCTGAAAGCCATGGAGATTCTCAATCTTGAGACCTTAATCTCTGTAAAGCTA 1625  
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Db 1626 AAATAAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTACAGAGGACTGTAAA 1685  
Qy 1755 CACAGCAGGCTCAAGTGTCTCTGAAACATTTGAGTTGGAATCAGCTGTTTAGAAC 1814  
Db 1686 CACAGCAGGCTCAAGTGTCTCTGAAACATTTGAGTTGGAATCAGCTGTTTAGAAC 1745  
Qy 1815 CACACACTTACTTTTCTGCTCTACACCTGCTGATATTTTCTTAGGAAATATATCTTT 1874  
Db 1746 CACACACTTACTTTTCTGCTCTACACCTGCTGATATTTTCTTAGGAAATATATCTTT 1805  
Qy 1875 TACAAGTAAACAAAATAAAAACTCTTATAAATTTCTATTTTATCTGAGTTACAGAAATG 1934  
Db 1806 TACAAGTAAACAAAATAAAAACTCTTATAAATTTCTATTTTATCTGAGTTACAGAAATG 1865  
Qy 1935 ATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAAATAAATTCACAAACATTT 1994  
Db 1866 ATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAAATAAATTCACAAACATTT 1925  
Qy 1995 GCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTCTGTAAATGGAATTT 2054  
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Db 1986 ATTCTCTCAAAAAATGTCATATAGTAGAAGCGCTATCTGGGAAGCTATTTTTTTCAGTTTTG 2045  
Qy 2115 ATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGTCTGAGACTAATCTTATTC 2174  
Db 2046 ATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGTCTGAGACTAATCTTATTC 2105  
Qy 2175 ATTTTCTCTAATATGCAACCAATTAACCTTAATTTATTTATTAACATACCTAAGAAAGTA 2234  
Db 2106 ATTTTCTCTAATATGCAACCAATTAACCTTAATTTATTTATTAACATACCTAAGAAAGTA 2165  
Qy 2235 CATTTGTTACCTCTATATACCAAGCACAATTTTAAAGTGCCATTAACAAATGTTATCACTA 2294  
Db 2166 CATTTGTTACCTCTATATACCAAGCACAATTTTAAAGTGCCATTAACAAATGTTATCACTA 2225  
Qy 2295 GCCCTCCTTTTCCAAACAAGAGGACTGAGAGATGCAAGAAATTTTGTGACAAAAAATTT 2354  
Db 2226 GCCCTCCTTTTCCAAACAAGAGGACTGAGAGATGCAAGAAATTTTGTGACAAAAAATTT 2285  
Qy 2355 AAAGCATTTAGAAAA 2369  
Db 2286 AAAGCATTTAGAAAA 2300

## RESULT 12

US-09-232-160-13

; Sequence 13, Application US/09232160

; Patent No. 6368794

; GENERAL INFORMATION:

; APPLICANT: Steve Daniel

; APPLICANT: James Gilmore

; APPLICANT: Susan G. Stuart

; APPLICANT: Laura Stuve

; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL

; TITLE OF INVENTION: PROLIFERATION

; FILE REFERENCE: PA-0003 US

; CURRENT APPLICATION NUMBER: US/09/232.160

; CURRENT FILING DATE: 1999-01-15									
; NUMBER OF SEQ ID NOS: 23									
; SOFTWARE: PERL Program									
; SEQ ID NO 13									
; LENGTH: 2029									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
; FEATURE: -									
; OTHER INFORMATION: 304710									
US-09-232-160-13									
Query Match 84.1%; Score 1994; DB 3; Length 2029;									
Best Local Similarity 99.8%; Pred No. 0;									
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;									
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Qy	61	GTTCAGAACTCTCCATCCGACTAGTTATTTAGGATCTGGCTCTCATATCACAGTGGC	120						
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Qy	121	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCAGTGGCCAGGTGCTTCAGCCTG	180						
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Qy	361	TTGGCCGCAAGGACCAAGTTGAAACAGCTTTGAAAGCTAGCTTTGAACTTGCAGCTAT	420						
Db	384	TTGGCCGCAAGGACCAAGTTGAAACAGCTTTGAAAGCTAGCTTTGAACTTGCAGCTAT	443						
Qy	421	GGCTGGTGGAGATGGATTCGTGTCTATCTAGGATTCAGCAAAACCCCAAGTGGG	480						
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Db	624	GATCCATATTCACACTCAAACTGCAACAACAACAAGATTTATTTGTCAGTGACAGT	683						
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Db	804	GAAGTACCACTGTCTACAGAACTGAACCAATTTGTTGAAAAATAAGCAGCATTCAG	863						
Qy	841	AATGAGCTGCTGGTGGAGGTGTCCTCCAGGCTCTGCTAGTGTCTCTCTCTCTCTCT	900						

Db	864	AATGAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTAGTGTCTCTCTCTCTCT	923
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Db	924	TTTGGTGTGAGCTGTGCTTTGGATTTTGTCTATGTCAAAAGGTATGTGAAGGCTTCCCT	983
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Db	1284	TCAGGACTGCCATTTGGACTATGGAGTGACCAAAAGAGAAATGCCCTTCTCTTATTGTAAC	1343
Qy	1321	CCTGTCTGGATCTTATCTCTCTACCTCAAAAGCTTCCACGGCTTTCTAGCTGGCTAT	1380
Db	1344	CCTGTCTGGATCTTATCTCTCTACCTCAAAAGCTTCCACGGCTTTCTAGCTGGCTAT	1403
Qy	1381	GTCTCTAATATATCCCACTGGGAGAAAGGAGTTTGGAAAGTGAAGGACCTAAAAACATC	1440
Db	1404	GTCTCTAATATATCCCACTGGGAGAAAGGAGTTTGGAAAGTGAAGGACCTAAAAACATC	1463
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Db	1464	TCATCAGTATCCAGTGGTAAAAAGCCCTCTCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGC	1523
Qy	1501	CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGGCAGCTCAGACCTTCTTCA	1560
Db	1524	CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGGCAGCTCAGACCTTCTTCA	1583
Qy	1561	GCTCTGAAAGAGAAACAGTATCCACCTGACATGCTCTCTGAGCCGGTAAAGAGCAA	1620
Db	1584	GCTCTGAAAGAGAAACAGTATCCACCTGACATGCTCTCTGAGCCGGTAAAGAGCAA	1643
Qy	1621	AGAAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1680
Db	1644	AGAAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1703
Qy	1681	TCTCTGTAAGCTAAAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA	1740
Db	1704	TCTCTGTAAGCTAAAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA	1763
Qy	1741	GCAGGAGTGTAAACACAGACAGGCTCAAAAGTGTCTCTGTAACACATTCAGTTTGGAAAT	1800
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Db	1824	CACCTGTTAGAACACACACACTTACTTTTCTGGTCTCTACACCTGCTGATATTTCTCT	1883
Qy	1861	AGGAAATATATCTTTTCAAGTAAACAAAACTCTTATAAATTTCTATTTTATCT	1920
Db	1884	AGGAAATATATCTTTTCAAGTAAACAAAACTCTTATAAATTTCTATTTTATCT	1943
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Db	1944	GAGTTACAGAAATGATTAAGGAGTACTCAGTAATTTGTTTAAAAAGTATATAAA	2003



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; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1896
; TYPE: DNA
; ORGANISM: Mouse
US-09-724-864-28

Query Match      25.4%; Score 603.6; DB 3; Length 1896;
Best Local Similarity 76.2%; Pred. No. 1.7e-163;
Matches 786; Conservative 0; Mismatches 234; Indels 12; Gaps 3;

Qy 140 GCTCTGAAGGGTAGGACACAGATGCGCAGGTGCTTTCAGCTGGTGTGCTTCTCACTTCCA 199
Db 42 GCCCGGAGGATCTGCACATGCTCCAGCACACTAGCTGTGTACTCTCGCTCTTA 101
Qy 200 TCTGGACACAGAGCTCTCTGTCACAGCTCTTTGCGTGACAGAGCTTTCCATCCAGG 259
Db 102 TTTGGACCACTAGGACCCAGCTCCAGGTGCGGACCTCGTCAAGACCTTTCCAT--TT 158
Qy 260 TGTCATGCAGAAATTATGGGATCACCTTGTGACNMAAAGCGCAACAGCAGCTGAATT 319
Db 159 CTACATGCAGAAATCATGGCGCTTGCCCTTTGGGCGAGAAACAAACCCACAGATGAAT 218
Qy 320 TCACAGAAGCTTAAGGAGGCGCTGTAGGCTGTGCGACTAAGTTTGGCGGCAAGACCAAG 379
Db 219 TCACAGAAGCCACAGGCGCTGTAGATGCTGGGACTGACTCTGGCCAGGAGGACCAAG 278
Qy 380 TTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTTCAGCTATGCTGCGGTTGGAGATGAT 439
Db 279 TAGAGTCAGCGCAAAATCTGGCTTTGAGACTTGCAGCTATGGATGGGTTGGAGACAGT 338
Qy 440 TCGTGGTCATCTCTAGGATTAAGCCAAACCCCAAGTGTGGGAAAAATGGGTTGGGTGCC 499
Db 339 TCTCTGTCTCCCTCGGATTTTCTCAAACCCCAAGTGTGGGAAAGTGGCAAGGTGTCC 398
Qy 500 TGATTGGAGGTTTCCAGTGAGCGGCACAGTTTTCAGAGCTATTGTTACAACTCATCTGATA 559
Db 399 TGATTGGAGTCTCTCTCCAGCCAAAGTTTCAAGGCTATTGCCAACACTCATCTCCACA 458
Qy 560 CTTGGACTAATCTGTGATTCACGAAATTAATCACCAACCAAGATGCCATATTCACACTC 619
Db 459 CTTGGGTTAATCTCTGATTCACGAAATCGTTACCACATTTTACCCCGTTGGACACTC 518
Qy 620 AACTGCAACACAAACACAGAAATTTATGTCAGTGACAGTACCTACTCGGTGGCATCCC 679
Db 519 A-----AACACCCGCAACAGAGTTTCTGTGTCAGCAGCGCGCTACTTGGCTTCATCCC 572
Qy 680 CTTACTCTACAATACCTGCGCCCTACTACTCTCTCTGTCCTCAGCTTCCACTTCTATTTC 739
Db 573 CTGACTCCACAACTCTG---TTTCTGCAACCCCGGCTCCACCTTTGACCTTCAATGG 629
Qy 740 CACGAGAAAAAATATGATTTGTCACAGAGTTTATGGAACCAACTAGCACCACTGCTA 799
Db 630 CACGGAAGACAAAAAGATTGTTATACGGAAGTTTATACAGAACCTTATCACCATGCTA 689
Qy 800 CAGAACTGAACCATTTGTTGAAATAAAGCAGCAATTCAGAAATGAAGCTGCTGGGTTTG 859
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Qy 860 GAGTGTCCCAACAGGCTCTGCTAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 919
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Qy 980 AGAAGGAATGATCGAAACCAAAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCCTA 1039
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Db 870 AGAAGGAATGATCGAAACCAAGGTTGTAAAGGAAGAGGCTGTGACGCTCAACGCTA 929
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Qy 1160 CTGGTTTCTTTC 1171
Db 1050 CAAGTTTCATGC 1061

RESULT 15
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; Sequence 11, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-892-880-11

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Matches 334; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy	1586	ACCTGACATCTCTTCTGAGCCCGGTAAGAGCAAAAGAAATGGCAGAAAAAGTTTAGCCCT	1645
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Db	159	GAAGCCCATGGAGANTCTCATAACTTGAGACCTAATCTCTGTAAAGCTAAAAATAAAGAAA	100
Qy	1706	TAGAACAAAGCTGAGGATACGACAGTACACTGTTCAGCAGGGACTGTAAACACACAGACAGG	1765
Db	99	TAGAACAAAGCTGAGGATACGACAGTACACTGTTCAGCAGGGACTGTAAACACACAGACAGG	40
Qy	1766	TCAAAGTGTCTCTGAAACACATTGAGTTGGAATCACT	1804
Db	39	TCAAAGTGTCTCTGAAACACATTGAGTTGGAATCACT	1

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Job time : 493 secs



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Scoring table: IDENTITY_NUC

Searched:  Gapop 10.0 , Gapext 1.0
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
                Maximum Match 100%

Database :      N_Geneseq 16Dec04:*
Listing first 1500 summaries
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3:  _geneseqn2000s:*
4:  _geneseqn2001as:*
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9:  _geneseqn2003bs:*
10: _geneseqn2003cs:*
11: _geneseqn2003ds:*
12: _geneseqn2004as:*
13: _geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No.   Score  Match Length DB ID      Description
RESULT 1
ID AAX52250 standard; DNA; 2372 BP.
DE Protein PRO263 cDNA clone DNA34431-1171.
PN WO9314328-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2372; DB 2; Length 2372;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 2
ID ADC78520 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA.
PN WO20015796-A2.
PD 23-MAR-2000.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2372; DB 3; Length 2372;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 3
ID AAF72408 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2372; DB 4; Length 2372;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 4
ID AAF92060 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH ) GENENTECH INC.
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RESULT 5
ID ABS74380 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2372; DB 8; Length 2372;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 6
ID ABL88087 standard; cDNA; 2372 BP.
DE Human PRO263 cDNA sequence SEQ ID NO:31.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2372; DB 6; Length 2372;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 7
ID ABL95576 standard; cDNA; 2372 BP.
DE Human angiogenesis related cDNA PRO263 SEQ ID NO: 31.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2372; DB 6; Length 2372;
  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 8
ID ACA60164 standard; cDNA; 2372 BP.
DE Human cDNA for secreted/transmembrane protein PRO263.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
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  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 9
ID ACD07564 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
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RESULT 10
ID ACA91166 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
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  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 11
ID ACD81543 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
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  Best Local Similarity 100.0%; Pred. No. 0;
RESULT 12
ID ACA60365 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 2372; DB 8; Length 2372;
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RESULT 13
ID ABX71612 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 14
ID ACH06944 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO263 cDNA.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 15
ID ACA58812 standard; cDNA; 2372 BP.
DE cDNA encoding human secreted polypeptide PRO263.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 16
ID ACA63988 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 17
ID ACA91252 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 18
ID ACD45151 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane polypeptide PRO263 cDNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 19
ID ABX96181 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #38.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 20
ID ACA05502 standard; cDNA; 2372 BP.
DE cDNA encoding human secreted protein PRO263.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
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ID ACA93699 standard; cDNA; 2372 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO263.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 22
ID ACD19807 standard; cDNA; 2372 BP.
DE Human secreted / transmembrane polypeptide PRO263 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 23
ID ACA67273 standard; cDNA; 2372 BP.
DE cDNA encoding human secreted polypeptide PRO263.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 24
ID ACH66246 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
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ID ACD02300 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 26
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DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
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DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
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PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
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DE Human PRO polynucleotide #3.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 8; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
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ID ACA63375 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #3.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
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RESULT 31
ID ACD19807 standard; cDNA; 2372 BP.
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DE Human secreted / transmembrane polypeptide PRO263 cDNA.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
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DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003092002-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 33  
ID ADB17062 standard; cDNA; 2372 BP.  
DE Human cDNA clone (SeqID 5) encoding the transmembrane PRO protein.  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 9; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 34  
ID ACH03578 standard; cDNA; 2372 BP.  
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PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
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RESULT 35  
ID ADA18261 standard; cDNA; 2372 BP.  
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PN US2003030971-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 9; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 36  
ID ACD66954 standard; cDNA; 2372 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO263.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 37  
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PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 9; Length 2372;  
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PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
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ID ACD83115 standard; cDNA; 2372 BP.  
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PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
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PN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
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RESULT 41  
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PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
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PA (GETH ) GENENTECH INC.  
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PN US2003054401-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 44  
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PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
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PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
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RESULT 46  
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PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
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PN US2003049622-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 9; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 48  
ID ADA41957 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003082540-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 9; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 49  
ID ADA17304 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003017498-A1.

PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 9; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 50  
ID ADA42807 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003054351-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 9; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 51  
ID ACD23655 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #36.  
PN US2003064923-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 9; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 52  
ID AD885578 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 9; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 53  
ID ADB77726 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 54  
ID ADB74862 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 55  
ID ADB68257 standard; cDNA; 2372 BP.  
DE Human PRO263 cDNA.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 56  
ID ADB68064 standard; cDNA; 2372 BP.  
DE Human PRO263 cDNA.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 57  
ID ADB90881 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 58  
ID ADC28508 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003059772-A1.  
PD 27-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 59  
ID ADC39708 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003059828-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 60  
ID ADC40222 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003059829-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 61  
ID ADC19046 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003036061-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 62  
ID ADC34346 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003036094-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 63  
ID ADC29401 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003049676-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 64  
ID ADC28932 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003049677-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 65  
ID ADC40817 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003054400-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 66  
ID ADC19474 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003054441-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 67  
ID ADC06961 standard; cDNA; 2372 BP.  
DE Human PRO263 cDNA.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.

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Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 68
ID ADCL17140 standard; cDNA; 2372 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 5).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 69
ID ADC33922 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 70
ID ADC12992 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 71
ID ADC14838 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 72
ID ADC52333 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 73
ID ADC12444 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 74
ID ADD10320 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 75
ID ADD11280 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 76
ID ADD04005 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 77
ID ADD03581 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 78
ID ADD37073 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 79
ID ADD36009 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 80
ID ADE34833 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 81
ID ADG01010 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 82
ID ADG08563 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 83
ID ADF95184 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 84
ID ADH24037 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180318-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 85
ID ADH34063 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 2372; DB 10; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 96  
ID ADH29896 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 97  
ID ADH23867 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 98  
ID ADH85271 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 99  
ID ADH24547 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 90  
ID ADH37403 standard; cDNA; 2372 BP.  
DE Human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 91  
ID ADH01992 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 92  
ID ADH37573 standard; cDNA; 2372 BP.  
DE Human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 93  
ID ADH85611 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 94  
ID ADH24207 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 95

ID ADH38501 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 96  
ID ADH83622 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 97  
ID ADH29430 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 98  
ID ADH27546 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 99  
ID ADH37743 standard; cDNA; 2372 BP.  
DE Human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 100  
ID ADH37920 standard; cDNA; 2372 BP.  
DE Human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 101  
ID ADH57340 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 102  
ID ADH59316 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003039972-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 103  
ID ADH53482 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;  
Pred. No. 0;  
RESULT 104  
ID ADH53652 standard; cDNA; 2372 BP.

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DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 105
ID ADH91988 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 106
ID ADH49843 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 107
ID ADI25353 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 108
ID ADH90146 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 109
ID ADI25523 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 110
ID ADH97697 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 111
ID ADI38095 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 112
ID ADI03545 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 113
ID ADI11902 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2002192659-A1.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 114
ID ADH89976 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 115
ID ADH98377 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 116
ID ADI11052 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 117
ID ADI11562 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 118
ID ADH98207 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 119
ID ADH98547 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 120
ID ADH98037 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 121
ID ACA59060 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #36.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2372; DB 10; Length 2372;
RESULT 122
ID ACA58457 standard; cDNA; 2372 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2002192659-A1.
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PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 123  
ID AD105025 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 124  
ID AD103375 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 125  
ID AD104770 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 126  
ID ADH78224 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003181668-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 127  
ID AD119568 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 128  
ID ADH90316 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 129  
ID AD103035 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 130  
ID ADH77884 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 131  
ID ADH97867 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181674-A1.  
PD 25-SEP-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 132  
ID AD101252 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 133  
ID AD101947 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 134  
ID AD103205 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 135  
ID AD111392 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 136  
ID AD102294 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 137  
ID AD111732 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 138  
ID AD105369 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 139  
ID ADH79441 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 10; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 140  
ID AD119398 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.





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RESULT 159
ID ADE73378 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 160
ID ADE411281 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #16.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 161
ID ADE73913 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 162
ID ADE99467 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US200311576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 163
ID ADE98586 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 164
ID ADE99013 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 165
ID ADG40483 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) CURNAY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 166
ID ADF73877 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 167
ID ADF73453 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 168
ID ADH06575 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 169
ID ADH06405 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 170
ID ADG68826 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 171
ID ADH27716 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 172
ID ADH25057 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 173
ID ADH33689 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 174
ID ADG92296 standard; cDNA; 2372 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 175
ID ADH02332 standard; cDNA; 2372 BP.
DE Human PRO polynucleotide #3.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2372; DB 12; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 176
ID ADH07939 standard; cDNA; 2372 BP.
DE Novel human secreted and transmembrane protein PRO263 cDNA.
PN US2003180845-A1.
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PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 177  
ID ADG69336 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 178  
ID ADH39157 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 179  
ID ADG92723 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003027146-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 180  
ID ADG83897 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 181  
ID ADG85441 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 182  
ID ADH06235 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 183  
ID ADH30231 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 184  
ID ADH24377 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 185  
ID ADG59506 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180844-A1.  
PD 25-SEP-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 186  
ID ADH07769 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 187  
ID ADG85781 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 188  
ID ADH39327 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 189  
ID ADH33519 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 190  
ID ADH33859 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 191  
ID ADH01069 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 192  
ID ADG69676 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 193  
ID ADH02162 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 194  
ID ADG69166 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Query Match	100.0%;	Score 2372;	DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 195				
ID ADG85951 standard; cDNA; 2372 BP.				
DE Novel human secreted and transmembrane protein PRO263 cDNA.				
PN US2003180862-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 2372;	DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 196				
ID ADH24887 standard; cDNA; 2372 BP.				
DE Novel human secreted and transmembrane protein PRO263 cDNA.				
PN US2003180909-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 2372;	DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 197				
ID ADH39504 standard; cDNA; 2372 BP.				
DE Novel human secreted and transmembrane protein PRO263 cDNA.				
PN US2003180915-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 2372;	DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 198				
ID ADH02502 standard; cDNA; 2372 BP.				
DE Human PRO polynucleotide #3.				
PN US2003180840-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 2372;	DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 199				
ID ADG68996 standard; cDNA; 2372 BP.				
DE Novel human secreted and transmembrane protein PRO263 cDNA.				
PN US2003180849-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 2372;	DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 200				
ID ADH07599 standard; cDNA; 2372 BP.				
DE Novel human secreted and transmembrane protein PRO263 cDNA.				
PN US2003180850-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 2372;	DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 201				
ID ADG86121 standard; cDNA; 2372 BP.				
DE Novel human secreted and transmembrane protein PRO263 cDNA.				
PN US2003180863-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 2372;	DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 202				
ID ADH24717 standard; cDNA; 2372 BP.				
DE Novel human secreted and transmembrane protein PRO263 cDNA.				
PN US2003180908-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 2372;	DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 203				
ID ADH25765 standard; cDNA; 2372 BP.				
DE Novel human secreted and transmembrane protein PRO263 cDNA.				
PN US2003180911-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 2372;	DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 204				
ID ADH25765 standard; cDNA; 2372 BP.				
DE Novel human secreted and transmembrane protein PRO263 cDNA.				
PN US2003180911-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 2372;	DB 12;	Length 2372;

Best Local Similarity	100.0%;	Pred. No. 0;	
RESULT 204			
ID	ADH38331 standard; cDNA; 2372 BP.		
DE	Novel human secreted and transmembrane protein PRO263 cDNA.		
FN	US2003180922-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 2372; DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;	
RESULT 205			
ID	ADH20512 standard; cDNA; 2372 BP.		
DE	Human secreted/transmembrane protein cDNA, #40.		
FN	US2004005553-A1.		
PD	08-JAN-2004.		
PA	(GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 2372; DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;	
RESULT 206			
ID	ADH57170 standard; cDNA; 2372 BP.		
DE	Novel human secreted and transmembrane protein PRO263 cDNA.		
FN	US2003181642-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 2372; DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;	
RESULT 207			
ID	ADH43464 standard; cDNA; 2372 BP.		
DE	Human PRO polynucleotide #16.		
FN	US2003224984-A1.		
PD	04-DEC-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 2372; DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;	
RESULT 208			
ID	ADH07367 standard; cDNA; 2372 BP.		
DE	Human secreted/transmembrane protein cDNA, #40.		
FN	US2004006211-A1.		
PD	08-JAN-2004.		
PA	(DESN/) DESNOYERS L.		
PA	(GODD/) GODDARD A.		
PA	(GODO/) GODOWSKI P J.		
PA	(GURN/) GURNEY A L.		
PA	(MATH/) MATHER J P.		
PA	(WILL/) WILLIAMS P M.		
PA	(WOOD/) WOOD W I.		
Query Match	100.0%;	Score 2372; DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;	
RESULT 209			
ID	ADH52158 standard; cDNA; 2372 BP.		
DE	Novel human secreted and transmembrane protein PRO263 cDNA.		
FN	US2003180921-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 2372; DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;	
RESULT 210			
ID	ADH59912 standard; cDNA; 2372 BP.		
DE	Human secreted/transmembrane protein cDNA, #40.		
FN	US2003215904-A1.		
PD	20-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 2372; DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;	
RESULT 211			
ID	ADH49524 standard; cDNA; 2372 BP.		
DE	Novel human secreted and transmembrane protein PRO263 cDNA.		
FN	US2003180857-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 2372; DB 12;	Length 2372;
Best Local Similarity	100.0%;	Pred. No. 0;	
RESULT 212			
ID	ADH06940 standard; cDNA; 2372 BP.		

DE Human secreted/transmembrane protein cDNA, #40.  
PN US2004005665-A1.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P M.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;  
Pred. No. 0;  
RESULT 213  
ID ADH90486 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;  
Pred. No. 0;  
RESULT 214  
ID ADI11222 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;  
Pred. No. 0;  
RESULT 215  
ID ADI18682 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003152999-A1.  
PD 14-AUG-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;  
Pred. No. 0;  
RESULT 216  
ID ADH98887 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;  
Pred. No. 0;  
RESULT 217  
ID ADI02117 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003190699-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;  
Pred. No. 0;  
RESULT 218  
ID ADH90656 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;  
Pred. No. 0;  
RESULT 219  
ID ADI37665 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003096340-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;  
Pred. No. 0;  
RESULT 220  
ID ADH97461 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003190610-A1.  
PD 09-OCT-2003.

PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;  
Pred. No. 0;  
RESULT 221  
ID ADI65829 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003148371-A1.  
PD 07-AUG-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;  
Pred. No. 0;  
RESULT 222  
ID ADH60572 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2004023331-A1.  
PD 05-FEB-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;  
Pred. No. 0;  
RESULT 223  
ID ADJ99629 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003187238-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;  
Pred. No. 0;  
RESULT 224  
ID ADL08822 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003186358-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;  
Pred. No. 0;  
RESULT 225  
ID ADJ98531 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;  
Pred. No. 0;  
RESULT 226  
ID ADJ98701 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;  
Pred. No. 0;  
RESULT 227  
ID ADH78660 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;  
Pred. No. 0;  
RESULT 228  
ID ADJ99094 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 12; Length 2372;  
Pred. No. 0;

RESULT 229  
ID ADJ99264 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 230  
ID ADJ98882 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 231  
ID ADH79030 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 232  
ID ADK00890 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 233  
ID ADK14411 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 234  
ID ADM25163 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003096233-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 235  
ID ADM29913 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003190611-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 236  
ID ADK82809 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #16.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 237  
ID ADM80860 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #3.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 238  
ID ADM25163 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003096233-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 239  
ID ADQ06235 standard; cDNA; 2372 BP.  
DE Human PRO polynucleotide #38.  
PN US6686451-B1.  
PD 03-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 240  
ID ADH79030 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 241  
ID ADK14411 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 242  
ID ADS74635 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane cDNA #40.  
PN US2004185531-A1.  
PD 23-SEP-2004.  
PA (ASHK/) ASHKENAZI A.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FILV/) FILVAROFF E.  
PA (FERR/) FERRARA N.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI C J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (MATH/) MATHER J P.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 2372; DB 13; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 243  
ID ADT03672 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003152922-A1.  
PD 14-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 13; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 244  
ID ADS74635 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane cDNA #40.  
PN US2004185531-A1.  
PD 23-SEP-2004.  
PA (ASHK/) ASHKENAZI A.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI C J.  
PA (GURN/) GURNEY A L.

RESULT 239  
ID ADH79030 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 12; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 240  
ID ADH79030 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (ASHK/) ASHKENAZI A.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI C J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (MATH/) MATHER J P.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 2372; DB 13; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 241  
ID ADT03672 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003152922-A1.  
PD 14-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2372; DB 13; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 242  
ID ADS74635 standard; cDNA; 2372 BP.  
DE Human secreted/transmembrane cDNA #40.  
PN US2004185531-A1.  
PD 23-SEP-2004.  
PA (ASHK/) ASHKENAZI A.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI C J.  
PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (MATH/) MATH J.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (STEM/) STEWART T A.  
PA (TUNA/) TUNAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match  
Best Local Similarity 100.0%; Score 2372; DB 13; Length 2372;  
RESULT 243  
ID ADC52143 standard; cDNA; 2372 BP.  
DE Novel human secreted and transmembrane protein PRO263 cDNA.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 99.9%; Score 2370.4; DB 12; Length 2372;  
RESULT 244  
ID ADQ25003 standard; DNA; 2667 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7823.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 99.9%; Score 2369; DB 12; Length 2667;  
RESULT 245  
ID ADRA1319 standard; cDNA; 2369 BP.  
DE Human CD-like molecule HEMFC27 cDNA, SEQ ID NO:118.  
PN WO200226930-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 98.8%; Score 2343; DB 7; Length 2369;  
RESULT 246  
ID ABL90698 standard; cDNA; 2369 BP.  
DE Human polynucleotide SEQ ID NO 1260.  
PN WO200193004-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 98.7%; Score 2342.2; DB 6; Length 2369;  
RESULT 247  
ID ABA09223 standard; cDNA; 2324 BP.  
DE Human PRO263 homologue-encoding cDNA, SEQ ID NO:999.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 97.5%; Score 2313.2; DB 4; Length 2324;  
RESULT 248  
ID AAV22687 standard; DNA; 2313 BP.  
DE DNA encoding a CD44-like protein.  
PN WO9806839-A1.  
PD 19-FEB-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 96.6%; Score 2290.2; DB 2; Length 2313;  
RESULT 249  
ID ADP65684 standard; DNA; 2313 BP.  
DE Human extracellular link domain containing 1 (XLKDI) DNA.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match  
Best Local Similarity 96.2%; Score 2282.2; DB 11; Length 2313;  
RESULT 250  
ID ADM67137 standard; DNA; 2313 BP.  
DE Human homologue of murine adipocyte specific DNA SeqID 273.  
PN WO2004011618-A2.  
PD 05-FEB-2004.

PA (HMGE-) HMGENE INC.  
Query Match  
Best Local Similarity 96.2%; Score 2282.2; DB 12; Length 2313;  
RESULT 251  
ID ADN05865 standard; cDNA; 2313 BP.  
DE Antipsoriatic cDNA sequence #1164.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 96.2%; Score 2282.2; DB 12; Length 2313;  
RESULT 252  
ID ADQ21088 standard; DNA; 2313 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3908.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 96.2%; Score 2282.2; DB 12; Length 2313;  
RESULT 253  
ID ADE71449 standard; cDNA; 2027 BP.  
DE Human cDNA encoding PDEBC #2.  
PN US2003124543-A1.  
PD 03-JUL-2003.  
PA (STUA/) STUART S G.  
PA (STRE/) STREETER D G.  
Query Match  
Best Local Similarity 84.1%; Score 1994; DB 12; Length 2027;  
RESULT 254  
ID AA298172 standard; cDNA; 2029 BP.  
DE Human signal peptide containing protein HSPP-64 cDNA SEQ ID NO:198.  
PN WO200006610-A2.  
PD 06-JAN-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match  
Best Local Similarity 84.1%; Score 1994; DB 3; Length 2029;  
RESULT 255  
ID ADE71445 standard; cDNA; 2029 BP.  
DE Human cDNA encoding PDEBC Incyte 3044710CB1.  
PN US2003124543-A1.  
PD 03-JUL-2003.  
PA (STUA/) STUART S G.  
PA (STRE/) STREETER D G.  
Query Match  
Best Local Similarity 84.1%; Score 1994; DB 12; Length 2029;  
RESULT 256  
ID AAC59803 standard; DNA; 2967 BP.  
DE Human secreted protein encoding DNA clone vb28 1.  
PN WO200055375-A1.  
PD 21-SEP-2000.  
PA (ALPH-) ALPHAGENE INC.  
Query Match  
Best Local Similarity 73.1%; Score 1733; DB 3; Length 2967;  
RESULT 257  
ID AAF93818 standard; cDNA; 1755 BP.  
DE Human cDNA encoding a membrane or secretory protein clone PSEC0135.  
PN EP1067182-A2.  
PD 10-JAN-2001.  
PA (HELI-) HELIX RES INST.  
Query Match  
Best Local Similarity 72.2%; Score 1712.4; DB 5; Length 1755;  
RESULT 258  
ID ADD04999 standard; cDNA; 1680 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2003104469-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 43.4%; Score 1029; DB 10; Length 1680;  
RESULT 259  
ID ACA10111 standard; cDNA; 1127 BP.  
DE Human NOVX polynucleotide #1.  
PN WO200290504-A2.





DE Primer specific for DNA encoding secretory/membrane protein SEQ ID 594.  
PN EP1067182-A2.  
PA (HELI-) HELIX RES INST.  
Query Match 19.3%; Score 458.8; DB 5; Length 591;  
Best Local Similarity 88.9%; Pred. No. 3e-104;  
RESULT 275  
ID AAX41156 standard; cDNA; 451 BP.  
DE Human secreted protein 5' EST SEQ ID NO:100.  
PN WO906548-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Query Match 19.0%; Score 450; DB 2; Length 451;  
Best Local Similarity 100.0%; Pred. No. 4.3e-102;  
RESULT 276  
ID ACH22904 standard; cDNA; 486 BP.  
DE Human adult ovary cDNA #1284.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRNA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 18.5%; Score 440; DB 9; Length 486;  
Best Local Similarity 100.0%; Pred. No. 1.4e-99;  
RESULT 277  
ID ACH22239 standard; cDNA; 472 BP.  
DE Human adult ovary cDNA #619.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRNA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 17.7%; Score 419.4; DB 9; Length 472;  
Best Local Similarity 99.8%; Pred. No. 2e-94;  
RESULT 278  
ID ACH30085 standard; cDNA; 499 BP.  
DE Human testis cDNA #471.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRNA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 17.1%; Score 406; DB 9; Length 499;  
Best Local Similarity 99.8%; Pred. No. 4.5e-91;  
RESULT 279  
ID ACH17082 standard; cDNA; 441 BP.  
DE Human adult heart cDNA #1396.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRNA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 17.0%; Score 403; DB 9; Length 441;  
Best Local Similarity 100.0%; Pred. No. 2.4e-90;  
RESULT 280  
ID ACH20895 standard; cDNA; 411 BP.  
DE Human adult liver cDNA #507.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRNA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 16.7%; Score 397; DB 9; Length 411;

Best Local Similarity 98.8%; Pred. No. 7.4e-89;  
RESULT 281  
ID ADE71448 standard; cDNA; 820 BP.  
DE Dog cDNA encoding PDEBC variant Incyte 704113673J1.  
PN US2003124543-A1.  
PD 03-JUL-2003.  
PA (STUA/) STUART S G.  
PA (STRE/) STREETER D G.  
Query Match 16.3%; Score 387.6; DB 12; Length 820;  
Best Local Similarity 77.5%; Pred. No. 2.3e-86;  
RESULT 282  
ID AAX41003 standard; cDNA; 363 BP.  
DE Human secreted protein 5' EST SEQ ID NO: 215.  
PN WO9906554-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Query Match 14.5%; Score 343; DB 2; Length 363;  
Best Local Similarity 97.0%; Pred. No. 2.3e-75;  
RESULT 283  
ID AAX51631 standard; cDNA; 373 BP.  
DE Human secreted protein 5' EST SEQ ID NO:210.  
PN WO9906549-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Query Match 14.0%; Score 331.8; DB 2; Length 373;  
Best Local Similarity 99.4%; Pred. No. 1.5e-72;  
RESULT 284  
ID ADE71446 standard; cDNA; 559 BP.  
DE Rat cDNA encoding PDEBC variant Incyte 702127782H1.  
PN US2003124543-A1.  
PD 03-JUL-2003.  
PA (STUA/) STUART S G.  
PA (STRE/) STREETER D G.  
Query Match 13.9%; Score 328.6; DB 12; Length 559;  
Best Local Similarity 78.4%; Pred. No. 1.1e-71;  
RESULT 285  
ID AAF17836 standard; cDNA; 241 BP.  
DE Human breast cancer associated 23232 coding sequence.  
PN WO200060076-A2.  
PD 12-OCT-2000.  
PA (CORI-) CORIXA CORP.  
Query Match 10.1%; Score 239; DB 4; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2e-49;  
RESULT 286  
ID AAS47266 standard; cDNA; 241 BP.  
DE Human breast cancer cDNA clone 23232.  
PN WO200179286-A2.  
PD 25-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 10.1%; Score 239; DB 4; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2e-49;  
RESULT 287  
ID ABG63867 standard; cDNA; 241 BP.  
DE Human breast tumour polynucleotide #319.  
PN US2002085998-A1.  
PD 04-JUL-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 10.1%; Score 239; DB 6; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2e-49;  
RESULT 288  
ID ABT33079 standard; DNA; 241 BP.  
DE Human tumour-related DNA sequence - SEQ ID NO 324.  
PN WO200283956-A1.  
PD 24-OCT-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 10.1%; Score 239; DB 10; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2e-49;  
RESULT 289  
ID ADL92986 standard; cDNA; 241 BP.  
DE Human breast cancer-associated polypeptide cDNA #319.  
PN US2003166022-A1.  
PD 04-SEP-2003.  
PA (CORI-) CORIXA CORP.

Query Match 10.1%; Score 239; DB 11; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2e-49;  
RESULT 290  
ID ADE44276 standard; cDNA; 241 BP.  
DE Human cDNA associated with breast cancer #319.  
PN US2003104366-A1.  
PD 05-JUN-2003.  
PA (JIAN/) JIANG Y.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (XUJ/) XU J.  
PA (HARL/) HARLOCKER S L.  
Query Match 10.1%; Score 239; DB 12; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2e-49;  
RESULT 291  
ID ABL63797 standard; DNA; 308 BP.  
DE Breast cancer related gene sequence SEQ ID NO:2134.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 10.0%; Score 238; DB 6; Length 308;  
Best Local Similarity 91.0%; Pred. No. 3.9e-49;  
RESULT 292  
ID ABL63384 standard; DNA; 308 BP.  
DE Breast cancer related gene sequence SEQ ID NO:1721.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 10.0%; Score 238; DB 6; Length 308;  
Best Local Similarity 91.0%; Pred. No. 3.9e-49;  
RESULT 293  
ID ABL63798 standard; DNA; 308 BP.  
DE Breast cancer related gene sequence SEQ ID NO:2135.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 10.0%; Score 238; DB 6; Length 308;  
Best Local Similarity 91.0%; Pred. No. 3.9e-49;  
RESULT 294  
ID ABN95189 standard; DNA; 308 BP.  
DE Gene #1687 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.0%; Score 238; DB 6; Length 308;  
Best Local Similarity 91.0%; Pred. No. 3.9e-49;  
RESULT 295  
ID AAF17835 standard; cDNA; 241 BP.  
DE Human breast cancer associated 23182 coding sequence.  
PN WO200060076-A2.  
PD 12-OCT-2000.  
PA (CORI-) CORIXA CORP.  
Query Match 10.0%; Score 237; DB 4; Length 241;  
Best Local Similarity 100.0%; Pred. No. 6.2e-49;  
RESULT 296  
ID AAG47265 standard; cDNA; 241 BP.  
DE Human breast cancer cDNA clone 23182.  
PN WO200179286-A2.  
PD 25-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 10.0%; Score 237; DB 4; Length 241;  
Best Local Similarity 100.0%; Pred. No. 6.2e-49;  
RESULT 297  
ID AB863866 standard; cDNA; 241 BP.  
DE Human breast tumour polynucleotide #318.  
PN US2002085998-A1.  
PD 04-JUL-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 10.0%; Score 237; DB 6; Length 241;  
Best Local Similarity 100.0%; Pred. No. 6.2e-49;  
RESULT 298  
ID ABT33078 standard; DNA; 241 BP.  
DE Human tumour-related DNA sequence - SEQ ID NO 323.

PN WO200283956-A1.  
PD 24-OCT-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 10.0%; Score 237; DB 10; Length 241;  
Best Local Similarity 100.0%; Pred. No. 6.2e-49;  
RESULT 299  
ID ADL92985 standard; cDNA; 241 BP.  
DE Human breast cancer-associated polypeptide cDNA #318.  
PN US2003166022-A1.  
PD 04-SEP-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 10.0%; Score 237; DB 11; Length 241;  
Best Local Similarity 100.0%; Pred. No. 6.2e-49;  
RESULT 300  
ID ADE4275 standard; cDNA; 241 BP.  
DE Human cDNA associated with breast cancer #318.  
PN US2003104366-A1.  
PD 05-JUN-2003.  
PA (JIAN/) JIANG Y.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (XUJ/) XU J.  
PA (HARL/) HARLOCKER S L.  
Query Match 10.0%; Score 237; DB 12; Length 241;  
Best Local Similarity 100.0%; Pred. No. 6.2e-49;  
RESULT 301  
ID ABL65603 standard; DNA; 239 BP.  
DE Lung cancer related gene sequence SEQ ID NO:3940.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 9.5%; Score 226.2; DB 6; Length 239;  
Best Local Similarity 95.4%; Pred. No. 3.1e-46;  
RESULT 302  
ID ABL63605 standard; DNA; 239 BP.  
DE Breast cancer related gene sequence SEQ ID NO:1942.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 9.5%; Score 226.2; DB 6; Length 239;  
Best Local Similarity 95.4%; Pred. No. 3.1e-46;  
RESULT 303  
ID ABL66203 standard; DNA; 239 BP.  
DE Lung cancer related gene sequence SEQ ID NO:4540.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 9.5%; Score 226.2; DB 6; Length 239;  
Best Local Similarity 95.4%; Pred. No. 3.1e-46;  
RESULT 304  
ID ABL64015 standard; DNA; 239 BP.  
DE Breast cancer related gene sequence SEQ ID NO:2352.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 9.5%; Score 226.2; DB 6; Length 239;  
Best Local Similarity 95.4%; Pred. No. 3.1e-46;  
RESULT 305  
ID ABN94227 standard; DNA; 239 BP.  
DE Gene #725 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 9.5%; Score 226.2; DB 6; Length 239;  
Best Local Similarity 95.4%; Pred. No. 3.1e-46;  
RESULT 306  
ID ADE71447 standard; cDNA; 279 BP.  
DE Rat cDNA encoding PDEBC variant Incyte 701647942H1.  
PN US2003124543-A1.  
PD 03-JUL-2003.  
PA (STUA/) STUART S G.  
PA (STRE/) STREETER D G.  
Query Match 8.9%; Score 212.2; DB 12; Length 279;

Best Local Similarity 86.1%; Pred. No. 1.1e-42;  
RESULT 307  
ID ABA44110 standard; DNA; 469 BP.  
DE Human foetal liver single exon nucleic acid probe #2415.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 7.6%; Score 179.2; DB 4; Length 469;  
Best Local Similarity 98.0%; Pred. No. 2.4e-34;  
RESULT 308  
ID AAI33763 standard; DNA; 469 BP.  
DE Probe #2449 used to measure gene expression in human placenta sample.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 7.6%; Score 179.2; DB 4; Length 469;  
Best Local Similarity 98.0%; Pred. No. 2.4e-34;  
RESULT 309  
ID ABA231859 standard; DNA; 469 BP.  
DE Probe #2325 for gene expression analysis in human heart cell sample.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 7.6%; Score 179.2; DB 4; Length 469;  
Best Local Similarity 98.0%; Pred. No. 2.4e-34;  
RESULT 310  
ID AAK72829 standard; DNA; 469 BP.  
DE Human bone marrow expressed single exon probe SEQ ID NO: 2386.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 7.6%; Score 179.2; DB 4; Length 469;  
Best Local Similarity 98.0%; Pred. No. 2.4e-34;  
RESULT 311  
ID ABS27409 standard; DNA; 469 BP.  
DE Human liver single exon probe, SEQ ID No 2399.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 7.6%; Score 179.2; DB 4; Length 469;  
Best Local Similarity 98.0%; Pred. No. 2.4e-34;  
RESULT 312  
ID ABS02280 standard; DNA; 469 BP.  
DE Human genome-derived single exon probe from lung SEQ ID No 2271.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 7.6%; Score 179.2; DB 6; Length 469;  
Best Local Similarity 98.0%; Pred. No. 2.4e-34;  
RESULT 313  
ID AAI33382 standard; DNA; 457 BP.  
DE Probe #2068 used to measure gene expression in human placenta sample.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 7.4%; Score 175; DB 4; Length 457;  
Best Local Similarity 94.8%; Pred. No. 2.7e-33;  
RESULT 314  
ID ABS01959 standard; DNA; 457 BP.  
DE Human genome-derived single exon probe from lung SEQ ID No 1950.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 7.4%; Score 175; DB 6; Length 457;  
Best Local Similarity 94.8%; Pred. No. 2.7e-33;  
RESULT 315  
ID ABA66678 standard; DNA; 141 BP.  
DE Human foetal liver single exon nucleic acid probe #14983.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 5.4%; Score 129; DB 4; Length 141;  
Best Local Similarity 99.3%; Pred. No. 5.1e-22;

RESULT 316  
ID AAI46891 standard; DNA; 141 BP.  
DE Probe #15577 used to measure gene expression in human placenta sample.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 5.4%; Score 129; DB 4; Length 141;  
Best Local Similarity 99.3%; Pred. No. 5.1e-22;  
RESULT 317  
ID ABA33740 standard; DNA; 141 BP.  
DE Probe #12206 for gene expression analysis in human heart cell sample.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 5.4%; Score 129; DB 4; Length 141;  
Best Local Similarity 99.3%; Pred. No. 5.1e-22;  
RESULT 318  
ID AAK40837 standard; DNA; 141 BP.  
DE Human bone marrow expressed single exon probe SEQ ID NO: 15394.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 5.4%; Score 129; DB 4; Length 141;  
Best Local Similarity 99.3%; Pred. No. 5.1e-22;  
RESULT 319  
ID ABS40414 standard; DNA; 141 BP.  
DE Human liver single exon probe, SEQ ID No 15404.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 5.4%; Score 129; DB 4; Length 141;  
Best Local Similarity 99.3%; Pred. No. 5.1e-22;  
RESULT 320  
ID ABS14788 standard; DNA; 141 BP.  
DE Human genome-derived single exon probe ORF from lung SEQ ID No 14779.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 5.4%; Score 129; DB 6; Length 141;  
Best Local Similarity 99.3%; Pred. No. 5.1e-22;  
RESULT 321  
ID AAI46523 standard; DNA; 106 BP.  
DE Probe #15209 used to measure gene expression in human placenta sample.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 4.5%; Score 106; DB 4; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2.6e-16;  
RESULT 322  
ID ABS14478 standard; DNA; 106 BP.  
DE Human genome-derived single exon probe ORF from lung SEQ ID No 14469.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 4.5%; Score 106; DB 6; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2.6e-16;  
RESULT 323  
ID ABN38121 standard; DNA; 60 BP.  
DE Human spliced transcript detection oligonucleotide SEQ ID NO:10869.  
PN WO200210449-A2.  
PD 07-FEB-2002.  
PA (COMP-) COMPUGEN INC.  
Query Match 2.5%; Score 60; DB 6; Length 60;  
Best Local Similarity 100.0%; Pred. No. 6.4e-05;  
RESULT 324  
ID ABQ56694 standard; cDNA; 641 BP.  
DE Human colon cancer related nucleotide sequence SEQ ID NO:389.  
PN WO200229086-A2.  
PD 11-APR-2002.  
PA (FARB ) BAYER CORP.  
Query Match 2.5%; Score 58.2; DB 6; Length 641;  
Best Local Similarity 38.9%; Pred. No. 0.00051;  
RESULT 325

Query Match 2.4%; Score 57.4; DB 13; Length 110000;  
Best Local Similarity 46.4%; Pred. No. 0.0079;  
RESULT 326  
ID AB210100 standard; DNA; 8056 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #240.  
PN WO20027272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.4%; Score 56.8; DB 8; Length 8056;  
Best Local Similarity 44.9%; Pred. No. 0.0035;  
RESULT 327  
ID ADA71938 standard; DNA; 2000 BP.  
DE Rice gene, SEQ ID 5263.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 2.4%; Score 56.6; DB 8; Length 2000;  
Best Local Similarity 9.0%; Pred. No. 0.0021;  
RESULT 328  
ID ABK39932 standard; DNA; 6216 BP.  
DE Human chemically pretreated gene sequence #7 strand 1.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.4%; Score 56.6; DB 6; Length 6216;  
Best Local Similarity 49.0%; Pred. No. 0.0035;  
RESULT 329  
ID ABL70139 standard; DNA; 6216 BP.  
DE Chemically treated cell signalling DNA sequence#15.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.4%; Score 56.6; DB 6; Length 6216;  
Best Local Similarity 49.0%; Pred. No. 0.0035;  
RESULT 330  
ID AB210246 standard; DNA; 8056 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #386.  
PN WO20027272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.4%; Score 55.8; DB 8; Length 8056;  
Best Local Similarity 45.7%; Pred. No. 0.0063;  
RESULT 331  
ID ACC43051 standard; DNA; 339 BP.  
DE Nucleotide sequence of a chicken CD44-hyaluronic acid binding domain.  
PN WO2003018044-A1.  
PD 06-MAR-2003.  
PA (STRO/) STROEMBLAD S.  
PA (KOGG/) KOGERMAN P.  
PA (PAEL/) PAELL T.  
Query Match 2.3%; Score 55.4; DB 8; Length 339;  
Best Local Similarity 50.2%; Pred. No. 0.0019;  
RESULT 332  
ID AB210246 standard; DNA; 8056 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #386.  
PN WO20027272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.3%; Score 55.2; DB 8; Length 8056;  
Best Local Similarity 44.7%; Pred. No. 0.0088;  
RESULT 333  
ID ABQ67093 standard; DNA; 83391 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 123.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.3%; Score 55; DB 6; Length 83391;  
Best Local Similarity 45.9%; Pred. No. 0.028;  
RESULT 334  
ID AA70187 standard; DNA; 11922 BP.  
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:320.  
PN WO200252728-A2.  
PD 11-MAY-2000.

PA (HOFF/) HOFFMAN S.  
PA (CARU/) CARUCCI D.  
PA (GARD/) GARDNER M.  
PA (VENT/) VENTER J C.  
Query Match 2.3%; Score 54.2; DB 3; Length 11922;  
Best Local Similarity 49.0%; Pred. No. 0.019;  
RESULT 335  
ID ABL32467 standard; DNA; 15373 BP.  
DE Human immune system associated gene SEQ ID NO: 440.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.3%; Score 54.2; DB 6; Length 15373;  
Best Local Similarity 46.5%; Pred. No. 0.021;  
RESULT 336  
ID ABL32542 standard; DNA; 11790 BP.  
DE Human immune system associated gene SEQ ID NO: 515.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.3%; Score 53.8; DB 6; Length 11790;  
Best Local Similarity 46.2%; Pred. No. 0.023;  
RESULT 337  
ID AAH93026 standard; DNA; 700 BP.  
DE Human inflammatory bowel disease related gene fragment IGR3319a.  
PN WO200142511-A2.  
PD 14-JUN-2001.  
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.  
Query Match 2.3%; Score 53.6; DB 4; Length 700;  
Best Local Similarity 47.6%; Pred. No. 0.0076;  
RESULT 338  
ID AAS45340 standard; DNA; 6544 BP.  
DE Chemically pretreated genomic DNA associated with cell cycle #23.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.2%; Score 53; DB 4; Length 6544;  
Best Local Similarity 44.0%; Pred. No. 0.029;  
RESULT 339  
ID ABL32646 standard; DNA; 6544 BP.  
DE Human immune system associated gene SEQ ID NO: 619.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.2%; Score 53; DB 6; Length 6544;  
Best Local Similarity 44.0%; Pred. No. 0.029;  
RESULT 340  
ID ABL33979 standard; DNA; 8101 BP.  
DE Human immune system associated gene SEQ ID NO: 1952.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.2%; Score 53; DB 6; Length 8101;  
Best Local Similarity 45.0%; Pred. No. 0.031;  
RESULT 341  
ID ABL33317 standard; DNA; 13574 BP.  
DE Human immune system associated gene SEQ ID NO: 1290.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.2%; Score 53; DB 6; Length 13574;  
Best Local Similarity 48.7%; Pred. No. 0.039;  
RESULT 342  
ID ABL32656 standard; DNA; 9832 BP.  
DE Human immune system associated gene SEQ ID NO: 629.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.2%; Score 51.8; DB 6; Length 9832;  
Best Local Similarity 49.8%; Pred. No. 0.068;  
RESULT 343  
ID AAS46314 standard; DNA; 16750 BP.

DE Tumour suppressor gene derived chemically modified sequence #36.  
PN WO200168912-A2.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.2%; Score 51.6; DB 4; Length 16750;  
Best Local Similarity 44.0%; Pred. No. 0.097;  
RESULT 344  
ID ABLJ2521 standard; DNA; 16750 BP.  
DE Human immune system associated gene SEQ ID NO: 494.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.2%; Score 51.6; DB 6; Length 16750;  
Best Local Similarity 44.0%; Pred. No. 0.097;  
RESULT 345  
ID ADH10017 standard; DNA; 365186 BP.  
DE Human chromosome 2p21-22 fragment containing the DRIP gene.  
PN WO200309310-A1.  
PD 13-NOV-2003.  
PA (UYBR-) UNIV BREMEN.  
Query Match 2.2%; Score 51.6; DB 10; Length 110000;  
Best Local Similarity 46.2%; Pred. No. 0.22;  
RESULT 346  
ID ADRO1991 standard; DNA; 724 BP.  
DE A. GOSSEYPJII genomic DNA PAGI453RP.  
PN US6239264-B1.  
PD 29-MAY-2001.  
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.  
Query Match 2.2%; Score 51.2; DB 2; Length 724;  
Best Local Similarity 48.5%; Pred. No. 0.031;  
RESULT 347  
ID ABQ67074 standard; DNA; 20579 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 104.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.2%; Score 51.2; DB 6; Length 20579;  
Best Local Similarity 47.2%; Pred. No. 0.15;  
RESULT 348  
ID ABLJ4090 standard; DNA; 5407 BP.  
DE Human immune system associated gene SEQ ID NO: 2063.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.1%; Score 50.8; DB 6; Length 5407;  
Best Local Similarity 45.6%; Pred. No. 0.093;  
RESULT 349  
ID ABX39643 standard; CDNA; 392 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #4808.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 2.1%; Score 50.6; DB 8; Length 392;  
Best Local Similarity 52.1%; Pred. No. 0.033;  
RESULT 350  
ID ABLJ70350 standard; DNA; 5504 BP.  
DE Chemically treated cell signalling DNA sequence complementary to #120.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.1%; Score 50.6; DB 6; Length 5504;  
Best Local Similarity 43.8%; Pred. No. 0.11;  
RESULT 351  
ID AAS61309 standard; DNA; 5504 BP.  
DE Human gene regulation-associated gene oligonucleotide #264.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.1%; Score 50.6; DB 6; Length 5504;  
Best Local Similarity 43.8%; Pred. No. 0.11;

RESULT 352  
ID ABZ10100 standard; DNA; 8056 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #240.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.1%; Score 50.4; DB 8; Length 8056;  
Best Local Similarity 47.4%; Pred. No. 0.14;  
RESULT 353  
ID ABLJ34358 standard; DNA; 12237 BP.  
DE Human immune system associated gene SEQ ID NO: 2331.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.1%; Score 50.4; DB 6; Length 12237;  
Best Local Similarity 45.1%; Pred. No. 0.17;  
RESULT 354  
ID AAX52401 standard; DNA; 50 BP.  
DE Probe used to isolate a cDNA clone encoding PRO263.  
PN WO9914328-A2.  
PD 25-MAR-1999.  
PA (GETH) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 355  
ID ADC78525 standard; DNA; 50 BP.  
DE Human PRO protein-related probe SEQ ID 205.  
PN WO200015796-A2.  
PD 23-MAR-2000.  
PA (GETH) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 356  
ID AAF72559 standard; DNA; 50 BP.  
DE Human PRO polypeptide gene hybridisation probe SEQ ID NO: 205.  
PN WO200104311-A1.  
PD 18-JAN-2001.  
PA (GETH) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 357  
ID ACA60168 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein PRO263 probe.  
PN US2003003530-A1.  
PD 02-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 8; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 358  
ID ACD07568 standard; DNA; 50 BP.  
DE Novel human secreted and transmembrane protein PCR probe #31.  
PN US2002197671-A1.  
PD 26-DEC-2002.  
PA (GETH) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 8; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 359  
ID ABX71616 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein PRO263 probe.  
PN US2002132240-A1.  
PD 19-SEP-2002.  
PA (GETH) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 8; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 360  
ID ACH06948 standard; DNA; 50 BP.  
DE Human secreted/transmembrane polypeptide PRO263 probe.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 8; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 361

ID ABX96185 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein cDNA, #38, probe.  
PN US2002160374-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 8; Length 50;  
RESULT 362  
ID ACA05506 standard; DNA; 50 BP.  
DE Human secreted protein PRO263 probe.  
PN US2003023054-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 8; Length 50;  
RESULT 363  
ID ACD20173 standard; DNA; 50 BP.  
DE Human secreted / transmembrane polypeptide PRO263 probe.  
PN US2003036060-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 8; Length 50;  
RESULT 364  
ID ACA54976 standard; DNA; 50 BP.  
DE Novel secreted and transmembrane protein associated primer #90.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 8; Length 50;  
RESULT 365  
ID ACD19811 standard; DNA; 50 BP.  
DE Human secreted / transmembrane polypeptide PRO263 probe.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 9; Length 50;  
RESULT 366  
ID ADB29410 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003092002-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 9; Length 50;  
RESULT 367  
ID ADA18266 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003039971-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 9; Length 50;  
RESULT 368  
ID ACD66958 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein PRO263 probe.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 9; Length 50;  
RESULT 369  
ID ACD83119 standard; DNA; 50 BP.  
DE Human PRO probe #40.  
PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 9; Length 50;  
RESULT 370  
ID ADA16241 standard; DNA; 50 BP.

DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 9; Length 50;  
RESULT 371  
ID ADA42386 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003054401-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 9; Length 50;  
RESULT 372  
ID ACD23297 standard; DNA; 50 BP.  
DE Human PRO probe #37.  
PN US2003064367-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 9; Length 50;  
RESULT 373  
ID ADA16665 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 9; Length 50;  
RESULT 374  
ID ADA13094 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003049622-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 9; Length 50;  
RESULT 375  
ID ADA41962 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003082540-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 9; Length 50;  
RESULT 376  
ID ADA17309 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003017498-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 9; Length 50;  
RESULT 377  
ID ADA42812 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003054351-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 9; Length 50;  
RESULT 378  
ID ACD23659 standard; DNA; 50 BP.  
DE Human PRO probe #37.  
PN US2003064923-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 2.1%; Score 50; DB 9; Length 50;  
RESULT 379  
ID ADB77731 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.

PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 380  
ID ADB74867 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 381  
ID ADC28513 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003059772-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 382  
ID ADC39713 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003059828-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 383  
ID ADC40227 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003059829-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 384  
ID ADC19051 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003036061-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 385  
ID ADC34351 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003036094-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 386  
ID ADC29406 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003049676-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 387  
ID ADC28937 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003049677-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 388  
ID ADC40822 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003054400-A1.

PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 389  
ID ADC19479 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003054441-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 390  
ID ADC3927 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003073077-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 391  
ID ADC12997 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003073079-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 392  
ID ADC12449 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003082541-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 393  
ID ADD05004 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003104469-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 394  
ID ADD04010 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003104381-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 395  
ID ADD03586 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003108983-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 396  
ID ADE34838 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003077583-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC. 2.1%; Score 50; DB 10; Length 50;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 397  
ID ADH59321 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003039972-A1.  
PD 27-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 10; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 398  
ID AD138100 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 10; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 399  
ID ACA59064 standard; DNA; 50 BP.  
DE Human PRO probe #37.  
PN US2002146709-A1.  
PD 10-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 10; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 400  
ID ACA58461 standard; DNA; 50 BP.  
DE Probe #38 used to isolate cDNA encoding a human PRO polypeptide.  
PN US2002192859-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 10; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 401  
ID ADJ26368 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003054349-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 10; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 402  
ID ADE79283 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003135025-A1.  
PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 12; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 403  
ID ADE79707 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003130489-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 12; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 404  
ID ADE73383 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003129592-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 12; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 405  
ID ADE73918 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003148370-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 12; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 406  
ID ADE99472 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003211576-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.

Query Match 2.1%; Score 50; DB 12; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 407  
ID ADE98591 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003211569-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 12; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 408  
ID ADE99018 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003211568-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 12; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 409  
ID ADG40488 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003225253-A1.  
PD 04-DEC-2003.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 2.1%; Score 50; DB 12; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 410  
ID ADF73882 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003180312-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 12; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 411  
ID ADF73458 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003166051-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 12; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 412  
ID ADG92301 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003027145-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 12; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 413  
ID ADG92728 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2003027146-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 12; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 414  
ID ADH20517 standard; DNA; 50 BP.  
DE Human secreted/transmembrane protein, #40, DNA probe #1.  
PN US2004005553-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 2.1%; Score 50; DB 12; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
RESULT 415



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ID ADH07372 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 2.1%; Score 50; DB 12; Length 50;
Pred. No. 0.019;
RESULT 416
ID ADH5917 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.1%; Score 50; DB 12; Length 50;
Pred. No. 0.019;
RESULT 417
ID ADH06945 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 2.1%; Score 50; DB 12; Length 50;
Pred. No. 0.019;
RESULT 418
ID ADI18687 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.1%; Score 50; DB 12; Length 50;
Pred. No. 0.019;
RESULT 419
ID ADI65407 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.1%; Score 50; DB 12; Length 50;
Pred. No. 0.019;
RESULT 420
ID ADI37670 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.1%; Score 50; DB 12; Length 50;
Pred. No. 0.019;
RESULT 421
ID ADH97466 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.1%; Score 50; DB 12; Length 50;
Pred. No. 0.019;
RESULT 422
ID ADI65834 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.1%; Score 50; DB 12; Length 50;
Pred. No. 0.019;
RESULT 423
ID ADH60577 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 2.1%; Score 50; DB 12; Length 50;
Pred. No. 0.019;
RESULT 424
ID ADJ99634 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.1%; Score 50; DB 12; Length 50;
Pred. No. 0.019;
RESULT 425
ID ADL08827 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.1%; Score 50; DB 12; Length 50;
Pred. No. 0.019;
RESULT 426
ID ADM25168 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.1%; Score 50; DB 12; Length 50;
Pred. No. 0.019;
RESULT 427
ID ADM29918 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.1%; Score 50; DB 12; Length 50;
Pred. No. 0.019;
RESULT 428
ID ADO06240 standard; DNA; 50 BP.
DE Human PRO probe #37.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.1%; Score 50; DB 12; Length 50;
Pred. No. 0.019;
RESULT 429
ID ADRI1092 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.1%; Score 50; DB 12; Length 50;
Pred. No. 0.019;
RESULT 430
ID ADRI8001 standard; DNA; 50 BP.
DE Human secreted/transmembrane protein, #40, DNA probe #1.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
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PA (FERR/) FERRARA N.  
 PA (FILV/) FILVAROFF E.  
 PA (FONG/) FONG S.  
 PA (GAOW/) GAO W.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GRIM/) GRIMALDI C J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (KLJA/) KLJAVIN I J.  
 PA (MATH/) MATHER J P.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (ROYM/) ROY M A.  
 PA (STEW/) STEWART T A.  
 PA (TUMA/) TUMAS D.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match 2.1%; Score 50; DB 13; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 0.019;  
 RESULT 431  
 ID AD703677 standard; DNA; 50 BP.  
 DE Human secreted/transmembrane protein, #40, DNA probe #1.  
 PN US2003152922-A1.  
 PD 14-AUG-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 2.1%; Score 50; DB 13; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 0.019;  
 RESULT 432  
 ID ADS74640 standard; DNA; 50 BP.  
 DE Human secreted/transmembrane protein, #40, DNA probe #1.  
 PN US2004185531-A1.  
 PD 23-SEP-2004.  
 PA (ASHK/) ASHKENAZI A.  
 PA (BOTS/) BOTSTEIN D.  
 PA (DESN/) DESNOYERS L.  
 PA (EATO/) EATON D L.  
 PA (FERR/) FERRARA N.  
 PA (FILV/) FILVAROFF E.  
 PA (FONG/) FONG S.  
 PA (GAOW/) GAO W.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GRIM/) GRIMALDI C J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (KLJA/) KLJAVIN I J.  
 PA (MATH/) MATHER J P.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (ROYM/) ROY M A.  
 PA (STEW/) STEWART T A.  
 PA (TUMA/) TUMAS D.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match 2.1%; Score 50; DB 13; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 0.019;  
 RESULT 433  
 ID AB066998 standard; DNA; 37515 BP.  
 DE Human angiogenesis associated polynucleotide SEQ ID NO 28.  
 PN WO200246454-A2.  
 PD 13-JUN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 2.1%; Score 50; DB 6; Length 37515;  
 Best Local Similarity 45.0%; Pred. No. 0.35;  
 RESULT 434  
 ID ADP71270 standard; DNA; 600 BP.  
 DE Human aggrecan B-B' domain gene region SeqID5.  
 PN JP2004154038-A.

PD 03-JUN-2004.  
 PA (SESK) SEIRAGAKU KOGYO CO LTD.  
 Query Match 2.1%; Score 49.6; DB 12; Length 600;  
 Best Local Similarity 51.9%; Pred. No. 0.071;  
 RESULT 435  
 ID ADU13490 standard; DNA; 6951 BP.  
 DE Osteoarthritis-associated polymorphic nucleotide #22.  
 PN WO2003054166-A2.  
 PD 03-JUL-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 2.1%; Score 49.6; DB 10; Length 6951;  
 Best Local Similarity 51.9%; Pred. No. 0.21;  
 RESULT 436  
 ID ADL13489 standard; DNA; 7137 BP.  
 DE Osteoarthritis-associated polymorphic nucleotide #21.  
 PN WO2003054166-A2.  
 PD 03-JUL-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 2.1%; Score 49.6; DB 10; Length 7137;  
 Best Local Similarity 51.9%; Pred. No. 0.21;  
 RESULT 437  
 ID ADP65694 standard; DNA; 7137 BP.  
 DE Human aggrecan 1 (chondroitin sulfate proteoglycan 1, large DNA.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Query Match 2.1%; Score 49.6; DB 11; Length 7137;  
 Best Local Similarity 51.9%; Pred. No. 0.21;  
 RESULT 438  
 ID ADP65777 standard; DNA; 7137 BP.  
 DE Human large aggregating cartilage proteoglycan core protein mRNA, DNA.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Query Match 2.1%; Score 49.6; DB 11; Length 7137;  
 Best Local Similarity 51.9%; Pred. No. 0.21;  
 RESULT 439  
 ID ABK31511 standard; DNA; 47108 BP.  
 DE Signal transduction associated gene modified complementary DNA #177.  
 PN WO200200926-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 2.1%; Score 49.6; DB 6; Length 47108;  
 Best Local Similarity 44.5%; Pred. No. 0.48;  
 RESULT 440  
 ID ABL33569 standard; DNA; 8305 BP.  
 DE Human immune system associated gene SEQ ID NO: 1542.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 2.1%; Score 49.4; DB 6; Length 8305;  
 Best Local Similarity 45.3%; Pred. No. 0.25;  
 RESULT 441  
 ID AB080553 standard; DNA; 47841 BP.  
 DE Human Canion gene fragment #3.  
 PN WO200246404-A2.  
 PD 13-JUN-2002.  
 PA (GEST) GENSET.  
 Query Match 2.1%; Score 49.4; DB 6; Length 47841;  
 Best Local Similarity 44.4%; Pred. No. 0.55;  
 RESULT 442  
 ID ABL34125 standard; DNA; 73334 BP.  
 DE Human immune system associated gene SEQ ID NO: 2098.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 2.1%; Score 49.4; DB 6; Length 73334;  
 Best Local Similarity 47.6%; Pred. No. 0.66;  
 RESULT 443  
 ID ABL92319 standard; DNA; 73334 BP.  
 DE Chemically treated DNA repair gene fragment complementary to#64.  
 PN WO200181622-A2.  
 PD 01-NOV-2001.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.1%; Score 49.4; DB 6; Length 73334;  
Best Local Similarity 47.6%; Pred. No. 0.66;  
RESULT 444  
ID ADR01499 standard; DNA; 663 BP.  
DE A. gossypii genomic DNA PAG1076UP.  
PN US6239264-B1.  
PD 29-MAY-2001.  
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.  
Query Match 2.1%; Score 49.2; DB 2; Length 663;  
Best Local Similarity 48.1%; Pred. No. 0.093;  
RESULT 445  
ID ADR02344 standard; DNA; 732 BP.  
DE A. gossypii genomic DNA PAG1633UP.  
PN US6239264-B1.  
PD 29-MAY-2001.  
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.  
Query Match 2.1%; Score 49.2; DB 2; Length 732;  
Best Local Similarity 48.3%; Pred. No. 0.097;  
RESULT 446  
ID ADR01842 standard; DNA; 854 BP.  
DE A. gossypii genomic DNA PAG1372UP.  
PN US6239264-B1.  
PD 29-MAY-2001.  
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.  
Query Match 2.1%; Score 49.2; DB 2; Length 854;  
Best Local Similarity 48.9%; Pred. No. 0.1;  
RESULT 447  
ID ABL33784 standard; DNA; 7461 BP.  
DE Human immune system associated gene SEQ ID NO: 1757.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.1%; Score 49.2; DB 6; Length 7461;  
Best Local Similarity 44.8%; Pred. No. 0.27;  
RESULT 448  
ID AAS46815 standard; DNA; 21354 BP.  
DE Tumour suppressor gene derived chemically modified sequence #512.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.1%; Score 49.2; DB 4; Length 21354;  
Best Local Similarity 47.2%; Pred. No. 0.43;  
RESULT 449  
ID ABL67703 standard; DNA; 302250 BP.  
DE Oesophagus cancer related gene sequence SEQ ID NO:6040.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 2.1%; Score 49.2; DB 6; Length 302250;  
Best Local Similarity 47.2%; Pred. No. 1.4;  
RESULT 450  
ID AAS46292 standard; DNA; 5430 BP.  
DE Tumour suppressor gene derived chemically modified sequence #14.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.1%; Score 49; DB 4; Length 5430;  
Best Local Similarity 48.0%; Pred. No. 0.26;  
RESULT 451  
ID AAS46429 standard; DNA; 6106 BP.  
DE Tumour suppressor gene derived chemically modified sequence #151.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.1%; Score 49; DB 4; Length 6106;  
Best Local Similarity 45.9%; Pred. No. 0.28;  
RESULT 452  
ID ABK40031 standard; DNA; 6106 BP.  
DE Human chemically pretreated gene sequence #57 strand 1.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.

Query Match 2.1%; Score 49; DB 6; Length 6106;  
Best Local Similarity 45.9%; Pred. No. 0.28;  
RESULT 453  
ID ABL33472 standard; DNA; 6106 BP.  
DE Human immune system associated gene SEQ ID NO: 1445.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.1%; Score 49; DB 6; Length 6106;  
Best Local Similarity 45.9%; Pred. No. 0.28;  
RESULT 454  
ID ABL33207 standard; DNA; 15767 BP.  
DE Human immune system associated gene SEQ ID NO: 1180.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.1%; Score 49; DB 6; Length 15767;  
Best Local Similarity 48.9%; Pred. No. 0.42;  
RESULT 455  
ID ABL34553 standard; DNA; 15767 BP.  
DE Human metastasis associated gene SEQ ID NO: 106.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.1%; Score 49; DB 6; Length 15767;  
Best Local Similarity 48.9%; Pred. No. 0.42;  
RESULT 456  
ID ADS99814 standard; DNA; 15767 BP.  
DE Complement of bisulphite treated metastasis-associated human gene #53.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 2.1%; Score 49; DB 7; Length 15767;  
Best Local Similarity 48.9%; Pred. No. 0.42;  
RESULT 457  
ID ADR01595 standard; DNA; 860 BP.  
DE A. gossypii genomic DNA PAG1240UP.  
PN US6239264-B1.  
PD 29-MAY-2001.  
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.  
Query Match 2.1%; Score 48.8; DB 2; Length 860;  
Best Local Similarity 50.0%; Pred. No. 0.13;  
RESULT 458  
ID ABL32426 standard; DNA; 9810 BP.  
DE Human immune system associated gene SEQ ID NO: 399.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.1%; Score 48.8; DB 6; Length 9810;  
Best Local Similarity 44.9%; Pred. No. 0.38;  
RESULT 459  
ID ABL33299 standard; DNA; 12025 BP.  
DE Human immune system associated gene SEQ ID NO: 1272.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.1%; Score 48.8; DB 6; Length 12025;  
Best Local Similarity 45.6%; Pred. No. 0.42;  
RESULT 460  
ID ABL33485 standard; DNA; 13202 BP.  
DE Human immune system associated gene SEQ ID NO: 1458.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.1%; Score 48.8; DB 6; Length 13202;  
Best Local Similarity 46.1%; Pred. No. 0.44;  
RESULT 461  
ID ABL33530 standard; DNA; 13712 BP.  
DE Human immune system associated gene SEQ ID NO: 1503.  
PN WO200200928-A2.  
PD 03-JAN-2002.

PA (EPiG-) EPIGENOMICS AG.  
Query Match 2.1%; Score 48.8; DB 6; Length 13712;  
Best Local Similarity 46.1%; Pred. No. 0.45;  
RESULT 462  
ID ABL56203 standard; DNA; 32392 BP.  
DE AMEPV genome fragment#5.  
PN WO200212526-A2.  
PD 14-FEB-2002.  
PA (UYFL) UNIV FLORIDA.  
Query Match 2.1%; Score 48.8; DB 6; Length 32392;  
Best Local Similarity 45.5%; Pred. No. 0.65;  
RESULT 463  
ID ABK31200 standard; DNA; 6154 BP.  
DE Signal transduction associated gene modified DNA #22.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 48.6; DB 6; Length 6154;  
Best Local Similarity 45.8%; Pred. No. 0.35;  
RESULT 464  
ID ABL70167 standard; DNA; 6154 BP.  
DE Chemically treated cell signalling DNA sequence#29.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 48.6; DB 6; Length 6154;  
Best Local Similarity 45.8%; Pred. No. 0.35;  
RESULT 465  
ID AAS61112 standard; DNA; 6154 BP.  
DE Human gene regulation-associated gene oligonucleotide #67.  
PN WO20017375-A2.  
PD 18-OCT-2001.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 48.6; DB 6; Length 6154;  
Best Local Similarity 45.8%; Pred. No. 0.35;  
RESULT 466  
ID AAX20257 standard; DNA; 10749 BP.  
DE Borrelia burgdorferi polynucleotide sequence #10.  
PN WO9858943-A1.  
PD 30-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (MEDI-) MEDIMMUNE INC.  
Query Match 2.0%; Score 48.6; DB 2; Length 10749;  
Best Local Similarity 47.5%; Pred. No. 0.45;  
RESULT 467  
ID ABL34053 standard; DNA; 11172 BP.  
DE Human immune system associated gene SEQ ID NO: 2026.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 48.6; DB 6; Length 11172;  
Best Local Similarity 49.2%; Pred. No. 0.46;  
RESULT 468  
ID ABL32191 standard; DNA; 17137 BP.  
DE Human immune system associated gene SEQ ID NO: 164.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 48.6; DB 6; Length 17137;  
Best Local Similarity 43.4%; Pred. No. 0.55;  
RESULT 469  
ID ABO67160 standard; DNA; 6775 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 190.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 48.4; DB 6; Length 6775;  
Best Local Similarity 47.4%; Pred. No. 0.41;  
RESULT 470  
Query Match 2.0%; Score 48.4; DB 6; Length 110000;  
Best Local Similarity 48.2%; Pred. No. 1.4;  
RESULT 471  
ID ACH93277 standard; DNA; 334 BP.

DE Human genome derived single exon probe #26472.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 2.0%; Score 48.2; DB 12; Length 334;  
Best Local Similarity 52.8%; Pred. No. 0.12;  
RESULT 472  
ID ACH79577 standard; DNA; 538 BP.  
DE Human genome derived single exon probe #12772.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 2.0%; Score 48.2; DB 12; Length 538;  
Best Local Similarity 52.8%; Pred. No. 0.15;  
RESULT 473  
ID ABA06490 standard; CDNA; 972 BP.  
DE Human cDNA SEQ ID NO: 156.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.0%; Score 48.2; DB 4; Length 972;  
Best Local Similarity 52.8%; Pred. No. 0.2;  
RESULT 474  
ID ABV83827 standard; CDNA; 972 BP.  
DE Human polynucleotide SEQ ID NO 156.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 2.0%; Score 48.2; DB 6; Length 972;  
Best Local Similarity 52.8%; Pred. No. 0.2;  
RESULT 475  
ID AAV41923 standard; CDNA; 1587 BP.  
DE Nucleotide sequence of the cDNA clone BEF (HSXCK41).  
PN WO9831800-A2.  
PD 23-JUL-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (AUCK-) AUCKLAND UNISERVICES LTD.  
Query Match 2.0%; Score 48.2; DB 2; Length 1587;  
Best Local Similarity 52.8%; Pred. No. 0.24;  
RESULT 476  
ID AAV34196 standard; DNA; 1720 BP.  
DE Human secreted protein gene 43 clone HSXCK41.  
PN WO9839446-A2.  
PD 11-SEP-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.0%; Score 48.2; DB 2; Length 1720;  
Best Local Similarity 52.8%; Pred. No. 0.25;  
RESULT 477  
ID ACD08067 standard; CDNA; 1720 BP.  
DE cDNA encoding novel human secreted protein #43.  
PN US2003027132-A1.  
PD 06-FEB-2003.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (FISC/) FISCHER C L.  
PA (SOPP/) SOPPET D R.  
PA (CART/) CARTER K C.  
PA (BEDN/) BEDNARIK D R.  
PA (ENDR/) ENDRESS G A.  
PA (YUGG/) YU G.  
PA (NIJJ/) NI J.  
PA (FENG/) FENG P.  
PA (YOUN/) YOUNG P E.  
PA (GREE/) GREENE J M.  
PA (FERR/) FERRIE A M.  
PA (DUAN/) DUAN R.  
PA (HUUJ/) HU J.

PA (FLOR/) FLORENCE K A.  
PA (OLSE/) OLSEN H S.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
PA (SHIY/) SHI Y.  
Query Match  
Best Local Similarity 2.0%; Score 48.2; DB 8; Length 1720;  
52.8%; Pred. No. 0.25;  
RESULT 478  
ID AAF29460 standard; cDNA; 2013 BP.  
DE Human TANGO 332 cDNA open reading frame.  
PN WO200100638-A2.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 2.0%; Score 48.2; DB 4; Length 2013;  
52.8%; Pred. No. 0.27;  
RESULT 479  
ID ACD66767 standard; cDNA; 2013 BP.  
DE Secreted polypeptide-related cDNA #51.  
PN US200302279-A1.  
PD 30-JAN-2003.  
PA (FRAS/) FRASER C C.  
PA (BARN/) BARNES T M.  
PA (SHAR/) SHARP J D.  
PA (KIRS/) KIRST S J.  
PA (MYER/) MYERS P S.  
PA (LEIB/) LEIBY K R.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (WRIG/) WRIGHTON N.  
PA (MACK/) MACKAY C R.  
PA (GOOD/) GOODEARL A D J.  
Query Match  
Best Local Similarity 2.0%; Score 48.2; DB 8; Length 2013;  
52.8%; Pred. No. 0.27;  
RESULT 480  
ID ADB90775 standard; cDNA; 2013 BP.  
DE Human TANGO 332 open reading frame.  
PN US2003082586-A1.  
PD 01-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 2.0%; Score 48.2; DB 9; Length 2013;  
52.8%; Pred. No. 0.27;  
RESULT 481  
ID ADF71510 standard; cDNA; 2013 BP.  
DE Human TANGO 332 CDS.  
PN US2003175733-A1.  
PD 18-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 2.0%; Score 48.2; DB 10; Length 2013;  
52.8%; Pred. No. 0.27;  
RESULT 482  
ID ADQ10328 standard; cDNA; 2013 BP.  
DE Human polynucleotide #58.  
PN US2004121396-A1.  
PD 24-JUN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 2013;  
52.8%; Pred. No. 0.27;  
RESULT 483  
ID AAX20297 standard; DNA; 2496 BP.  
DE Borrelia burgdorferi polynucleotide sequence #50.  
PN WO9858943-A1.  
PD 30-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (MEDI-) MEDIMUNE INC.  
Query Match  
Best Local Similarity 2.0%; Score 48.2; DB 2; Length 2496;  
45.6%; Pred. No. 0.3;  
RESULT 484  
ID AAF29459 standard; cDNA; 2730 BP.  
DE Human TANGO 332 cDNA.  
PN WO200100638-A2.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 2.0%; Score 48.2; DB 4; Length 2730;  
52.8%; Pred. No. 0.31;  
RESULT 485  
ID ACD66766 standard; cDNA; 2730 BP.  
DE Secreted polypeptide-related cDNA #50.  
PN US200302279-A1.  
PD 30-JAN-2003.  
PA (FRAS/) FRASER C C.  
PA (BARN/) BARNES T M.  
PA (SHAR/) SHARP J D.  
PA (KIRS/) KIRST S J.  
PA (MYER/) MYERS P S.  
PA (LEIB/) LEIBY K R.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (WRIG/) WRIGHTON N.  
PA (MACK/) MACKAY C R.  
PA (GOOD/) GOODEARL A D J.  
Query Match  
Best Local Similarity 2.0%; Score 48.2; DB 8; Length 2730;  
52.8%; Pred. No. 0.31;  
RESULT 486  
ID ADB90774 standard; cDNA; 2730 BP.  
DE Human cDNA encoding TANGO 332.  
PN US2003082586-A1.  
PD 01-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 2.0%; Score 48.2; DB 9; Length 2730;  
52.8%; Pred. No. 0.31;  
RESULT 487  
ID ADF71509 standard; cDNA; 2730 BP.  
DE Human TANGO 332 cDNA.  
PN US2003175733-A1.  
PD 18-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 2.0%; Score 48.2; DB 10; Length 2730;  
52.8%; Pred. No. 0.31;  
RESULT 488  
ID ADQ10327 standard; cDNA; 2730 BP.  
DE Human polynucleotide #57.  
PN US2004121396-A1.  
PD 24-JUN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 2730;  
52.8%; Pred. No. 0.31;  
RESULT 489  
ID AAD48133 standard; DNA; 2878 BP.  
DE Human chondroitin sulphate proteoglycan BEHAB/brevican DNA.  
PN WO200276510-A1.  
PD 03-OCT-2002.  
PA (AGYT-) AGY THERAPEUTICS INC.  
Query Match  
Best Local Similarity 2.0%; Score 48.2; DB 8; Length 2878;  
52.8%; Pred. No. 0.32;  
RESULT 490  
ID ADN38941 standard; cDNA; 2878 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:259.  
PN WO2003042861-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match  
Best Local Similarity 2.0%; Score 48.2; DB 11; Length 2878;  
52.8%; Pred. No. 0.32;  
RESULT 491  
ID ADK67783 standard; DNA; 2878 BP.  
DE Human glycosylation-variant BEHAB isoform coding sequence.  
PN WO2004013356-A1.  
PD 12-FEB-2004.  
PA (UYVA-) UNIV YALE.  
Query Match  
Best Local Similarity 2.0%; Score 48.2; DB 12; Length 2878;  
52.8%; Pred. No. 0.32;  
RESULT 492  
ID ACN37482 standard; cDNA; 3275 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA323924, SEQ ID NO:394.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH-) GENENTECH INC.

Query Match 2.0%; Score 48.2; DB 13; Length 3275;  
Best Local Similarity 52.8%; Pred. No. 0.33;  
RESULT 493  
ID ADH18923 standard; cDNA; 3293 BP.  
DE Human cell adhesion and extracellular matrix CADECM-19 cDNA - SEQ 50.  
PN WO2003094843-A2.  
PD 20-NOV-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 2.0%; Score 48.2; DB 12; Length 3293;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 494  
ID AD128068 standard; cDNA; 3438 BP.  
DE ECWAD gene clone 6755002CB1.  
PN WO200202634-A2.  
PD 10-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 2.0%; Score 48.2; DB 6; Length 3438;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 495  
ID ADQ83194 standard; cDNA; 3467 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #8.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 2.0%; Score 48.2; DB 12; Length 3467;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 496  
ID ADQ85107 standard; cDNA; 3467 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1921.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 2.0%; Score 48.2; DB 12; Length 3467;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 497  
ID AAA91017 standard; DNA; 3476 BP.  
DE Human secreted protein PRO6018 coding sequence.  
PN WO200075317-A2.  
PD 14-DEC-2000.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 4; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 498  
ID ABK69986 standard; DNA; 3476 BP.  
DE cDNA encoding human Pro peptide #26.  
PN WO200224888-A2.  
PD 28-MAR-2002.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 6; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 499  
ID ADA01319 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003068779-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 9; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 500  
ID ADA43748 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003064474-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 9; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 501  
ID ADA43516 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.

PN US2003073196-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 9; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 502  
ID ADA01191 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003068782-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 9; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 503  
ID ADA01075 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003068780-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 9; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 504  
ID ADA43632 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003073190-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 9; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 505  
ID ADA06894 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003068781-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 9; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 506  
ID ADA08382 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003068783-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 9; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 507  
ID ADB99675 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide SEQ ID 51.  
PN US2003082728-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 9; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 508  
ID ADB86958 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003082726-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 9; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 509  
ID ADB66113 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003082729-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 9; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 510  
ID ADB99791 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide SEQ ID 51.  
PN US2003073192-A1.

PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 10; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 511  
ID ADB99446 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003082731-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 10; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 512  
ID ADB65997 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003082732-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 10; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 513  
ID ADC23395 standard; cDNA; 3476 BP.  
DE Human cDNA clone (SeqID 51) encoding the transmembrane PRO protein.  
PN US2003073193-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 10; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 514  
ID ADC26088 standard; cDNA; 3476 BP.  
DE Human PRO6018 cDNA.  
PN US2003073194-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 10; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 515  
ID ADE04915 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003068778-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 10; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 516  
ID ADE11221 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003073191-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 10; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 517  
ID ADB88152 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003082733-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 10; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 518  
ID ADP95447 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003064473-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 10; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 519  
ID ADE06377 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003073195-A1.  
PD 17-APR-2003.

PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 10; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 520  
ID ADE38152 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119120-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 10; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 521  
ID ADB88268 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003073189-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 10; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 522  
ID ADD90849 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003073188-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 10; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 523  
ID ADF99404 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003078401-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 10; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 524  
ID ADG06497 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003077742-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 10; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 525  
ID ADG05448 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003077741-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 10; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 526  
ID ADG82449 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003077744-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 10; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 527  
ID ADE51702 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104560-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC. 2.0%; Score 48.2; DB 12; Length 3476;  
Query Match  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 528  
ID ADE51818 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104561-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.

Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 529  
ID ADE337676 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104564-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 530  
ID ADE37560 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104565-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 531  
ID ADD95331 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003138901-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 532  
ID ADE338031 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003104566-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 533  
ID ADE76120 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003124665-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 534  
ID ADE339443 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119117-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 535  
ID ADE04247 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003096364-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 536  
ID ADE339844 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138896-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 537  
ID ADE19709 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138903-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;

Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 538  
ID ADE77287 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003124666-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 539  
ID ADE65395 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119116-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 540  
ID ADE76004 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003124663-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 541  
ID ADE37915 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119119-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 542  
ID ADE64525 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119114-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 543  
ID ADE38860 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003096363-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 544  
ID ADE51934 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104562-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 545  
ID ADD90965 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003138902-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 546  
ID ADE38744 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003108996-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;



RESULT 547  
ID ADE37444 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104563-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 548  
ID ADE06261 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138898-A1.  
PD 24-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 549  
ID ADD90120 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003138904-A1.  
PD 24-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 550  
ID ADE38628 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119086-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 551  
ID ADE39559 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119118-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 552  
ID ADDB9164 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138897-A1.  
PD 24-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 553  
ID ADE88931 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138899-A1.  
PD 24-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 554  
ID ADE19825 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003138900-A1.  
PD 24-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 555  
ID ADE77403 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003124667-A1.  
PD 03-JUL-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 556

ID ADE65279 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119113-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 557  
ID ADE39327 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119115-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 558  
ID ADE38512 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003104559-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 559  
ID ADG11065 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003170809-A1.  
PD 11-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 560  
ID ADG10949 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003077743-A1.  
PD 24-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 561  
ID ADH31477 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119139-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 562  
ID ADH38725 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119140-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 563  
ID ADH29360 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119137-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 564  
ID ADH23663 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119143-A1.  
PD 26-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 565  
ID ADH26993 standard; cDNA; 3476 BP.

DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119135-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 566  
ID ADH38261 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119124-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 567  
ID ADH26877 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119134-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 568  
ID ADH38145 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119123-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 569  
ID ADH38841 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119141-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 570  
ID ADH23779 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003119142-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 571  
ID ADH40155 standard; cDNA; 3476 BP.  
DE Human PRO6018 cDNA.  
PN US2003119132-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 572  
ID ADH40039 standard; cDNA; 3476 BP.  
DE Human PRO6018 cDNA.  
PN US2003119133-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 573  
ID ADH31361 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003119138-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 574  
ID ADH29239 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.

PN US2003119136-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 575  
ID ADH49454 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119127-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 576  
ID ADH51918 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119125-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 577  
ID ADH49773 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119128-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 578  
ID ADH52374 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119130-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 579  
ID ADH52490 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119129-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 580  
ID ADH58487 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119121-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 581  
ID ADH51802 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119126-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 582  
ID ADH58363 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119122-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 583  
ID ADH13560 standard; cDNA; 3476 BP.  
DE Novel human secreted and transmembrane protein PRO6018 cDNA.  
PN US2003119131-A1.

PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 584  
ID ADK00816 standard; cDNA; 3476 BP.  
DE Human PRO polynucleotide #26.  
PN US2003186373-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 585  
ID ADL08557 standard; cDNA; 3476 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO6018.  
PN US2003186372-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 3476;  
Best Local Similarity 52.8%; Pred. No. 0.34;  
RESULT 586  
ID ACN42086 standard; cDNA; 4353 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:961.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 2.0%; Score 48.2; DB 13; Length 4353;  
Best Local Similarity 52.8%; Pred. No. 0.38;  
RESULT 587  
ID ACN42085 standard; cDNA; 4391 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:960.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 2.0%; Score 48.2; DB 13; Length 4391;  
Best Local Similarity 52.8%; Pred. No. 0.38;  
RESULT 588  
ID ACN42084 standard; cDNA; 4536 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:959.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 2.0%; Score 48.2; DB 13; Length 4536;  
Best Local Similarity 52.8%; Pred. No. 0.39;  
RESULT 589  
ID ACN42083 standard; cDNA; 4545 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:958.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 2.0%; Score 48.2; DB 13; Length 4545;  
Best Local Similarity 52.8%; Pred. No. 0.39;  
RESULT 590  
ID ACN42082 standard; cDNA; 4659 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:957.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 2.0%; Score 48.2; DB 13; Length 4659;  
Best Local Similarity 52.8%; Pred. No. 0.39;  
RESULT 591  
ID ADR06936 standard; cDNA; 4966 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 442.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 2.0%; Score 48.2; DB 13; Length 4966;  
Best Local Similarity 54.1%; Pred. No. 0.4;  
RESULT 592  
ID AAS28917 standard; DNA; 5430 BP.  
DE Human immunoglobulin encoding genomic DNA SEQ ID NO 279.  
PN WO200155315-A2.  
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.0%; Score 48.2; DB 4; Length 5430;  
Best Local Similarity 52.8%; Pred. No. 0.42;  
RESULT 593  
ID ADB31758 standard; DNA; 5430 BP.  
DE Human novel protein DNA SEQ ID NO 279.  
PN US2003077806-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 2.0%; Score 48.2; DB 10; Length 5430;  
Best Local Similarity 52.8%; Pred. No. 0.42;  
RESULT 594  
ID AAS46429 standard; DNA; 6106 BP.  
DE Tumour suppressor gene derived chemically modified sequence #151.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 48.2; DB 4; Length 6106;  
Best Local Similarity 44.7%; Pred. No. 0.44;  
RESULT 595  
ID ABK40031 standard; DNA; 6106 BP.  
DE Human chemically pretreated gene sequence #57 strand 1.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 48.2; DB 6; Length 6106;  
Best Local Similarity 44.7%; Pred. No. 0.44;  
RESULT 596  
ID ABL33472 standard; DNA; 6106 BP.  
DE Human immune system associated gene SEQ ID NO: 1445.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 48.2; DB 6; Length 6106;  
Best Local Similarity 44.7%; Pred. No. 0.44;  
RESULT 597  
ID ADH12179 standard; cDNA; 9646 BP.  
DE Human CHD5 (chromodomain, helicase, DNA-binding 5)-encoding cDNA.  
PN WO2003106650-A2.  
PD 24-DEC-2003.  
PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.  
Query Match 2.0%; Score 48.2; DB 12; Length 9646;  
Best Local Similarity 54.1%; Pred. No. 0.54;  
RESULT 598  
ID ADQ17729 standard; DNA; 143239 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 546.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 2.0%; Score 48.2; DB 12; Length 143239;  
Best Local Similarity 44.9%; Pred. No. 1.8;  
RESULT 599  
ID ADS89278 standard; DNA; 5286 BP.  
DE Oligonucleotide of the invention SEQ ID NO:294.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 48; DB 13; Length 5286;  
Best Local Similarity 45.3%; Pred. No. 0.46;  
RESULT 600  
ID ADS89552 standard; DNA; 5286 BP.  
DE Oligonucleotide of the invention SEQ ID NO:568.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 48; DB 13; Length 5286;  
Best Local Similarity 45.3%; Pred. No. 0.46;  
RESULT 601  
ID ABK28414 standard; DNA; 5362 BP.  
DE DNA transcription associated complementary genomic DNA #144.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.

Query Match 2.0%; Score 48; DB 6; Length 5362;  
Best Local Similarity 44.9%; Pred. No. 0.47;  
RESULT 602  
ID ACN42826 standard; cDNA; 7678 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1701.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 2.0%; Score 48; DB 13; Length 7678;  
Best Local Similarity 51.4%; Pred. No. 0.55;  
RESULT 603  
ID ACN42825 standard; cDNA; 7975 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1700.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 2.0%; Score 48; DB 13; Length 7975;  
Best Local Similarity 51.4%; Pred. No. 0.56;  
RESULT 604  
ID ABK31511 standard; DNA; 47108 BP.  
DE Signal transduction associated gene modified complementary DNA #177.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.8; DB 6; Length 47108;  
Best Local Similarity 46.5%; Pred. No. 1.4;  
RESULT 605  
ID AAH93026 standard; DNA; 700 BP.  
DE Human inflammatory bowel disease related gene fragment IGR3319a.  
PN WO200142511-A2.  
PD 14-JUN-2001.  
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.  
PA (ELLJ-) ELLIPSIS BIOTHERAPEUTICS CORP.  
Query Match 2.0%; Score 47.6; DB 4; Length 700;  
Best Local Similarity 47.5%; Pred. No. 0.24;  
RESULT 606  
ID ABL33527 standard; DNA; 9965 BP.  
DE Human immune system associated gene SEQ ID NO: 1500.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.6; DB 6; Length 9965;  
Best Local Similarity 45.3%; Pred. No. 0.77;  
RESULT 607  
ID AAS46660 standard; DNA; 12578 BP.  
DE Tumour suppressor gene derived chemically modified sequence #382.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.6; DB 4; Length 12578;  
Best Local Similarity 48.6%; Pred. No. 0.86;  
RESULT 608  
ID AAS46395 standard; DNA; 12781 BP.  
DE Tumour suppressor gene derived chemically modified sequence #107.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.6; DB 4; Length 12781;  
Best Local Similarity 49.6%; Pred. No. 0.86;  
RESULT 609  
ID ABL92228 standard; DNA; 12781 BP.  
DE Chemically treated DNA repair gene fragment#19.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.6; DB 6; Length 12781;  
Best Local Similarity 49.6%; Pred. No. 0.86;  
RESULT 610  
ID ADB54127 standard; DNA; 12781 BP.  
DE Pretreated genomic DNA region 51.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.

Query Match 2.0%; Score 47.6; DB 10; Length 12781;  
Best Local Similarity 49.6%; Pred. No. 0.86;  
RESULT 611  
ID ADB54255 standard; DNA; 12781 BP.  
DE Pretreated genomic DNA region 179.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.6; DB 10; Length 12781;  
Best Local Similarity 49.6%; Pred. No. 0.86;  
RESULT 612  
ID ABL56203 standard; DNA; 32392 BP.  
DE AmbPV genome fragment#5.  
PN WO200212526-A2.  
PD 14-FEB-2002.  
PA (UYFL) UNIV FLORIDA.  
Query Match 2.0%; Score 47.6; DB 6; Length 32392;  
Best Local Similarity 44.8%; Pred. No. 1.3;  
RESULT 613  
ID ABL34073 standard; DNA; 40862 BP.  
DE Human immune system associated gene SEQ ID NO: 2046.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.4; DB 6; Length 40862;  
Best Local Similarity 50.2%; Pred. No. 1.6;  
RESULT 614  
ID ADH30232 standard; DNA; 161671 BP.  
DE Human PLOD2 DNA.  
PN US2003124535-A1.  
PD 03-JUL-2003.  
PA (VITI-) VITIVITY INC.  
Query Match 2.0%; Score 47.4; DB 12; Length 161671;  
Best Local Similarity 46.7%; Pred. No. 3;  
RESULT 615  
ID AAL15210 standard; cDNA; 883 BP.  
DE Human breast cancer expressed polynucleotide 7667.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.0%; Score 47.2; DB 4; Length 883;  
Best Local Similarity 39.8%; Pred. No. 0.33;  
RESULT 616  
ID ACN85231 standard; DNA; 960 BP.  
DE Breast cancer related marker, seq id 6381.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 2.0%; Score 47.2; DB 11; Length 960;  
Best Local Similarity 39.8%; Pred. No. 0.35;  
RESULT 617  
ID AAS46694 standard; DNA; 5413 BP.  
DE Tumour suppressor gene derived chemically modified sequence #417.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.2; DB 4; Length 5413;  
Best Local Similarity 46.9%; Pred. No. 0.74;  
RESULT 618  
ID ABK28374 standard; DNA; 6074 BP.  
DE DNA transcription associated complementary genomic DNA #124.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.2; DB 6; Length 6074;  
Best Local Similarity 45.9%; Pred. No. 0.78;  
RESULT 619  
ID AAS46433 standard; DNA; 6174 BP.  
DE Tumour suppressor gene derived chemically modified sequence #155.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.2; DB 4; Length 6174;

Best Local Similarity 44.4%; Pred. No. 0.79;  
RESULT 620  
ID ABL32216 standard; DNA; 6191 BP.  
DE Human immune system associated gene SEQ ID NO: 1189.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.2; DB 6; Length 6191;  
Best Local Similarity 44.8%; Pred. No. 0.79;  
RESULT 621  
ID ABK31306 standard; DNA; 6191 BP.  
DE Signal transduction associated gene modified DNA #75.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.2; DB 6; Length 6191;  
Best Local Similarity 44.8%; Pred. No. 0.79;  
RESULT 622  
ID ABL70281 standard; DNA; 6191 BP.  
DE Chemically treated cell signalling DNA sequence#86.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.2; DB 6; Length 6191;  
Best Local Similarity 44.8%; Pred. No. 0.79;  
RESULT 623  
ID ABN80160 standard; DNA; 6191 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 177.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.2; DB 6; Length 6191;  
Best Local Similarity 44.8%; Pred. No. 0.79;  
RESULT 624  
ID ABL32628 standard; DNA; 7669 BP.  
DE Human immune system associated gene SEQ ID NO: 601.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.2; DB 6; Length 7669;  
Best Local Similarity 51.4%; Pred. No. 0.87;  
RESULT 625  
ID ABL32191 standard; DNA; 17137 BP.  
DE Human immune system associated gene SEQ ID NO: 164.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.2; DB 6; Length 17137;  
Best Local Similarity 44.8%; Pred. No. 1.2;  
RESULT 626  
ID AAS4665 standard; DNA; 17144 BP.  
DE Tumour suppressor gene derived chemically modified sequence #387.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.2; DB 4; Length 17144;  
Best Local Similarity 53.2%; Pred. No. 1.2;  
RESULT 627  
ID ABN80227 standard; DNA; 19236 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 244.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47.2; DB 6; Length 19236;  
Best Local Similarity 49.5%; Pred. No. 1.3;  
RESULT 628  
ID AA161373 standard; DNA; 513445 BP.  
DE Soybean 318013 region A3, SEQ ID NO: 4.  
PN WO200151627-A2.  
PD 19-JUL-2001.  
PA (MONS) MONSANTO CO.  
Query Match 2.0%; Score 47.2; DB 5; Length 110000;  
Best Local Similarity 47.3%; Pred. No. 2.8;

RESULT 629  
ID AAS46740 standard; DNA; 4045 BP.  
DE Tumour suppressor gene derived chemically modified sequence #464.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47; DB 4; Length 4045;  
Best Local Similarity 51.2%; Pred. No. 0.73;  
RESULT 630  
ID AAD22381 standard; DNA; 5006 BP.  
DE Cotton oleoyl-PC delta12-desaturase (ghFAD2-1) gene.  
PN WO200179499-A1.  
PD 25-OCT-2001.  
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
Query Match 2.0%; Score 47; DB 5; Length 5006;  
Best Local Similarity 47.2%; Pred. No. 0.81;  
RESULT 631  
ID AAS46601 standard; DNA; 7057 BP.  
DE Tumour suppressor gene derived chemically modified sequence #323.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47; DB 4; Length 7057;  
Best Local Similarity 46.4%; Pred. No. 0.94;  
RESULT 632  
ID ABL33848 standard; DNA; 7057 BP.  
DE Human immune system associated gene SEQ ID NO: 1821.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47; DB 6; Length 7057;  
Best Local Similarity 46.4%; Pred. No. 0.94;  
RESULT 633  
ID ABL34594 standard; DNA; 7057 BP.  
DE Human metastasis associated gene SEQ ID NO: 147.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47; DB 6; Length 7057;  
Best Local Similarity 46.4%; Pred. No. 0.94;  
RESULT 634  
ID ABL70407 standard; DNA; 7057 BP.  
DE Chemically treated cell signalling DNA sequence#149.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47; DB 6; Length 7057;  
Best Local Similarity 46.4%; Pred. No. 0.94;  
RESULT 635  
ID AAS61354 standard; DNA; 7057 BP.  
DE Human gene regulation-associated gene oligonucleotide #309.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47; DB 6; Length 7057;  
Best Local Similarity 46.4%; Pred. No. 0.94;  
RESULT 636  
ID ADS99855 standard; DNA; 7057 BP.  
DE Bisulphite treated human gene associated with metastasis #74.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK)/ OLEK A.  
PA (PIEP)/ PIEPENBROCK C.  
PA (BERL)/ BERLIN K.  
Query Match 2.0%; Score 47; DB 7; Length 7057;  
Best Local Similarity 46.4%; Pred. No. 0.94;  
RESULT 637  
ID ABQ67025 standard; DNA; 11964 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 55.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47; DB 6; Length 11964;

Best Local Similarity 46.5%; Pred. No. 1.2;  
RESULT 638  
ID ABK40038 standard; DNA; 16258 BP.  
DE Human chemically pretreated gene sequence #60 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47; DB 6; Length 16258;  
Best Local Similarity 45.3%; Pred. No. 1.4;  
RESULT 639  
ID ABL70376 standard; DNA; 16258 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#133.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 47; DB 6; Length 16258;  
Best Local Similarity 45.3%; Pred. No. 1.4;  
RESULT 640  
ID ACN44758 standard; DNA; 172569 BP.  
DE Human genomic sequence HCG20145.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 2.0%; Score 47; DB 11; Length 172569;  
Best Local Similarity 54.3%; Pred. No. 3.8;  
RESULT 641  
ID ADL38504 standard; DNA; 319 BP.  
DE Human ovarian cancer DNA marker #12394.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.0%; Score 46.8; DB 5; Length 319;  
Best Local Similarity 44.7%; Pred. No. 0.27;  
RESULT 642  
ID ADI73373 standard; DNA; 319 BP.  
DE Human ovarian cancer DNA marker #6115.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.0%; Score 46.8; DB 5; Length 319;  
Best Local Similarity 44.7%; Pred. No. 0.27;  
RESULT 643  
ID ADS89604 standard; DNA; 2987 BP.  
DE Oligonucleotide of the invention SEQ ID NO:620.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.8; DB 13; Length 2987;  
Best Local Similarity 44.4%; Pred. No. 0.72;  
RESULT 644  
ID ADS89330 standard; DNA; 2987 BP.  
DE Oligonucleotide of the invention SEQ ID NO:346.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.8; DB 13; Length 2987;  
Best Local Similarity 44.4%; Pred. No. 0.72;  
RESULT 645  
ID AAF29464 standard; cDNA; 3153 BP.  
DE Murine brevidin cDNA.  
PN WO200100638-A2.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 2.0%; Score 46.8; DB 4; Length 3153;  
Best Local Similarity 54.7%; Pred. No. 0.74;  
RESULT 646  
ID ACD66770 standard; cDNA; 3153 BP.  
DE Secreted polypeptide-related cDNA #76.  
PN US200302279-A1.  
PD 30-JAN-2003.  
PA (FRAS/) FRASER C C.  
PA (BARN/) BARNES T M.  
PA (SHAR/) SHARP J D.  
Query Match 2.0%; Score 46.8; DB 6; Length 6301;  
Best Local Similarity 44.4%; Pred. No. 0.98;  
RESULT 647  
ID ADB90788 standard; cDNA; 3153 BP.  
DE Mouse cDNA encoding brevicin protein.  
PN US2003082586-A1.  
PD 01-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 2.0%; Score 46.8; DB 9; Length 3153;  
Best Local Similarity 54.7%; Pred. No. 0.74;  
RESULT 648  
ID ADF71523 standard; cDNA; 3153 BP.  
DE Murine brevidin protein cDNA.  
PN US2003175733-A1.  
PD 18-SEP-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 2.0%; Score 46.8; DB 10; Length 3153;  
Best Local Similarity 54.7%; Pred. No. 0.74;  
RESULT 649  
ID ADQ10339 standard; cDNA; 3153 BP.  
DE Human polynucleotide #61.  
PN US2004121396-A1.  
PD 24-JUN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 2.0%; Score 46.8; DB 12; Length 3153;  
Best Local Similarity 54.7%; Pred. No. 0.74;  
RESULT 650  
ID ABL33563 standard; DNA; 5987 BP.  
DE Human immune system associated gene SEQ ID NO: 1536.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.8; DB 6; Length 5987;  
Best Local Similarity 44.4%; Pred. No. 0.98;  
RESULT 651  
ID ABQ67102 standard; DNA; 5987 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 132.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.8; DB 6; Length 5987;  
Best Local Similarity 44.4%; Pred. No. 0.98;  
RESULT 652  
ID ADB54180 standard; DNA; 5987 BP.  
DE Pretreated genomic DNA region 104.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.8; DB 10; Length 5987;  
Best Local Similarity 44.4%; Pred. No. 0.98;  
RESULT 653  
ID ADB54308 standard; DNA; 5987 BP.  
DE Pretreated genomic DNA region 232.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.8; DB 10; Length 5987;  
Best Local Similarity 44.4%; Pred. No. 0.98;  
RESULT 654  
ID ABL32052 standard; DNA; 6301 BP.  
DE Human immune system associated gene SEQ ID NO: 25.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.8; DB 6; Length 6301;

Best Local Similarity 45.5%; Pred. No. 1;  
RESULT 655  
ID ABK31243 standard; DNA; 9760 BP.  
DE Signal transduction associated gene modified complementary DNA #43.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.8; DB 6; Length 9760;  
Best Local Similarity 45.8%; Pred. No. 1.2;  
RESULT 656  
ID ABL70198 standard; DNA; 9760 BP.  
DE Chemically treated cell signalling DNA sequence complementary to #44.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.8; DB 6; Length 9760;  
Best Local Similarity 45.8%; Pred. No. 1.2;  
RESULT 657  
ID AAS61156 standard; DNA; 9760 BP.  
DE Human gene regulation-associated gene oligonucleotide #111.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.8; DB 6; Length 9760;  
Best Local Similarity 45.8%; Pred. No. 1.2;  
RESULT 658  
ID AAS45494 standard; DNA; 12968 BP.  
DE Chemically pretreated genomic DNA associated with cell cycle #100.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.8; DB 4; Length 12968;  
Best Local Similarity 43.2%; Pred. No. 1.4;  
RESULT 659  
ID AAS46779 standard; DNA; 12968 BP.  
DE Tumour suppressor gene derived chemically modified sequence #504.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.8; DB 4; Length 12968;  
Best Local Similarity 43.2%; Pred. No. 1.4;  
RESULT 660  
ID ABL34085 standard; DNA; 12968 BP.  
DE Human immune system associated gene SEQ ID NO: 2058.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.8; DB 6; Length 12968;  
Best Local Similarity 43.2%; Pred. No. 1.4;  
RESULT 661  
ID ABK28424 standard; DNA; 12968 BP.  
DE DNA transcription associated complementary genomic DNA #149.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.8; DB 6; Length 12968;  
Best Local Similarity 43.2%; Pred. No. 1.4;  
RESULT 662  
ID ABN80285 standard; DNA; 12968 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 302.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.8; DB 6; Length 12968;  
Best Local Similarity 43.2%; Pred. No. 1.4;  
RESULT 663  
ID ABL56202 standard; DNA; 50000 BP.  
DE AmEPV genome fragment #4.  
PN WO200212526-A2.  
PD 14-FEB-2002.  
PA (UYFL) UNIV FLORIDA.  
Query Match 2.0%; Score 46.8; DB 6; Length 50000;  
Best Local Similarity 46.4%; Pred. No. 2.5;

RESULT 664  
ID ADQ59452 standard; DNA; 168198 BP.  
DE Human cancer-associated (CA) gene sequence SEQ ID NO: 88.  
PN WO2004058288-A1.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 2.0%; Score 46.8; DB 12; Length 168198;  
Best Local Similarity 48.8%; Pred. No. 4.3;  
RESULT 665  
ID AAC02796 standard; cDNA; 315 BP.  
DE Human secreted protein 5' EST, SEQ ID NO: 2794.  
PN EPI033401-A2.  
PD 06-SEP-2000.  
PA (GEST-) GENSET.  
Query Match 2.0%; Score 46.6; DB 3; Length 315;  
Best Local Similarity 51.9%; Pred. No. 0.3;  
RESULT 666  
ID AAL15210 standard; cDNA; 883 BP.  
DE Human breast cancer expressed polynucleotide 7667.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 2.0%; Score 46.6; DB 4; Length 883;  
Best Local Similarity 39.7%; Pred. No. 0.47;  
RESULT 667  
ID ACN85231 standard; DNA; 960 BP.  
DE Breast cancer related marker, seq id 6381.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 2.0%; Score 46.6; DB 11; Length 960;  
Best Local Similarity 39.7%; Pred. No. 0.49;  
RESULT 668  
ID ADA71938 standard; DNA; 2000 BP.  
DE Rice gene, SEQ ID 5263.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 2.0%; Score 46.6; DB 8; Length 2000;  
Best Local Similarity 8.8%; Pred. No. 0.68;  
RESULT 669  
ID ABN86507 standard; cDNA; 2747 BP.  
DE Rat glycoprotein CD44 polypeptide encoding cDNA.  
PN WO200238794-A2.  
PD 16-MAY-2002.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 2.0%; Score 46.6; DB 6; Length 2747;  
Best Local Similarity 50.5%; Pred. No. 0.78;  
RESULT 670  
ID ABK63681 standard; cDNA; 2747 BP.  
DE Rat sequence differentially expressed in response to a hepatotoxin #1588.  
PN WO200210453-A2.  
PD 07-FEB-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 2.0%; Score 46.6; DB 6; Length 2747;  
Best Local Similarity 50.5%; Pred. No. 0.78;  
RESULT 671  
ID AAQ14263 standard; cDNA; 3207 BP.  
DE p-meta-1 metastasis-specific variant of CD44 glycoprotein.  
PN DE4014510-A.  
PD 14-NOV-1991.  
PA (GESL) KERNFORSCHUNGSZENT KARLSRUHE.  
PA (UYKA-) UNIV KARLSRUHE.  
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.  
Query Match 2.0%; Score 46.6; DB 2; Length 3207;  
Best Local Similarity 50.5%; Pred. No. 0.83;  
RESULT 672  
ID ABL33248 standard; DNA; 5163 BP.  
DE Human immune system associated gene SEQ ID NO: 1221.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.

Query Match 2.0%; Score 46.6; DB 6; Length 5163;  
Best Local Similarity 45.5%; Pred. No. 1;  
RESULT 673  
ID ABL34598 standard; DNA; 7676 BP.  
DE Human metastasis associated gene SEQ ID NO: 151.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.6; DB 6; Length 7676;  
Best Local Similarity 46.2%; Pred. No. 1.2;  
RESULT 674  
ID ABL70409 standard; DNA; 7676 BP.  
DE Chemically treated cell signalling DNA sequence#150.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.6; DB 6; Length 7676;  
Best Local Similarity 46.2%; Pred. No. 1.2;  
RESULT 675  
ID ADS99859 standard; DNA; 7676 BP.  
DE Bisulphite treated human gene associated with metastasis #76.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 2.0%; Score 46.6; DB 7; Length 7676;  
Best Local Similarity 46.2%; Pred. No. 1.2;  
RESULT 676  
ID ABL33964 standard; DNA; 9180 BP.  
DE Human immune system associated gene SEQ ID NO: 1937.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.6; DB 6; Length 9180;  
Best Local Similarity 48.4%; Pred. No. 1.3;  
RESULT 677  
ID ABL32465 standard; DNA; 10891 BP.  
DE Human immune system associated gene SEQ ID NO: 438.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.6; DB 6; Length 10891;  
Best Local Similarity 45.0%; Pred. No. 1.4;  
RESULT 678  
ID ABL33512 standard; DNA; 11092 BP.  
DE Human immune system associated gene SEQ ID NO: 1485.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.6; DB 6; Length 11092;  
Best Local Similarity 44.4%; Pred. No. 1.4;  
RESULT 679  
ID ABL32298 standard; DNA; 12507 BP.  
DE Human immune system associated gene SEQ ID NO: 271.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.6; DB 6; Length 12507;  
Best Local Similarity 46.9%; Pred. No. 1.5;  
RESULT 680  
ID ABL34155 standard; DNA; 15548 BP.  
DE Human immune system associated gene SEQ ID NO: 2128.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.6; DB 6; Length 15548;  
Best Local Similarity 44.4%; Pred. No. 1.7;  
RESULT 681  
ID ABL34073 standard; DNA; 40862 BP.  
DE Human immune system associated gene SEQ ID NO: 2046.  
PN WO200200928-A2.  
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.6; DB 6; Length 40862;  
Best Local Similarity 47.8%; Pred. No. 2.6;  
RESULT 682  
ID ABL55643 standard; DNA; 50000 BP.  
DE AMEPV genome fragment#1.  
PN WO200212526-A2.  
PD 14-FEB-2002.  
PA (UYFL) UNIV FLORIDA.  
Query Match 2.0%; Score 46.6; DB 6; Length 50000;  
Best Local Similarity 47.3%; Pred. No. 2.8;  
RESULT 683  
ID ADQ97266 standard; DNA; 355211 BP.  
DE Human cancer associated sequence HD08-023, SEQ ID 242.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 2.0%; Score 46.6; DB 12; Length 110000;  
Best Local Similarity 48.4%; Pred. No. 4;  
RESULT 684  
Query Match 2.0%; Score 46.6; DB 13; Length 110000;  
Best Local Similarity 47.5%; Pred. No. 4;  
RESULT 685  
ID AAH54899 standard; DNA; 4092 BP.  
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4263.  
PN WO200134809-A2.  
PD 17-MAY-2001.  
PA (GLAX) GLAXO GROUP LTD.  
Query Match 2.0%; Score 46.4; DB 4; Length 4092;  
Best Local Similarity 46.3%; Pred. No. 1;  
RESULT 686  
ID ABL32714 standard; DNA; 4172 BP.  
DE Human immune system associated gene SEQ ID NO: 687.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.4; DB 6; Length 4172;  
Best Local Similarity 45.9%; Pred. No. 1.1;  
RESULT 687  
ID ABL92301 standard; DNA; 6040 BP.  
DE Chemically treated DNA repair gene fragment complementary to#55.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.4; DB 6; Length 6040;  
Best Local Similarity 47.0%; Pred. No. 1.2;  
RESULT 688  
ID ABL49370 standard; DNA; 6040 BP.  
DE Human polynucleotide associated with DNA replication SEQ ID NO 70.  
PN WO200177377-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.4; DB 6; Length 6040;  
Best Local Similarity 47.0%; Pred. No. 1.2;  
RESULT 689  
ID ABL70459 standard; DNA; 16228 BP.  
DE Chemically treated cell signalling DNA sequence#175.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.4; DB 6; Length 16228;  
Best Local Similarity 47.3%; Pred. No. 1.9;  
RESULT 690  
ID AAS61424 standard; DNA; 16228 BP.  
DE Human gene regulation-associated gene oligonucleotide #379.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.4; DB 6; Length 16228;  
Best Local Similarity 47.3%; Pred. No. 1.9;  
RESULT 691  
ID ABL34026 standard; DNA; 17594 BP.  
DE Human immune system associated gene SEQ ID NO: 1999.



PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.4; DB 6; Length 17594;  
Best Local Similarity 45.4%; Pred. No. 2;  
RESULT 692  
ID AAS46717 standard; DNA; 19131 BP.  
DE Tumour suppressor gene derived chemically modified sequence #440.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 2.0%; Score 46.4; DB 4; Length 19131;  
Best Local Similarity 58.8%; Pred. No. 2.1;  
RESULT 693  
ID AAN60472 standard; DNA; 4590 BP.  
DE Sequence encoding the ring-infected Erythrocyte Surface Antigen (RESA).  
PN WO8601802-A.  
PD 27-MAR-1986.  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
Query Match 1.9%; Score 46.2; DB 1; Length 4590;  
Best Local Similarity 44.6%; Pred. No. 1.2;  
RESULT 694  
ID ADS89612 standard; DNA; 4930 BP.  
DE Oligonucleotide of the invention SEQ ID NO:628.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46.2; DB 13; Length 4930;  
Best Local Similarity 46.0%; Pred. No. 1.3;  
RESULT 695  
ID AAS46331 standard; DNA; 5880 BP.  
DE Tumour suppressor gene derived chemically modified sequence #53.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46.2; DB 4; Length 5880;  
Best Local Similarity 43.5%; Pred. No. 1.4;  
RESULT 696  
ID ABK28177 standard; DNA; 5880 BP.  
DE DNA transcription associated genomic DNA #26.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46.2; DB 6; Length 5880;  
Best Local Similarity 43.5%; Pred. No. 1.4;  
RESULT 697  
ID ABL33763 standard; DNA; 5981 BP.  
DE Human immune system associated gene SEQ ID NO: 1736.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46.2; DB 6; Length 5981;  
Best Local Similarity 44.3%; Pred. No. 1.4;  
RESULT 698  
ID ADS89769 standard; DNA; 6001 BP.  
DE Oligonucleotide of the invention SEQ ID NO:785.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46.2; DB 13; Length 6001;  
Best Local Similarity 46.0%; Pred. No. 1.4;  
RESULT 699  
ID ABL33487 standard; DNA; 6831 BP.  
DE Human immune system associated gene SEQ ID NO: 1460.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46.2; DB 6; Length 6831;  
Best Local Similarity 45.9%; Pred. No. 1.5;  
RESULT 700  
ID ADS4312 standard; DNA; 7833 BP.  
DE Pretreated genomic DNA region 236.  
PN WO2003072821-A2.  
PD 05-DEC-2002.

PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46.2; DB 10; Length 7833;  
Best Local Similarity 46.0%; Pred. No. 1.6;  
RESULT 701  
ID ADE37779 standard; DNA; 7833 BP.  
DE Human chemically treated EVA4 nucleotide sequence SEQ ID NO:25.  
PN WO2003072820-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46.2; DB 10; Length 7833;  
Best Local Similarity 46.0%; Pred. No. 1.6;  
RESULT 702  
ID ADS89608 standard; DNA; 7833 BP.  
DE Oligonucleotide of the invention SEQ ID NO:624.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46.2; DB 13; Length 7833;  
Best Local Similarity 46.0%; Pred. No. 1.6;  
RESULT 703  
ID ABL32299 standard; DNA; 12507 BP.  
DE Human immune system associated gene SEQ ID NO: 272.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46.2; DB 6; Length 12507;  
Best Local Similarity 46.4%; Pred. No. 1.9;  
RESULT 704  
ID ABK28396 standard; DNA; 15743 BP.  
DE DNA transcription associated complementary genomic DNA #135.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46.2; DB 6; Length 15743;  
Best Local Similarity 46.2%; Pred. No. 2.1;  
RESULT 705  
ID AAS61427 standard; DNA; 19380 BP.  
DE Human gene regulation-associated gene oligonucleotide #382.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46.2; DB 6; Length 19380;  
Best Local Similarity 45.3%; Pred. No. 2.3;  
RESULT 706  
ID ADB37663 standard; DNA; 28993 BP.  
DE Human chemically pretreated EVA4 gene SEQ ID NO:5.  
PN WO2003072812-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46.2; DB 10; Length 28993;  
Best Local Similarity 44.0%; Pred. No. 2.8;  
RESULT 707  
ID ABL55643 standard; DNA; 50000 BP.  
DE AMEPV genome fragment#1.  
PN WO200212526-A2.  
PD 14-FEB-2002.  
PA (UYFL) UNIV FLORIDA.  
Query Match 1.9%; Score 46.2; DB 6; Length 50000;  
Best Local Similarity 48.6%; Pred. No. 3.5;  
RESULT 708  
ID ADH10017 standard; DNA; 365186 BP.  
DE Human chromosome 2p21-22 fragment containing the DRIP gene.  
PN WO2003093310-A1.  
PD 13-NOV-2003.  
PA (UYBR-) UNIV BREMEN.  
Query Match 1.9%; Score 46.2; DB 10; Length 110000;  
Best Local Similarity 44.4%; Pred. No. 5;  
RESULT 709  
ID ACA64845 standard; DNA; 115218 BP.  
DE Human HNRNP GP43 DNA corresponding to AL034397.  
PN DE10127572-A1.  
PD 05-DEC-2002.

PA (PATH-) PATHOARRAY GMBH.  
Query Match 1.9%; Score 46.2; DB 8; Length 115218;  
Best Local Similarity 45.9%; Pred. No. 5.1;  
RESULT 710  
ID AB032715 standard; DNA; 337344 BP.  
DE Human cancer-associated genomic DNA HD14-044.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 1.9%; Score 46.2; DB 13; Length 337344;  
Best Local Similarity 43.8%; Pred. No. 8.2;  
RESULT 711  
ID AAX99555 standard; DNA; 3057 BP.  
DE Nucleic acid sequence from U. urealyticum.  
PN WO9939007-A1.  
PD 05-AUG-1999.  
PA (UABR-) UAB RES FOUND.  
Query Match 1.9%; Score 46; DB 2; Length 3057;  
Best Local Similarity 43.1%; Pred. No. 1.2;  
RESULT 712  
ID AB067021 standard; DNA; 4661 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 51.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46; DB 6; Length 4661;  
Best Local Similarity 46.7%; Pred. No. 1.4;  
RESULT 713  
ID AB032430 standard; DNA; 6113 BP.  
DE Human immune system associated gene SEQ ID NO: 403.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46; DB 6; Length 6113;  
Best Local Similarity 45.2%; Pred. No. 1.6;  
RESULT 714  
ID ABL92204 standard; DNA; 6113 BP.  
DE Chemically treated DNA repair gene fragment#7.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46; DB 6; Length 6113;  
Best Local Similarity 45.2%; Pred. No. 1.6;  
RESULT 715  
ID AB049313 standard; DNA; 6113 BP.  
DE Human polynucleotide associated with DNA replication SEQ ID NO 13.  
PN WO200177377-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46; DB 6; Length 6113;  
Best Local Similarity 45.2%; Pred. No. 1.6;  
RESULT 716  
ID ABQ67062 standard; DNA; 9095 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 92.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46; DB 6; Length 9095;  
Best Local Similarity 43.4%; Pred. No. 1.9;  
RESULT 717  
ID ABK39994 standard; DNA; 9524 BP.  
DE Human chemically pretreated gene sequence #38 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46; DB 6; Length 9524;  
Best Local Similarity 47.5%; Pred. No. 1.9;  
RESULT 718  
ID ABL32839 standard; DNA; 9524 BP.  
DE Human immune system associated gene SEQ ID NO: 812.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.9%; Score 46; DB 6; Length 9524;  
Best Local Similarity 47.5%; Pred. No. 1.9;  
RESULT 719  
ID ABK31519 standard; DNA; 14316 BP.  
DE Signal transduction associated gene modified complementary DNA #181.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46; DB 6; Length 14316;  
Best Local Similarity 46.9%; Pred. No. 2.3;  
RESULT 720  
ID ABL70606 standard; DNA; 14316 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#248.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46; DB 6; Length 14316;  
Best Local Similarity 46.9%; Pred. No. 2.3;  
RESULT 721  
ID AAS61445 standard; DNA; 14316 BP.  
DE Human gene regulation-associated gene oligonucleotide #400.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46; DB 6; Length 14316;  
Best Local Similarity 46.9%; Pred. No. 2.3;  
RESULT 722  
ID ABK31343 standard; DNA; 15587 BP.  
DE Signal transduction associated gene modified complementary DNA #93.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46; DB 6; Length 15587;  
Best Local Similarity 50.9%; Pred. No. 2.4;  
RESULT 723  
ID ABL70304 standard; DNA; 15587 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#97.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46; DB 6; Length 15587;  
Best Local Similarity 50.9%; Pred. No. 2.4;  
RESULT 724  
ID AAS61238 standard; DNA; 15587 BP.  
DE Human gene regulation-associated gene oligonucleotide #193.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46; DB 6; Length 15587;  
Best Local Similarity 50.9%; Pred. No. 2.4;  
RESULT 725  
ID ABL32625 standard; DNA; 16217 BP.  
DE Human immune system associated gene SEQ ID NO: 598.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46; DB 6; Length 16217;  
Best Local Similarity 45.2%; Pred. No. 2.4;  
RESULT 726  
ID ABL33998 standard; DNA; 21537 BP.  
DE Human immune system associated gene SEQ ID NO: 1971.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 46; DB 6; Length 21537;  
Best Local Similarity 47.7%; Pred. No. 2.7;  
RESULT 727  
ID AAF12929 standard; cDNA; 1132 BP.  
DE Aspergillus oryzae EST SEQ ID NO:5452.  
PN WO200056762-A2.  
PD 28-SEP-2000.  
PA (NOVO ) NOVO NORDISK BIOTECH INC.  
PA (NOVO ) NOVO NORDISK AS.

Query Match 1.9%; Score 45.8; DB 3; Length 1132;  
Best Local Similarity 46.2%; Pred. No. 0.84;  
RESULT 728  
ID ADQ25148 standard; DNA; 1533 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7968.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 1.9%; Score 45.8; DB 12; Length 1533;  
Best Local Similarity 48.0%; Pred. No. 0.96;  
RESULT 729  
ID ABL33518 standard; DNA; 5520 BP.  
DE Human immune system associated gene SEQ ID NO: 1491.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.8; DB 6; Length 5520;  
Best Local Similarity 47.3%; Pred. No. 1.7;  
RESULT 730  
ID ABL32374 standard; DNA; 5659 BP.  
DE Human immune system associated gene SEQ ID NO: 347.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.8; DB 6; Length 5659;  
Best Local Similarity 51.2%; Pred. No. 1.7;  
RESULT 731  
ID ABK33931 standard; DNA; 5659 BP.  
DE Human DNA for staging of Astrocytomas #7.  
PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.8; DB 6; Length 5659;  
Best Local Similarity 51.2%; Pred. No. 1.7;  
RESULT 732  
ID ABL34486 standard; DNA; 5659 BP.  
DE Human metastasis associated gene SEQ ID NO: 39.  
PN WO200173736-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.8; DB 6; Length 5659;  
Best Local Similarity 51.2%; Pred. No. 1.7;  
RESULT 733  
ID ADS99747 standard; DNA; 5659 BP.  
DE Bisulphite treated human gene associated with metastasis #20.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 1.9%; Score 45.8; DB 7; Length 5659;  
Best Local Similarity 51.2%; Pred. No. 1.7;  
RESULT 734  
ID ADA20366 standard; DNA; 5659 BP.  
DE Prostate tumour related genomic DNA sample #16.  
PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.8; DB 8; Length 5659;  
Best Local Similarity 51.2%; Pred. No. 1.7;  
RESULT 735  
ID ADA84173 standard; DNA; 5659 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:31.  
PN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.8; DB 8; Length 5659;  
Best Local Similarity 51.2%; Pred. No. 1.7;  
RESULT 736  
ID ABL32505 standard; DNA; 6065 BP.  
DE Human immune system associated gene SEQ ID NO: 478.  
PN WO200200928-A2.  
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.8; DB 6; Length 6065;  
Best Local Similarity 51.7%; Pred. No. 1.8;  
RESULT 737  
ID ABL32030 standard; DNA; 6072 BP.  
DE Human immune system associated gene SEQ ID NO: 3.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.8; DB 6; Length 6072;  
Best Local Similarity 44.8%; Pred. No. 1.8;  
RESULT 738  
ID ABL32493 standard; DNA; 6120 BP.  
DE Human immune system associated gene SEQ ID NO: 466.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.8; DB 6; Length 6120;  
Best Local Similarity 45.3%; Pred. No. 1.8;  
RESULT 739  
ID ABL33140 standard; DNA; 6361 BP.  
DE Human immune system associated gene SEQ ID NO: 1113.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.8; DB 6; Length 6361;  
Best Local Similarity 46.9%; Pred. No. 1.8;  
RESULT 740  
ID ABL32357 standard; DNA; 7498 BP.  
DE Human immune system associated gene SEQ ID NO: 230.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.8; DB 6; Length 7498;  
Best Local Similarity 47.1%; Pred. No. 1.9;  
RESULT 741  
ID ABK31207 standard; DNA; 7508 BP.  
DE Signal transduction associated gene modified complementary DNA #25.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.8; DB 6; Length 7508;  
Best Local Similarity 44.4%; Pred. No. 1.9;  
RESULT 742  
ID AB210177 standard; DNA; 8093 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #317.  
PN WO200272722-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.8; DB 8; Length 8093;  
Best Local Similarity 46.4%; Pred. No. 2;  
RESULT 743  
ID ADB54267 standard; DNA; 8093 BP.  
DE Pretreated genomic DNA region 191.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.8; DB 10; Length 8093;  
Best Local Similarity 46.4%; Pred. No. 2;  
RESULT 744  
ID ADE84189 standard; DNA; 8093 BP.  
DE Human lymphoid cell proliferative disorder gene derived DNA #125.  
PN WO2003044226-A2.  
PD 30-MAY-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.8; DB 10; Length 8093;  
Best Local Similarity 46.4%; Pred. No. 2;  
RESULT 745  
ID ADS89565 standard; DNA; 8093 BP.  
DE Oligonucleotide of the invention SEQ ID NO:581.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.9%; Score 45.8; DB 13; Length 8093;  
 Best Local Similarity 46.4%; Pred. No. 2;  
 RESULT 746  
 ID ABL33949 standard; DNA; 18218 BP.  
 DE Human immune system associated gene SEQ ID NO: 1922.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 1.9%; Score 45.8; DB 6; Length 18218;  
 Best Local Similarity 45.7%; Pred. No. 2.8;  
 RESULT 747  
 ID ABL51601 standard; DNA; 319608 BP.  
 DE Human chromosome 13q31-q33 genomic nucleotide sequence.  
 PN WO200058510-A2.  
 PD 05-OCT-2000.  
 PA (GEST ) GENSET.  
 Query Match 1.9%; Score 45.8; DB 3; Length 319608;  
 Best Local Similarity 48.1%; Pred. No. 10;  
 RESULT 748  
 ID AAS09301 standard; DNA; 319608 BP.  
 DE Human schizophrenia associated gene g35030 and biallelic markers A1-A71.  
 Query Match 1.9%; Score 45.8; DB 5; Length 319608;  
 Best Local Similarity 48.1%; Pred. No. 10;  
 RESULT 749  
 ID AAX08523 standard; DNA; 6265 BP.  
 DE NBP46 (root lectin) genomic DNA.  
 PN WO9907223-A1.  
 PD 18-FEB-1999.  
 PA (REGC ) UNIV CALIFORNIA.  
 Query Match 1.9%; Score 45.6; DB 2; Length 6265;  
 Best Local Similarity 44.7%; Pred. No. 2;  
 RESULT 750  
 ID ABL32604 standard; DNA; 11155 BP.  
 DE Human immune system associated gene SEQ ID NO: 577.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 1.9%; Score 45.6; DB 6; Length 11155;  
 Best Local Similarity 45.5%; Pred. No. 2.6;  
 RESULT 751  
 Query Match 1.9%; Score 45.6; DB 6; Length 110000;  
 Best Local Similarity 46.8%; Pred. No. 7;  
 RESULT 752  
 ID ADS89278 standard; DNA; 5286 BP.  
 DE Oligonucleotide of the invention SEQ ID NO:294.  
 PN WO2004035803-A2.  
 PD 29-APR-2004.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 1.9%; Score 45.4; DB 13; Length 5286;  
 Best Local Similarity 45.4%; Pred. No. 2.1;  
 RESULT 753  
 ID ADS89552 standard; DNA; 5286 BP.  
 DE Oligonucleotide of the invention SEQ ID NO:568.  
 PN WO2004035803-A2.  
 PD 29-APR-2004.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 1.9%; Score 45.4; DB 13; Length 5286;  
 Best Local Similarity 45.4%; Pred. No. 2.1;  
 RESULT 754  
 ID AAX08523 standard; DNA; 6265 BP.  
 DE NBP46 (root lectin) genomic DNA.  
 PN WO9907223-A1.  
 PD 18-FEB-1999.  
 PA (REGC ) UNIV CALIFORNIA.  
 Query Match 1.9%; Score 45.4; DB 2; Length 6265;  
 Best Local Similarity 48.5%; Pred. No. 2.2;  
 RESULT 755  
 ID ABL32257 standard; DNA; 7498 BP.  
 DE Human immune system associated gene SEQ ID NO: 230.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 1.9%; Score 45.4; DB 6; Length 7498;

Best Local Similarity 44.8%; Pred. No. 2.4;  
 RESULT 756  
 ID ABL54354 standard; DNA; 9881 BP.  
 DE Chemically treated apoptosis gene complementary to gene #27.  
 PN WO200177164-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 1.9%; Score 45.4; DB 6; Length 9881;  
 Best Local Similarity 45.0%; Pred. No. 2.7;  
 RESULT 757  
 ID ABL33591 standard; DNA; 10279 BP.  
 DE Human immune system associated gene SEQ ID NO: 1564.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 1.9%; Score 45.4; DB 6; Length 10279;  
 Best Local Similarity 44.5%; Pred. No. 2.8;  
 RESULT 758  
 ID ABL92277 standard; DNA; 10279 BP.  
 DE Chemically treated DNA repair gene fragment complementary to#43.  
 PN WO200181622-A2.  
 PD 01-NOV-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 1.9%; Score 45.4; DB 6; Length 10279;  
 Best Local Similarity 44.5%; Pred. No. 2.8;  
 RESULT 759  
 ID AAD22328 standard; DNA; 10279 BP.  
 DE Chemically treated human genomic DNA #18 associated with DNA adducts.  
 PN WO200177378-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 1.9%; Score 45.4; DB 6; Length 10279;  
 Best Local Similarity 44.5%; Pred. No. 2.8;  
 RESULT 760  
 ID AAS45315 standard; DNA; 11260 BP.  
 DE Chemically pretreated complementary DNA associated with cell cycle #10.  
 PN WO200168911-A2.  
 PD 20-SEP-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 1.9%; Score 45.4; DB 4; Length 11260;  
 Best Local Similarity 47.2%; Pred. No. 2.9;  
 RESULT 761  
 ID ABK28154 standard; DNA; 11260 BP.  
 DE DNA transcription associated complementary genomic DNA #14.  
 PN WO200192565-A2.  
 PD 06-DEC-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 1.9%; Score 45.4; DB 6; Length 11260;  
 Best Local Similarity 47.2%; Pred. No. 2.9;  
 RESULT 762  
 ID AEN80039 standard; DNA; 11260 BP.  
 DE Human chemically modified disease associated gene SEQ ID NO 56.  
 PN WO200200927-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 1.9%; Score 45.4; DB 6; Length 11260;  
 Best Local Similarity 47.2%; Pred. No. 2.9;  
 RESULT 763  
 ID ABL34493 standard; DNA; 11996 BP.  
 DE Human metastasis associated gene SEQ ID NO: 46.  
 PN WO200177376-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 1.9%; Score 45.4; DB 6; Length 11996;  
 Best Local Similarity 48.1%; Pred. No. 3;  
 RESULT 764  
 ID ADS99754 standard; DNA; 11996 BP.  
 DE Complement of bisulphite treated metastasis-associated human gene #23.  
 PN US2003148327-A1.  
 PD 07-AUG-2003.  
 PA (OLEK/) OLEK A.  
 PA (FIEP/) FIEPENBROCK C.  
 PA (BERL/) BERLIN K.

Query Match 1.9%; Score 45.4; DB 7; Length 11996;  
Best Local Similarity 48.1%; Pred. No. 3;  
RESULT 765  
ID ABLJ32917 standard; DNA; 13420 BP.  
DE Human immune system associated gene SEQ ID NO: 890.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.4; DB 6; Length 13420;  
Best Local Similarity 53.0%; Pred. No. 3.1;  
RESULT 766  
ID ABL70543 standard; DNA; 15649 BP.  
DE Chemically treated cell signalling DNA sequence#217.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.4; DB 6; Length 15649;  
Best Local Similarity 54.5%; Pred. No. 3.3;  
RESULT 767  
ID ABL70604 standard; DNA; 34548 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#247.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.4; DB 6; Length 34548;  
Best Local Similarity 44.3%; Pred. No. 4.7;  
RESULT 768  
ID ABO67149 standard; DNA; 40324 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 179.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.4; DB 6; Length 40324;  
Best Local Similarity 46.5%; Pred. No. 5.1;  
RESULT 769  
ID ABL13728 standard; DNA; 151212 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #260.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.9%; Score 45.4; DB 10; Length 151212;  
Best Local Similarity 46.0%; Pred. No. 9.1;  
RESULT 770  
ID ABL13728 standard; DNA; 151212 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #260.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.9%; Score 45.4; DB 2; Length 1939;  
Best Local Similarity 46.1%; Pred. No. 1.5;  
RESULT 771  
ID ABL13728 standard; DNA; 151212 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #260.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.9%; Score 45.4; DB 2; Length 1939;  
Best Local Similarity 46.1%; Pred. No. 1.5;  
RESULT 772  
ID ABL13728 standard; DNA; 151212 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #260.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.9%; Score 45.4; DB 2; Length 1939;  
Best Local Similarity 46.1%; Pred. No. 1.5;  
RESULT 773  
ID ABL13728 standard; DNA; 151212 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #260.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.9%; Score 45.4; DB 2; Length 1939;  
Best Local Similarity 46.1%; Pred. No. 1.5;  
RESULT 774  
ID ABL13728 standard; DNA; 151212 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #260.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.9%; Score 45.4; DB 2; Length 1939;  
Best Local Similarity 46.1%; Pred. No. 1.5;  
RESULT 775  
ID ABL13728 standard; DNA; 151212 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #260.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.

ID ADS89338 standard; DNA; 4930 BP.  
DE Oligonucleotide of the invention SEQ ID NO:354.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.2; DB 13; Length 4930;  
Best Local Similarity 46.4%; Pred. No. 2.3;  
RESULT 776  
ID ABO67043 standard; DNA; 5267 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 73.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.2; DB 6; Length 5267;  
Best Local Similarity 44.8%; Pred. No. 2.3;  
RESULT 777  
ID ADS89495 standard; DNA; 6001 BP.  
DE Oligonucleotide of the invention SEQ ID NO:511.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.2; DB 13; Length 6001;  
Best Local Similarity 46.4%; Pred. No. 2.5;  
RESULT 778  
ID ADQ24856 standard; DNA; 6816 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7676.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 1.9%; Score 45.2; DB 12; Length 6816;  
Best Local Similarity 37.7%; Pred. No. 2.6;  
RESULT 779  
ID ABK31206 standard; DNA; 7508 BP.  
DE Signal transduction associated gene modified DNA #25.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.2; DB 6; Length 7508;  
Best Local Similarity 47.2%; Pred. No. 2.7;  
RESULT 780  
ID ADB54184 standard; DNA; 7833 BP.  
DE Pretreated genomic DNA region 108.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.2; DB 10; Length 7833;  
Best Local Similarity 46.4%; Pred. No. 2.8;  
RESULT 781  
ID ADE37769 standard; DNA; 7833 BP.  
DE Human chemically treated EYA4 nucleotide sequence SEQ ID NO:15.  
PN WO2003072820-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.2; DB 10; Length 7833;  
Best Local Similarity 46.4%; Pred. No. 2.8;  
RESULT 782  
ID ADS89334 standard; DNA; 7833 BP.  
DE Oligonucleotide of the invention SEQ ID NO:350.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.2; DB 13; Length 7833;  
Best Local Similarity 46.4%; Pred. No. 2.8;  
RESULT 783  
ID ABL34076 standard; DNA; 8876 BP.  
DE Human immune system associated gene SEQ ID NO: 2049.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.2; DB 6; Length 8876;  
Best Local Similarity 45.2%; Pred. No. 2.9;  
RESULT 784  
ID ABN79996 standard; DNA; 10710 BP.

DE Human chemically modified disease associated gene SEQ ID NO 13.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.2; DB 6; Length 10710;  
Best Local Similarity 51.0%; Pred. No. 3.2;  
RESULT 785  
ID ABU32487 standard; DNA; 17183 BP.  
DE Human immune system associated gene SEQ ID NO: 460.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.2; DB 6; Length 17183;  
Best Local Similarity 46.2%; Pred. No. 3.9;  
RESULT 786  
ID AA545393 standard; DNA; 17419 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #49.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.2; DB 4; Length 17419;  
Best Local Similarity 44.3%; Pred. No. 3.9;  
RESULT 787  
ID ABU33295 standard; DNA; 17419 BP.  
DE Human immune system associated gene SEQ ID NO: 1268.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.2; DB 6; Length 17419;  
Best Local Similarity 44.3%; Pred. No. 3.9;  
RESULT 788  
ID ABK28238 standard; DNA; 17419 BP.  
DE DNA transcription associated complementary genomic DNA #56.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45.2; DB 6; Length 17419;  
Best Local Similarity 44.3%; Pred. No. 3.9;  
RESULT 789  
ID ACN47153 standard; cDNA; 535 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-007-Q1-N6-G4, SEQ:1934.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (PENG/) PENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.9%; Score 45; DB 13; Length 535;  
Best Local Similarity 47.0%; Pred. No. 0.95;  
RESULT 790  
ID AD024856 standard; DNA; 6816 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7676.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 1.9%; Score 45; DB 12; Length 6816;  
Best Local Similarity 36.7%; Pred. No. 2.9;  
RESULT 791  
ID ABU33673 standard; DNA; 12142 BP.  
DE Human immune system associated gene SEQ ID NO: 1646.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45; DB 6; Length 12142;  
Best Local Similarity 43.7%; Pred. No. 3.8;  
RESULT 792  
ID ABU32630 standard; DNA; 14987 BP.  
DE Human immune system associated gene SEQ ID NO: 603.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45; DB 6; Length 14987;  
Best Local Similarity 47.1%; Pred. No. 4.1;

RESULT 793  
ID ABK40018 standard; DNA; 18133 BP.  
DE Human chemically pretreated gene sequence #50 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45; DB 6; Length 18133;  
Best Local Similarity 48.3%; Pred. No. 4.5;  
RESULT 794  
ID ABL32941 standard; DNA; 18133 BP.  
DE Human immune system associated gene SEQ ID NO: 914.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45; DB 6; Length 18133;  
Best Local Similarity 48.3%; Pred. No. 4.5;  
RESULT 795  
ID ABL32766 standard; DNA; 19659 BP.  
DE Human immune system associated gene SEQ ID NO: 739.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 45; DB 6; Length 19659;  
Best Local Similarity 48.6%; Pred. No. 4.7;  
RESULT 796  
ID AAX20253 standard; DNA; 26811 BP.  
DE Borrelia burgdorferi polynucleotide sequence #6.  
PN WO9858943-A1.  
PD 30-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (MEDI-) MEDIMMUNE INC.  
Query Match 1.9%; Score 45; DB 2; Length 26811;  
Best Local Similarity 48.0%; Pred. No. 5.3;  
RESULT 797  
ID ADO97050 standard; DNA; 687411 BP.  
DE Human cancer associated sequence HD08-001, SEQ ID 26.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 1.9%; Score 45; DB 12; Length 110000;  
Best Local Similarity 44.1%; Pred. No. 10;  
RESULT 798  
ID AAQ02047 standard; DNA; 3101 BP.  
DE Sequence encoding a circumsporozoite (CS)-related protein of Plasmodium falciparum.  
PN WO9001496-A.  
PD 22-FEB-1990.  
PA (REEX-) RES EXPLOITATION LTD.  
PA (THRE-) 3I RES EXPL LTD.  
Query Match 1.9%; Score 44.8; DB 2; Length 3101;  
Best Local Similarity 45.7%; Pred. No. 2.3;  
RESULT 799  
ID ABO67022 standard; DNA; 4661 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 52.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.8; DB 6; Length 4661;  
Best Local Similarity 47.0%; Pred. No. 2.8;  
RESULT 800  
ID ABL33161 standard; DNA; 5593 BP.  
DE Human immune system associated gene SEQ ID NO: 1134.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.8; DB 6; Length 5593;  
Best Local Similarity 50.5%; Pred. No. 3;  
RESULT 801  
ID ABL32738 standard; DNA; 6759 BP.  
DE Human immune system associated gene SEQ ID NO: 711.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.9%; Score 44.8; DB 6; Length 6759;  
Best Local Similarity 47.2%; Pred. No. 3.3;  
RESULT 802  
ID ABL34323 standard; DNA; 7231 BP.  
DE Chemically treated apoptosis gene #12.  
PN WO200177164-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.8; DB 6; Length 7231;  
Best Local Similarity 44.9%; Pred. No. 3.4;  
RESULT 803  
ID ABOQ67015 standard; DNA; 10048 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 45.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.8; DB 6; Length 10048;  
Best Local Similarity 46.7%; Pred. No. 3.9;  
RESULT 804  
ID ABOQ67074 standard; DNA; 20579 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 104.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.8; DB 6; Length 20579;  
Best Local Similarity 44.6%; Pred. No. 5.3;  
RESULT 805  
ID ABL70603 standard; DNA; 34548 BP.  
DE Chemically treated cell signalling DNA sequence#247.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.8; DB 6; Length 34548;  
Best Local Similarity 49.2%; Pred. No. 6.7;  
RESULT 806  
ID ADR02094 standard; DNA; 711 BP.  
DE A. gossypii genomic DNA PAG1504UP.  
PN US6239264-B1.  
PD 29-MAY-2001.  
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.  
Query Match 1.9%; Score 44.6; DB 2; Length 711;  
Best Local Similarity 48.3%; Pred. No. 1.4;  
RESULT 807  
ID AAS45313 standard; DNA; 5979 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #9.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.6; DB 4; Length 5979;  
Best Local Similarity 46.9%; Pred. No. 3.5;  
RESULT 808  
ID ABK28152 standard; DNA; 5979 BP.  
DE DNA transcription associated complementary genomic DNA #13.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.6; DB 6; Length 5979;  
Best Local Similarity 46.9%; Pred. No. 3.5;  
RESULT 809  
ID ABK28394 standard; DNA; 6063 BP.  
DE DNA transcription associated complementary genomic DNA #134.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.6; DB 6; Length 6063;  
Best Local Similarity 57.6%; Pred. No. 3.5;  
RESULT 810  
ID ABL28739 standard; DNA; 6759 BP.  
DE Human immune system associated gene SEQ ID NO: 712.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.6; DB 6; Length 6759;

Best Local Similarity 44.6%; Pred. No. 3.7;  
RESULT 811  
ID AAX20263 standard; DNA; 8905 BP.  
DE Borrelia burgdorferi polynucleotide sequence #16.  
PN WO9858943-A1.  
PD 30-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (MEDI-) MEDIMMUNE INC.  
Query Match 1.9%; Score 44.6; DB 2; Length 8905;  
Best Local Similarity 44.4%; Pred. No. 4.1;  
RESULT 812  
ID ABK40061 standard; DNA; 13784 BP.  
DE Human chemically pretreated gene sequence #72 strand 1.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.6; DB 6; Length 13784;  
Best Local Similarity 48.9%; Pred. No. 5;  
RESULT 813  
ID AAS45414 standard; DNA; 14649 BP.  
DE Chemically pretreated genomic DNA associated with cell cycle #60.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.6; DB 4; Length 14649;  
Best Local Similarity 44.6%; Pred. No. 5.2;  
RESULT 814  
ID ABK28267 standard; DNA; 14649 BP.  
DE DNA transcription associated genomic DNA #71.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.6; DB 6; Length 14649;  
Best Local Similarity 44.6%; Pred. No. 5.2;  
RESULT 815  
ID ABL33022 standard; DNA; 16236 BP.  
DE Human immune system associated gene SEQ ID NO: 995.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.6; DB 6; Length 16236;  
Best Local Similarity 45.7%; Pred. No. 5.4;  
RESULT 816  
ID ADB54246 standard; DNA; 16579 BP.  
DE Pretreated genomic DNA region 170.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.6; DB 10; Length 16579;  
Best Local Similarity 43.3%; Pred. No. 5.4;  
RESULT 817  
ID ADE37773 standard; DNA; 16579 BP.  
DE Human chemically treated TPEF nucleotide sequence SEQ ID NO:19.  
PN WO2003072820-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.6; DB 10; Length 16579;  
Best Local Similarity 43.3%; Pred. No. 5.4;  
RESULT 818  
ID ADS89548 standard; DNA; 16579 BP.  
DE Oligonucleotide of the invention SEQ ID NO:564.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.6; DB 13; Length 16579;  
Best Local Similarity 43.3%; Pred. No. 5.4;  
RESULT 819  
ID ABL70502 standard; DNA; 18283 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#196.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.6; DB 6; Length 18283;

Best Local Similarity 44.9%; Pred. No. 5.7;  
RESULT 820  
ID AAS61363 standard; DNA; 18283 BP.  
DE Human gene regulation-associated gene oligonucleotide #318.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.6; DB 6; Length 18283;  
Best Local Similarity 44.9%; Pred. No. 5.7;  
RESULT 821  
ID ABL56201 standard; DNA; 50000 BP.  
DE AmsEV genome fragment#3.  
PN WO200212526-A2.  
PD 14-FEB-2002.  
PA (UYFL) UNIV FLORIDA.  
Query Match 1.9%; Score 44.6; DB 6; Length 50000;  
Best Local Similarity 46.9%; Pred. No. 8.9;  
RESULT 822  
Query Match 1.9%; Score 44.6; DB 12; Length 82256;  
Best Local Similarity 46.3%; Pred. No. 11;  
RESULT 823  
ID ADC65260 standard; DNA; 96588 BP.  
DE Human PtpRK genomic sequence.  
PN WO2003045230-A2.  
PD 05-JUN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 1.9%; Score 44.6; DB 10; Length 96588;  
Best Local Similarity 53.8%; Pred. No. 12;  
RESULT 824  
ID ADA02780 standard; DNA; 96589 BP.  
DE Human PTPRK carcinoma associated gene, SEQ ID NO:1298.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 1.9%; Score 44.6; DB 9; Length 96589;  
Best Local Similarity 53.8%; Pred. No. 12;  
RESULT 825  
ID ADB72518 standard; DNA; 96589 BP.  
DE Human PTPRK gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 1.9%; Score 44.6; DB 10; Length 96589;  
Best Local Similarity 53.8%; Pred. No. 12;  
RESULT 826  
ID ADM74375 standard; DNA; 96589 BP.  
DE Human carcinoma associated (CA) nucleic acid #22.  
PN US2004072154-A1.  
PD 15-APR-2004.  
PA (MORR/) MORRIS D W.  
PA (ENGE/) ENGELHARD E K.  
Query Match 1.9%; Score 44.6; DB 12; Length 96589;  
Best Local Similarity 53.8%; Pred. No. 12;  
RESULT 827  
ID ABQ88126 standard; cDNA; 159400 BP.  
DE Human osteoblast differentiation related cDNA SEQ ID NO 33.  
PN WO200250301-A2.  
PD 27-JUN-2002.  
PA (GENE-) GENE LOGIC INC.  
PA (PROC) PROCTER & GAMBLE CO.  
Query Match 1.9%; Score 44.6; DB 6; Length 159400;  
Best Local Similarity 48.6%; Pred. No. 15;  
RESULT 828  
ID ABD32659 standard; DNA; 163382 BP.  
DE Human cancer-associated genomic DNA HD13-065.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 1.9%; Score 44.6; DB 13; Length 163382;  
Best Local Similarity 45.6%; Pred. No. 15;  
RESULT 829  
ID ADL43635 standard; DNA; 388 BP.  
DE Human ovarian cancer DNA marker #17525.

PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.9%; Score 44.4; DB 5; Length 388;  
Best Local Similarity 49.6%; Pred. No. 1.2;  
RESULT 830  
ID ADB09790 standard; DNA; 714 BP.  
DE Alloicoccus otitis antigenic protein encoding DNA SEQ ID NO:3835.  
PN WO2003048304-A2.  
PD 12-JUN-2003.  
PA (AMHP) WYETH HOLDINGS CORP.  
Query Match 1.9%; Score 44.4; DB 9; Length 714;  
Best Local Similarity 46.7%; Pred. No. 1.5;  
RESULT 831  
ID AAZ37082 standard; DNA; 1431 BP.  
DE DNA sequence encoding a yeast Scel endonuclease.  
PN EP972836-A2.  
PD 19-JAN-2000.  
PA (RIKA) INST PHYSICAL & CHEM RES.  
Query Match 1.9%; Score 44.4; DB 3; Length 1431;  
Best Local Similarity 48.6%; Pred. No. 2.1;  
RESULT 832  
ID ABZ10188 standard; DNA; 1501 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #328.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 8; Length 1501;  
Best Local Similarity 45.1%; Pred. No. 2.1;  
RESULT 833  
ID ADB84162 standard; DNA; 1501 BP.  
DE Human lymphoid cell proliferative disorder gene derived DNA #98.  
PN WO2003044226-A2.  
PD 30-MAY-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 10; Length 1501;  
Best Local Similarity 45.1%; Pred. No. 2.1;  
RESULT 834  
ID AAQ24134 standard; DNA; 1671 BP.  
DE 50 kD subunit of Scel.  
PN JP04104793-A.  
PD 07-APR-1992.  
PA (RIKA) RIKAGAKU KENKYUSHO.  
Query Match 1.9%; Score 44.4; DB 2; Length 1671;  
Best Local Similarity 48.6%; Pred. No. 2.2;  
RESULT 835  
ID ABZ59722 standard; DNA; 3410 BP.  
DE T. thermophila metallothionein gene (MTT1).  
PN WO2003006480-A1.  
PD 23-JAN-2003.  
PA (UVRP) UNIV ROCHESTER.  
Query Match 1.9%; Score 44.4; DB 8; Length 3410;  
Best Local Similarity 47.4%; Pred. No. 3;  
RESULT 836  
ID ABL34102 standard; DNA; 4993 BP.  
DE Human immune system associated gene SEQ ID NO: 2075.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 4993;  
Best Local Similarity 45.1%; Pred. No. 3.6;  
RESULT 837  
ID ADS89374 standard; DNA; 5034 BP.  
DE Oligonucleotide of the invention SEQ ID NO:390.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 13; Length 5034;  
Best Local Similarity 47.2%; Pred. No. 3.6;  
RESULT 838  
ID ADS89648 standard; DNA; 5034 BP.  
DE Oligonucleotide of the invention SEQ ID NO:664.  
PN WO2004035803-A2.



PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 13; Length 5034;  
Best Local Similarity 47.2%; Pred. No. 3.6;  
RESULT 839  
ID ABL33666 standard; DNA; 5798 BP.  
DE Human immune system associated gene SEQ ID NO: 1639.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 5798;  
Best Local Similarity 47.4%; Pred. No. 3.8;  
RESULT 840  
ID ABL32820 standard; DNA; 6123 BP.  
DE Human immune system associated gene SEQ ID NO: 793.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 6123;  
Best Local Similarity 46.4%; Pred. No. 3.9;  
RESULT 841  
ID ABK31185 standard; DNA; 6239 BP.  
DE Signal transduction associated gene modified complementary DNA #14.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 6239;  
Best Local Similarity 46.8%; Pred. No. 4;  
RESULT 842  
ID ABL70146 standard; DNA; 6239 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#18.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 6239;  
Best Local Similarity 46.8%; Pred. No. 4;  
RESULT 843  
ID AASE1072 standard; DNA; 6239 BP.  
DE Human gene regulation-associated gene oligonucleotide #27.  
PN WO20017375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 6239;  
Best Local Similarity 46.8%; Pred. No. 4;  
RESULT 844  
ID ABL92231 standard; DNA; 7168 BP.  
DE Chemically treated DNA repair gene fragment complementary to#20.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 7168;  
Best Local Similarity 47.0%; Pred. No. 4.2;  
RESULT 845  
ID AAD22318 standard; DNA; 7168 BP.  
DE Chemically treated human genomic DNA #8 associated with DNA adducts.  
PN WO20017378-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 7168;  
Best Local Similarity 47.0%; Pred. No. 4.2;  
RESULT 846  
ID ABN80026 standard; DNA; 7189 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 43.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 7189;  
Best Local Similarity 46.4%; Pred. No. 4.2;  
RESULT 847  
ID ABK31479 standard; DNA; 8032 BP.  
DE Signal transduction associated gene modified complementary DNA #161.  
PN WO200200926-A2.  
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 8032;  
Best Local Similarity 47.2%; Pred. No. 4.4;  
RESULT 848  
ID ABL70448 standard; DNA; 8032 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#169.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 8032;  
Best Local Similarity 47.2%; Pred. No. 4.4;  
RESULT 849  
ID AASE1409 standard; DNA; 8032 BP.  
DE Human gene regulation-associated gene oligonucleotide #364.  
PN WO20017375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 8032;  
Best Local Similarity 47.2%; Pred. No. 4.4;  
RESULT 850  
ID ABL33568 standard; DNA; 8305 BP.  
DE Human immune system associated gene SEQ ID NO: 1541.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 8305;  
Best Local Similarity 47.4%; Pred. No. 4.5;  
RESULT 851  
ID AA229911 standard; DNA; 8310 BP.  
DE cDNA encoding a SC4 protein of soybean.  
PN WO9953067-A2.  
PD 21-OCT-1999.  
PA (MIRAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.  
Query Match 1.9%; Score 44.4; DB 2; Length 8310;  
Best Local Similarity 44.2%; Pred. No. 4.5;  
RESULT 852  
ID ABL32668 standard; DNA; 11049 BP.  
DE Human immune system associated gene SEQ ID NO: 641.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 11049;  
Best Local Similarity 47.8%; Pred. No. 5.1;  
RESULT 853  
ID ABL92218 standard; DNA; 11049 BP.  
DE Chemically treated DNA repair gene fragment#14.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 11049;  
Best Local Similarity 47.8%; Pred. No. 5.1;  
RESULT 854  
ID ABL49321 standard; DNA; 11049 BP.  
DE Human polynucleotide associated with DNA replication SEQ ID NO 21.  
PN WO20017377-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 11049;  
Best Local Similarity 47.8%; Pred. No. 5.1;  
RESULT 855  
ID AAS46698 standard; DNA; 11694 BP.  
DE Tumour suppressor gene derived chemically modified sequence #421.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 4; Length 11694;  
Best Local Similarity 44.4%; Pred. No. 5.2;  
RESULT 856  
ID ABN79985 standard; DNA; 16633 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 2.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.9%; Score 44.4; DB 6; Length 16633;  
Best Local Similarity 47.1%; Pred. No. 6.1;  
RESULT 857  
ID ABL70501 standard; DNA; 18283 BP.  
DE Chemically treated cell signalling DNA sequence#196.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 18283;  
Best Local Similarity 44.7%; Pred. No. 6.4;  
RESULT 858  
ID AAS61362 standard; DNA; 18283 BP.  
DE Human gene regulation-associated gene oligonucleotide #317.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 18283;  
Best Local Similarity 44.7%; Pred. No. 6.4;  
RESULT 859  
ID ABO67060 standard; DNA; 34688 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 90.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 34688;  
Best Local Similarity 43.7%; Pred. No. 8.5;  
RESULT 860  
ID ABO67094 standard; DNA; 83391 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 124.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.4; DB 6; Length 83391;  
Best Local Similarity 45.7%; Pred. No. 12;  
RESULT 861  
Query Match 1.9%; Score 44.4; DB 9; Length 110000;  
Best Local Similarity 46.7%; Pred. No. 14;  
RESULT 862  
ID ADL37598 standard; DNA; 608 BP.  
DE Human ovarian cancer DNA marker #11478.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.9%; Score 44.2; DB 5; Length 608;  
Best Local Similarity 41.0%; Pred. No. 1.6;  
RESULT 863  
ID ADL72448 standard; DNA; 608 BP.  
DE Human ovarian cancer DNA marker #5190.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.9%; Score 44.2; DB 4; Length 697;  
Best Local Similarity 52.5%; Pred. No. 1.7;  
RESULT 864  
ID AAS28824 standard; cDNA; 697 BP.  
DE Human immunoglobulin encoding cDNA SEQ ID NO 70.  
PN WO200155315-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.9%; Score 44.2; DB 4; Length 697;  
Best Local Similarity 52.5%; Pred. No. 1.7;  
RESULT 865  
ID ABA06691 standard; cDNA; 697 BP.  
DE Human cDNA SEQ ID NO: 357.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.9%; Score 44.2; DB 4; Length 697;  
Best Local Similarity 52.5%; Pred. No. 1.7;  
RESULT 866  
ID ABV84028 standard; cDNA; 697 BP.  
DE Human polynucleotide SEQ ID NO 357.  
PN US2002090672-A1.

PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 1.9%; Score 44.2; DB 6; Length 697;  
Best Local Similarity 52.5%; Pred. No. 1.7;  
RESULT 867  
ID ADB31549 standard; cDNA; 697 BP.  
DE Human cDNA encoding a novel protein SEQ ID NO 70.  
PN US2003077606-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.9%; Score 44.2; DB 10; Length 697;  
Best Local Similarity 52.5%; Pred. No. 1.7;  
RESULT 868  
ID AAQ31693 standard; DNA; 731 BP.  
DE RsaI restriction fragment from Dd ras genomic clone.  
PN WO9220806-A2.  
PD 26-NOV-1992.  
PA (RMFD-) RMF DICTAGENE SA.  
Query Match 1.9%; Score 44.2; DB 2; Length 731;  
Best Local Similarity 43.0%; Pred. No. 1.7;  
RESULT 869  
ID AAZ17145 standard; cDNA; 1351 BP.  
DE Human gene expression product cDNA sequence SEQ ID NO:4616.  
PN WO9938972-A2.  
PD 05-AUG-1999.  
PA (CHIR-) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.9%; Score 44.2; DB 2; Length 1351;  
Best Local Similarity 37.6%; Pred. No. 2.3;  
RESULT 870  
ID ABZ17044 standard; DNA; 2000 BP.  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4849.  
PN WO200216655-A2.  
PD 28-FEB-2002.  
PA (SCRI) SCRIPPS RES INST.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 2000;  
Best Local Similarity 45.4%; Pred. No. 2.7;  
RESULT 871  
ID ADG65091 standard; DNA; 2000 BP.  
DE Promoter region sequence #3.  
PN EP1209228-A2.  
PD 29-MAY-2002.  
PA (RIKE) RIKEN KK.  
PA (TOYT) TOYOTA JIDOSHA KK.  
Query Match 1.9%; Score 44.2; DB 6; Length 2000;  
Best Local Similarity 45.4%; Pred. No. 2.7;  
RESULT 872  
ID ADA69322 standard; DNA; 2000 BP.  
DE Arabidopsis thaliana gene, SEQ ID 2645.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 1.9%; Score 44.2; DB 8; Length 2000;  
Best Local Similarity 45.4%; Pred. No. 2.7;  
RESULT 873  
ID ADS91270 standard; DNA; 2648 BP.  
DE alpha-1 tubulin coding sequence, SEQ ID 166.  
PN WO2004074479-A1.  
PD 02-SEP-2004.  
PA (PHYL-) PHYLOGICA LTD.  
Query Match 1.9%; Score 44.2; DB 13; Length 2648;  
Best Local Similarity 46.3%; Pred. No. 3.1;  
RESULT 874  
ID ABL32341 standard; DNA; 5349 BP.  
DE Human immune system associated gene SEQ ID NO: 314.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 5349;  
Best Local Similarity 51.4%; Pred. No. 4.2;

RESULT 875  
ID ABL31370 standard; DNA; 6012 BP.  
DE Signal transduction associated gene modified DNA #107.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 6012;  
Best Local Similarity 48.6%; Pred. No. 4.4;  
RESULT 876  
ID ABL70327 standard; DNA; 6012 BP.  
DE Chemically treated cell signalling DNA sequence#109.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 6012;  
Best Local Similarity 48.6%; Pred. No. 4.4;  
RESULT 877  
ID AAS61274 standard; DNA; 6012 BP.  
DE Human gene regulation-associated gene oligonucleotide #229.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 6012;  
Best Local Similarity 48.6%; Pred. No. 4.4;  
RESULT 878  
ID ABL32326 standard; DNA; 6109 BP.  
DE Human immune system associated gene SEQ ID NO: 299.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 6109;  
Best Local Similarity 45.6%; Pred. No. 4.4;  
RESULT 879  
ID AAS61077 standard; DNA; 6109 BP.  
DE Human gene regulation-associated gene oligonucleotide #32.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 6109;  
Best Local Similarity 45.6%; Pred. No. 4.4;  
RESULT 880  
ID ABL32890 standard; DNA; 6131 BP.  
DE Human immune system associated gene SEQ ID NO: 863.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 6131;  
Best Local Similarity 46.9%; Pred. No. 4.4;  
RESULT 881  
ID ABL31353 standard; DNA; 6147 BP.  
DE Signal transduction associated gene modified complementary DNA #98.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 6147;  
Best Local Similarity 44.1%; Pred. No. 4.4;  
RESULT 882  
ID ABL33047 standard; DNA; 6290 BP.  
DE Human immune system associated gene SEQ ID NO: 1020.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 6290;  
Best Local Similarity 43.8%; Pred. No. 4.5;  
RESULT 883  
ID ABL33930 standard; DNA; 7456 BP.  
DE Human immune system associated gene SEQ ID NO: 1903.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 7456;  
Best Local Similarity 53.1%; Pred. No. 4.8;  
RESULT 884

ID ABL92292 standard; DNA; 7456 BP.  
DE Chemically treated DNA repair gene fragment#51.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 7456;  
Best Local Similarity 53.1%; Pred. No. 4.8;  
RESULT 885  
ID ABL32530 standard; DNA; 7644 BP.  
DE Human immune system associated gene SEQ ID NO: 503.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 7644;  
Best Local Similarity 51.2%; Pred. No. 4.9;  
RESULT 886  
ID AAS46435 standard; DNA; 8093 BP.  
DE Tumour suppressor gene derived chemically modified sequence #157.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 4; Length 8093;  
Best Local Similarity 46.1%; Pred. No. 5;  
RESULT 887  
ID ABL33973 standard; DNA; 8093 BP.  
DE Human DNA for staging of Astrocytomas #29.  
PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 8093;  
Best Local Similarity 46.1%; Pred. No. 5;  
RESULT 888  
ID ABL92236 standard; DNA; 8093 BP.  
DE Chemically treated DNA repair gene fragment#23.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 8093;  
Best Local Similarity 46.1%; Pred. No. 5;  
RESULT 889  
ID ABL49331 standard; DNA; 8093 BP.  
DE Human MLH1 gene associated with DNA replication SEQ ID NO 31.  
PN WO200177377-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 8093;  
Best Local Similarity 46.1%; Pred. No. 5;  
RESULT 890  
ID ABL10031 standard; DNA; 8093 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #171.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 8; Length 8093;  
Best Local Similarity 46.1%; Pred. No. 5;  
RESULT 891  
ID ADA20360 standard; DNA; 8093 BP.  
DE Prostate tumour related genomic DNA sample #13.  
PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 8; Length 8093;  
Best Local Similarity 46.1%; Pred. No. 5;  
RESULT 892  
ID ADA84167 standard; DNA; 8093 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:25.  
PN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 8; Length 8093;  
Best Local Similarity 46.1%; Pred. No. 5;  
RESULT 893  
ID ABL54139 standard; DNA; 8093 BP.

DE Pretreated genomic DNA region 63.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 10; Length 8093;  
Best Local Similarity 46.1%; Pred. No. 5;  
RESULT 894  
ID ADB84113 standard; DNA; 8093 BP.  
DE Human lymphoid cell proliferative disorder gene derived DNA #49.  
PN WO2003044226-A2.  
PD 30-MAY-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 10; Length 8093;  
Best Local Similarity 46.1%; Pred. No. 5;  
RESULT 895  
ID ADS89291 standard; DNA; 8093 BP.  
DE Oligonucleotide of the invention SEQ ID NO:307.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 13; Length 8093;  
Best Local Similarity 46.1%; Pred. No. 5;  
RESULT 896  
ID ABK3068 standard; DNA; 9117 BP.  
DE Human immune system associated gene SEQ ID NO: 1041.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 9117;  
Best Local Similarity 51.4%; Pred. No. 5.3;  
RESULT 897  
ID AA545453 standard; DNA; 9515 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #79.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 4; Length 9515;  
Best Local Similarity 45.3%; Pred. No. 5.4;  
RESULT 898  
ID ABK28108 standard; DNA; 9515 BP.  
DE DNA transcription associated complementary genomic DNA #91.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 9515;  
Best Local Similarity 45.3%; Pred. No. 5.4;  
RESULT 899  
ID ABN80245 standard; DNA; 9515 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 262.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 9515;  
Best Local Similarity 45.3%; Pred. No. 5.4;  
RESULT 900  
ID ABK28452 standard; DNA; 11187 BP.  
DE DNA transcription associated complementary genomic DNA #163.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 11187;  
Best Local Similarity 44.8%; Pred. No. 5.8;  
RESULT 901  
ID ABU70501 standard; DNA; 18283 BP.  
DE Chemically treated cell signalling DNA sequence#196.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 18283;  
Best Local Similarity 50.2%; Pred. No. 7.2;  
RESULT 902  
ID AA561362 standard; DNA; 18283 BP.  
DE Human gene regulation-associated gene oligonucleotide #317.

PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 18283;  
Best Local Similarity 50.2%; Pred. No. 7.2;  
RESULT 903  
ID ABQ67006 standard; DNA; 33053 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 36.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44.2; DB 6; Length 33053;  
Best Local Similarity 45.7%; Pred. No. 9.3;  
RESULT 904  
ID ACN44010 standard; DNA; 198522 BP.  
DE Human genomic sequence hCG1643869.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 1.9%; Score 44.2; DB 11; Length 198522;  
Best Local Similarity 44.5%; Pred. No. 20;  
RESULT 905  
ID ABX46069 standard; cDNA; 419 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #11234.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.9%; Score 44; DB 8; Length 419;  
Best Local Similarity 47.5%; Pred. No. 1.5;  
RESULT 906  
ID ADQ22935 standard; DNA; 2288 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5755.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 1.9%; Score 44; DB 12; Length 2288;  
Best Local Similarity 50.5%; Pred. No. 3.2;  
RESULT 907  
ID AAS45511 standard; DNA; 3007 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #108.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 4; Length 3007;  
Best Local Similarity 46.3%; Pred. No. 3.6;  
RESULT 908  
ID ABK28445 standard; DNA; 3007 BP.  
DE DNA transcription associated genomic DNA #160.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 6; Length 3007;  
Best Local Similarity 46.3%; Pred. No. 3.6;  
RESULT 909  
ID ABQ67144 standard; DNA; 3151 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 174.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 6; Length 3151;  
Best Local Similarity 44.9%; Pred. No. 3.7;  
RESULT 910  
ID AAD48465 standard; DNA; 3750 BP.  
DE Brassica napus brevipedicellus (BnBP) genomic fragment DNA.  
PN WO200279463-A2.  
PD 10-OCT-2002.  
PA (CANA ) NAT RES COUNCIL CANADA.  
Query Match 1.9%; Score 44; DB 8; Length 3750;  
Best Local Similarity 44.6%; Pred. No. 4;  
RESULT 911

ID ABL32538 standard; DNA; 5820 BP.  
DE Human immune system associated gene SEQ ID NO: 511.  
PN WO200200928-A2.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 6; Length 5820;  
Best Local Similarity 44.5%; Pred. No. 4.9;  
RESULT 912  
ID ABK31237 standard; DNA; 6129 BP.  
DE Signal transduction associated gene modified complementary DNA #40.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 6; Length 6129;  
Best Local Similarity 44.9%; Pred. No. 5;  
RESULT 913  
ID ABL70538 standard; DNA; 6129 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#214.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 6; Length 6129;  
Best Local Similarity 44.9%; Pred. No. 5;  
RESULT 914  
ID AAS61150 standard; DNA; 6129 BP.  
DE Human gene regulation-associated gene oligonucleotide #105.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 6; Length 6129;  
Best Local Similarity 44.9%; Pred. No. 5;  
RESULT 915  
ID AAS61176 standard; DNA; 6223 BP.  
DE Human gene regulation-associated gene oligonucleotide #131.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 6; Length 6223;  
Best Local Similarity 45.4%; Pred. No. 5;  
RESULT 916  
ID AAS45422 standard; DNA; 6306 BP.  
DE Chemically pretreated genomic DNA associated with cell cycle #64.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 4; Length 6306;  
Best Local Similarity 48.0%; Pred. No. 5;  
RESULT 917  
ID ABL33260 standard; DNA; 6437 BP.  
DE Human immune system associated gene SEQ ID NO: 1233.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 6; Length 6437;  
Best Local Similarity 51.5%; Pred. No. 5.1;  
RESULT 918  
ID ABK31424 standard; DNA; 7321 BP.  
DE Signal transduction associated gene modified DNA #134.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 6; Length 7321;  
Best Local Similarity 57.1%; Pred. No. 5.4;  
RESULT 919  
ID ABL70385 standard; DNA; 7321 BP.  
DE Chemically treated cell signalling DNA sequence#138.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 6; Length 7321;  
Best Local Similarity 57.1%; Pred. No. 5.4;  
RESULT 920  
ID AAS61337 standard; DNA; 7321 BP.

DE Human gene regulation-associated gene oligonucleotide #292.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 6; Length 7321;  
Best Local Similarity 57.1%; Pred. No. 5.4;  
RESULT 921  
ID ABL32914 standard; DNA; 7522 BP.  
DE Human immune system associated gene SEQ ID NO: 887.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 6; Length 7522;  
Best Local Similarity 47.8%; Pred. No. 5.4;  
RESULT 922  
ID ABL33013 standard; DNA; 7597 BP.  
DE Human immune system associated gene SEQ ID NO: 986.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 6; Length 7597;  
Best Local Similarity 43.8%; Pred. No. 5.5;  
RESULT 923  
ID AAS46445 standard; DNA; 8952 BP.  
DE Tumour suppressor gene derived chemically modified sequence #167.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 4; Length 8952;  
Best Local Similarity 50.0%; Pred. No. 5.9;  
RESULT 924  
ID ABQ67026 standard; DNA; 11964 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 56.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 6; Length 11964;  
Best Local Similarity 44.9%; Pred. No. 6.7;  
RESULT 925  
ID ABQ66975 standard; DNA; 13627 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 5.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 6; Length 13627;  
Best Local Similarity 45.8%; Pred. No. 7.1;  
RESULT 926  
ID ABL33345 standard; DNA; 17674 BP.  
DE Human immune system associated gene SEQ ID NO: 1318.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 6; Length 17674;  
Best Local Similarity 45.1%; Pred. No. 7.9;  
RESULT 927  
ID AAS46794 standard; DNA; 56153 BP.  
DE Tumour suppressor gene derived chemically modified sequence #520.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.9%; Score 44; DB 4; Length 56153;  
Best Local Similarity 45.6%; Pred. No. 13;  
RESULT 928  
ID ABQ99654 standard; DNA; 95109 BP.  
DE Human membrane spanning 4-domain family, subfamily A genomic sequence.  
PN WO200262946-A2.  
PD 15-AUG-2002.  
PA (UYDU-) UNIV DUKE.  
Query Match 1.9%; Score 44; DB 6; Length 95109;  
Best Local Similarity 46.4%; Pred. No. 17;  
RESULT 929  
ID ABL33598 standard; DNA; 5487 BP.  
DE Human immune system associated gene SEQ ID NO: 1571.

PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 5487;  
Best Local Similarity 49.0%; Pred. No. 5.3;  
RESULT 930  
ID ABL34448 standard; DNA; 6127 BP.  
DE Human metastasis associated gene SEQ ID NO: 1.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 6127;  
Best Local Similarity 49.4%; Pred. No. 5.6;  
RESULT 931  
ID ABL70119 standard; DNA; 6127 BP.  
DE Chemically treated cell signalling DNA sequence#5.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 6127;  
Best Local Similarity 49.4%; Pred. No. 5.6;  
RESULT 932  
ID ADS99709 standard; DNA; 6127 BP.  
DE Bisulphite treated human gene associated with metastasis #1.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 1.8%; Score 43.8; DB 7; Length 6127;  
Best Local Similarity 49.4%; Pred. No. 5.6;  
RESULT 933  
ID AAS46497 standard; DNA; 6233 BP.  
DE Tumour suppressor gene derived chemically modified sequence #219.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 4; Length 6233;  
Best Local Similarity 48.0%; Pred. No. 5.6;  
RESULT 934  
ID ABL32323 standard; DNA; 6418 BP.  
DE Human immune system associated gene SEQ ID NO: 296.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 6418;  
Best Local Similarity 46.0%; Pred. No. 5.7;  
RESULT 935  
ID AAS61074 standard; DNA; 6418 BP.  
DE Human gene regulation-associated gene oligonucleotide #29.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 6418;  
Best Local Similarity 46.0%; Pred. No. 5.7;  
RESULT 936  
ID ABL34541 standard; DNA; 6811 BP.  
DE Human metastasis associated gene SEQ ID NO: 94.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 6811;  
Best Local Similarity 51.9%; Pred. No. 5.8;  
RESULT 937  
ID ABL70264 standard; DNA; 6811 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#77.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 6811;  
Best Local Similarity 51.9%; Pred. No. 5.8;  
RESULT 938  
ID ADS99802 standard; DNA; 6811 BP.

DE Complement of bisulphite treated metastasis-associated human gene #47.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 1.8%; Score 43.8; DB 7; Length 6811;  
Best Local Similarity 51.9%; Pred. No. 5.8;  
RESULT 939  
ID AB210178 standard; DNA; 8093 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #318.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 8; Length 8093;  
Best Local Similarity 47.0%; Pred. No. 6.3;  
RESULT 940  
ID ADB54268 standard; DNA; 8093 BP.  
DE Pretreated genomic DNA region 192.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 10; Length 8093;  
Best Local Similarity 47.0%; Pred. No. 6.3;  
RESULT 941  
ID ADB84190 standard; DNA; 8093 BP.  
DE Human lymphoid cell proliferative disorder gene derived DNA #126.  
PN WO2003044226-A2.  
PD 30-MAY-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 10; Length 8093;  
Best Local Similarity 47.0%; Pred. No. 6.3;  
RESULT 942  
ID ADS89566 standard; DNA; 8093 BP.  
DE Oligonucleotide of the invention SEQ ID NO:582.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 13; Length 8093;  
Best Local Similarity 47.0%; Pred. No. 6.3;  
RESULT 943  
ID ABQ67126 standard; DNA; 8227 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 156.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 8227;  
Best Local Similarity 45.8%; Pred. No. 6.3;  
RESULT 944  
ID ABL34492 standard; DNA; 11996 BP.  
DE Human metastasis associated gene SEQ ID NO: 45.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 11996;  
Best Local Similarity 45.6%; Pred. No. 7.5;  
RESULT 945  
ID ADS99753 standard; DNA; 11996 BP.  
DE Bisulphite treated human gene associated with metastasis #23.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 1.8%; Score 43.8; DB 7; Length 11996;  
Best Local Similarity 45.6%; Pred. No. 7.5;  
RESULT 946  
ID ABL34358 standard; DNA; 12237 BP.  
DE Human immune system associated gene SEQ ID NO: 2331.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 12237;

Best Local Similarity 47.3%; Pred. No. 7.6;  
RESULT 947  
ID ABL33194 standard; DNA; 14861 BP.  
DE Human immune system associated gene SEQ ID NO: 1167.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 14861;  
Best Local Similarity 47.6%; Pred. No. 8.2;  
RESULT 948  
ID ABL70553 standard; DNA; 14861 BP.  
DE Chemically treated cell signalling DNA sequence#222.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 14861;  
Best Local Similarity 47.6%; Pred. No. 8.2;  
RESULT 949  
ID AAS61202 standard; DNA; 14861 BP.  
DE Human gene regulation-associated gene oligonucleotide #157.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 14861;  
Best Local Similarity 47.6%; Pred. No. 8.2;  
RESULT 950  
ID AAS46506 standard; DNA; 14919 BP.  
DE Tumour suppressor gene derived chemically modified sequence #228.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 4; Length 14919;  
Best Local Similarity 44.8%; Pred. No. 8.2;  
RESULT 951  
ID ABK28395 standard; DNA; 15743 BP.  
DE DNA transcription associated genomic DNA #135.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 15743;  
Best Local Similarity 48.3%; Pred. No. 8.4;  
RESULT 952  
ID ABL33090 standard; DNA; 16724 BP.  
DE Human immune system associated gene SEQ ID NO: 1063.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 16724;  
Best Local Similarity 52.9%; Pred. No. 8.7;  
RESULT 953  
ID ABL34536 standard; DNA; 16724 BP.  
DE Human metastasis associated gene SEQ ID NO: 89.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 16724;  
Best Local Similarity 52.9%; Pred. No. 8.7;  
RESULT 954  
ID ABL70259 standard; DNA; 16724 BP.  
DE Chemically treated cell signalling DNA sequence#75.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 16724;  
Best Local Similarity 52.9%; Pred. No. 8.7;  
RESULT 955  
ID ADS99797 standard; DNA; 16724 BP.  
DE Bisulphite treated human gene associated with metastasis #45.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.

Query Match 1.8%; Score 43.8; DB 7; Length 16724;  
Best Local Similarity 52.9%; Pred. No. 8.7;  
RESULT 956  
ID ABK39952 standard; DNA; 17703 BP.  
DE Human chemically pretreated gene sequence #17 strand 1.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 17703;  
Best Local Similarity 44.7%; Pred. No. 8.9;  
RESULT 957  
ID ABL32254 standard; DNA; 18154 BP.  
DE Human immune system associated gene SEQ ID NO: 227.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 18154;  
Best Local Similarity 44.6%; Pred. No. 9;  
RESULT 958  
ID ABL32254 standard; DNA; 18154 BP.  
DE Human immune system associated gene SEQ ID NO: 227.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.8; DB 6; Length 18154;  
Best Local Similarity 44.1%; Pred. No. 9;  
RESULT 959  
ID AAC66747 standard; DNA; 555 BP.  
DE DNA marker B.  
PN WO200063432-A1.  
PD 26-OCT-2000.  
PA (ENZA-) ENZA ZADEN ENKHUIZER ZAADHANDEL BV.  
Query Match 1.8%; Score 43.6; DB 3; Length 555;  
Best Local Similarity 46.4%; Pred. No. 2.2;  
RESULT 960  
ID ABO40113 standard; DNA; 583 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 26704.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 583;  
Best Local Similarity 47.7%; Pred. No. 2.2;  
RESULT 961  
ID ABO40112 standard; DNA; 583 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 26703.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 583;  
Best Local Similarity 47.7%; Pred. No. 2.2;  
RESULT 962  
ID AAK03309 standard; DNA; 1988 BP.  
DE Human brain expressed single exon probe SEQ ID NO: 3300.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.8%; Score 43.6; DB 4; Length 1988;  
Best Local Similarity 44.5%; Pred. No. 3.8;  
RESULT 963  
ID ABZ10164 standard; DNA; 3128 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #304.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 8; Length 3128;  
Best Local Similarity 55.2%; Pred. No. 4.6;  
RESULT 964  
ID ADS89612 standard; DNA; 4930 BP.  
DE Oligonucleotide of the invention SEQ ID NO: 628.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 13; Length 4930;

Best Local Similarity 46.2%; Pred. No. 5.7;  
RESULT 965  
ID ABL34176 standard; DNA; 5368 BP.  
DE Human immune system associated gene SEQ ID NO: 2149.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 5368;  
Best Local Similarity 45.6%; Pred. No. 5.9;  
RESULT 966  
ID ABL34091 standard; DNA; 5407 BP.  
DE Human immune system associated gene SEQ ID NO: 2064.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 5407;  
Best Local Similarity 44.7%; Pred. No. 5.9;  
RESULT 967  
ID ABL33870 standard; DNA; 5511 BP.  
DE Human immune system associated gene SEQ ID NO: 1843.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 5511;  
Best Local Similarity 46.4%; Pred. No. 6;  
RESULT 968  
ID ADS89769 standard; DNA; 6001 BP.  
DE Oligonucleotide of the invention SEQ ID NO: 785.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 13; Length 6001;  
Best Local Similarity 46.2%; Pred. No. 6.2;  
RESULT 969  
ID ADS84206 standard; DNA; 6028 BP.  
DE Human lymphoid cell proliferative disorder gene derived DNA #142.  
PN WO2003044226-A2.  
PD 30-MAY-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 10; Length 6028;  
Best Local Similarity 55.2%; Pred. No. 6.2;  
RESULT 970  
ID AAS46430 standard; DNA; 6106 BP.  
DE Tumour suppressor gene derived chemically modified sequence #152.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 4; Length 6106;  
Best Local Similarity 43.8%; Pred. No. 6.2;  
RESULT 971  
ID ABK40032 standard; DNA; 6106 BP.  
DE Human chemically pretreated gene sequence #57 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 6106;  
Best Local Similarity 43.8%; Pred. No. 6.2;  
RESULT 972  
ID ABL33473 standard; DNA; 6106 BP.  
DE Human immune system associated gene SEQ ID NO: 1446.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 6106;  
Best Local Similarity 43.8%; Pred. No. 6.2;  
RESULT 973  
ID ABL70354 standard; DNA; 6107 BP.  
DE Chemically treated cell signalling DNA sequence complementary to #122.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 6107;  
Best Local Similarity 45.0%; Pred. No. 6.2;

RESULT 974  
ID AAS61315 standard; DNA; 6107 BP.  
DE Human gene regulation-associated gene oligonucleotide #270.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 6107;  
Best Local Similarity 45.0%; Pred. No. 6.2;  
RESULT 975  
ID AAS46574 standard; DNA; 6126 BP.  
DE Tumour suppressor gene derived chemically modified sequence #296.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 4; Length 6126;  
Best Local Similarity 47.2%; Pred. No. 6.2;  
RESULT 976  
ID ABL33831 standard; DNA; 6126 BP.  
DE Human immune system associated gene SEQ ID NO: 1804.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 6126;  
Best Local Similarity 47.2%; Pred. No. 6.2;  
RESULT 977  
ID ABL32623 standard; DNA; 6161 BP.  
DE Human immune system associated gene SEQ ID NO: 596.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 6161;  
Best Local Similarity 47.4%; Pred. No. 6.3;  
RESULT 978  
ID ABL33586 standard; DNA; 6227 BP.  
DE Human immune system associated gene SEQ ID NO: 1559.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 6227;  
Best Local Similarity 44.3%; Pred. No. 6.3;  
RESULT 979  
ID ABL92260 standard; DNA; 6227 BP.  
DE Chemically treated DNA repair gene fragment #35.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 6227;  
Best Local Similarity 44.3%; Pred. No. 6.3;  
RESULT 980  
ID ABZ79546 standard; DNA; 6459 BP.  
DE Radish Rfl DNA # SEQ ID 1.  
PN JP2002355042-A.  
PD 10-DEC-2002.  
PA (MITU) MITSUBISHI CHEM CORP.  
Query Match 1.8%; Score 43.6; DB 8; Length 6459;  
Best Local Similarity 46.0%; Pred. No. 6.4;  
RESULT 981  
ID AAK86101 standard; DNA; 6558 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 40913.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.8%; Score 43.6; DB 4; Length 6558;  
Best Local Similarity 44.5%; Pred. No. 6.4;  
RESULT 982  
ID AAL37138 standard; DNA; 6558 BP.  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3503.  
PN WO200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.8%; Score 43.6; DB 4; Length 6558;  
Best Local Similarity 44.5%; Pred. No. 6.4;  
RESULT 983



ID ABA21372 standard; DNA; 6558 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 13703.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 1.8%; Score 43.6; DB 5; Length 6558;  
Best Local Similarity 44.5%; Pred. No. 6.4;  
RESULT 984  
ID ABX60126 standard; cDNA; 6558 BP.  
DE cDNA encoding novel human musculoskeletal system antigen #2470.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 1.8%; Score 43.6; DB 8; Length 6558;  
Best Local Similarity 44.5%; Pred. No. 6.4;  
RESULT 985  
ID ADJ30876 standard; DNA; 6558 BP.  
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3503.  
PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 1.8%; Score 43.6; DB 12; Length 6558;  
Best Local Similarity 44.5%; Pred. No. 6.4;  
RESULT 986  
ID ABK31451 standard; DNA; 7131 BP.  
DE Signal transduction associated gene modified complementary DNA #147.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 7131;  
Best Local Similarity 43.4%; Pred. No. 6.7;  
RESULT 987  
ID ABL70428 standard; DNA; 7131 BP.  
DE Chemically treated cell signalling DNA sequence complementary to #159.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 7131;  
Best Local Similarity 43.4%; Pred. No. 6.7;  
RESULT 988  
ID AAS61361 standard; DNA; 7131 BP.  
DE Human gene regulation-associated gene oligonucleotide #316.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 7131;  
Best Local Similarity 43.4%; Pred. No. 6.7;  
RESULT 989  
ID ABL32982 standard; DNA; 7143 BP.  
DE Human immune system associated gene SEQ ID NO: 955.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 7143;  
Best Local Similarity 45.4%; Pred. No. 6.7;  
RESULT 990  
ID ABL33775 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1748.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 7503;  
Best Local Similarity 57.2%; Pred. No. 6.8;  
RESULT 991  
ID ADB54312 standard; DNA; 7833 BP.  
DE Pretreated genomic DNA region 236.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 10; Length 7833;  
Best Local Similarity 46.2%; Pred. No. 7;

RESULT 992  
ID ADB37779 standard; DNA; 7833 BP.  
DE Human chemically treated EYA4 nucleotide sequence SEQ ID NO:25.  
PN WO2003072820-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 10; Length 7833;  
Best Local Similarity 46.2%; Pred. No. 7;  
RESULT 993  
ID ADS89608 standard; DNA; 7833 BP.  
DE Oligonucleotide of the invention SEQ ID NO:624.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 13; Length 7833;  
Best Local Similarity 46.2%; Pred. No. 7;  
RESULT 994  
ID AAS45432 standard; DNA; 8866 BP.  
DE Chemically pretreated genomic DNA associated with cell cycle #69.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 4; Length 8866;  
Best Local Similarity 46.4%; Pred. No. 7.4;  
RESULT 995  
ID ABR28279 standard; DNA; 8866 BP.  
DE DNA transcription associated genomic DNA #77.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 8866;  
Best Local Similarity 46.4%; Pred. No. 7.4;  
RESULT 996  
ID ADS89686 standard; DNA; 8900 BP.  
DE Oligonucleotide of the invention SEQ ID NO:702.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 13; Length 8900;  
Best Local Similarity 47.4%; Pred. No. 7.4;  
RESULT 997  
ID ADS89412 standard; DNA; 8900 BP.  
DE Oligonucleotide of the invention SEQ ID NO:428.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 13; Length 8900;  
Best Local Similarity 47.4%; Pred. No. 7.4;  
RESULT 998  
ID ABR28453 standard; DNA; 10467 BP.  
DE DNA transcription associated genomic DNA #164.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 10467;  
Best Local Similarity 53.5%; Pred. No. 7.9;  
RESULT 999  
ID ADB54222 standard; DNA; 11913 BP.  
DE Pretreated genomic DNA region 146.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 10; Length 11913;  
Best Local Similarity 46.5%; Pred. No. 8.4;  
RESULT 1000  
ID ADS89520 standard; DNA; 11913 BP.  
DE Oligonucleotide of the invention SEQ ID NO:536.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 13; Length 11913;  
Best Local Similarity 46.5%; Pred. No. 8.4;

ID ABL32299 standard; DNA; 12507 BP.  
DE Human immune system associated gene SEQ ID NO: 272.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 12507;  
Best Local Similarity 49.3%; Pred. No. 8.6;  
RESULT 1002  
ID ABL33712 standard; DNA; 13326 BP.  
DE Human immune system associated gene SEQ ID NO: 1685.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 13326;  
Best Local Similarity 49.0%; Pred. No. 8.8;  
RESULT 1003  
ID ABL34070 standard; DNA; 13503 BP.  
DE Human immune system associated gene SEQ ID NO: 2043.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 13503;  
Best Local Similarity 47.8%; Pred. No. 8.8;  
RESULT 1004  
ID AAS46356 standard; DNA; 14537 BP.  
DE Tumour suppressor gene derived chemically modified sequence #78.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 4; Length 14537;  
Best Local Similarity 46.0%; Pred. No. 9.1;  
RESULT 1005  
ID ABL34469 standard; DNA; 16173 BP.  
DE Human metastasis associated gene SEQ ID NO: 22.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 16173;  
Best Local Similarity 45.9%; Pred. No. 9.6;  
RESULT 1006  
ID ADS99730 standard; DNA; 16173 BP.  
DE Complement of bisulphite treated metastasis-associated human gene #11.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 1.8%; Score 43.6; DB 7; Length 16173;  
Best Local Similarity 45.9%; Pred. No. 9.6;  
RESULT 1007  
ID ABL33702 standard; DNA; 18624 BP.  
DE Human immune system associated gene SEQ ID NO: 1675.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 18624;  
Best Local Similarity 50.5%; Pred. No. 10;  
RESULT 1008  
ID ABL33933 standard; DNA; 19734 BP.  
DE Human immune system associated gene SEQ ID NO: 1906.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 19734;  
Best Local Similarity 45.4%; Pred. No. 10;  
RESULT 1009  
ID ABK31510 standard; DNA; 47108 BP.  
DE Signal transduction associated gene modified DNA #177.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 47108;  
Best Local Similarity 45.7%; Pred. No. 15;

RESULT 1010  
ID ABL55644 standard; DNA; 50000 BP.  
DE AmEPV genome fragment#2.  
PN WO200212526-A2.  
PD 14-FEB-2002.  
PA (UYFL) UNIV FLORIDA.  
Query Match 1.8%; Score 43.6; DB 6; Length 50000;  
Best Local Similarity 48.7%; Pred. No. 16;  
RESULT 1011  
ID AQO67093 standard; DNA; 83391 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 123.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.6; DB 6; Length 83391;  
Best Local Similarity 45.6%; Pred. No. 20;  
RESULT 1012  
ID AQO97960 standard; DNA; 390183 BP.  
DE Human cancer associated sequence HD11-029, SEQ ID 937.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 1.8%; Score 43.6; DB 12; Length 110000;  
Best Local Similarity 47.5%; Pred. No. 22;  
RESULT 1013  
ID ABX41811 standard; cDNA; 337 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #6976.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 1.8%; Score 43.4; DB 8; Length 337;  
Best Local Similarity 53.2%; Pred. No. 2;  
RESULT 1014  
ID AQO14987 standard; DNA; 547 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1578.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 547;  
Best Local Similarity 44.9%; Pred. No. 2.4;  
RESULT 1015  
ID AQO14986 standard; DNA; 547 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1577.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 547;  
Best Local Similarity 44.9%; Pred. No. 2.4;  
RESULT 1016  
ID AQO89354 standard; cDNA; 830 BP.  
DE Human prostate expressed polynucleotide SEQ ID NO 610.  
PN WO200255700-A2.  
PD 18-JUL-2002.  
PA (CHIR) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.8%; Score 43.4; DB 6; Length 830;  
Best Local Similarity 51.9%; Pred. No. 2.9;  
RESULT 1017  
ID ADB82297 standard; cDNA; 830 BP.  
DE Human cDNA sequence useful for the treatment of cancer (seqID 609).  
PN WO2003050236-A2.  
PD 19-JUN-2003.  
PA (CHIR) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.8%; Score 43.4; DB 9; Length 830;  
Best Local Similarity 51.9%; Pred. No. 2.9;  
RESULT 1018  
ID ASI99480 standard; cDNA; 2196 BP.  
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:441.  
PN WO200188188-A2.

PD 22-NOV-2001.  
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
Query Match 1.8%; Score 43.4; DB 6; Length 2196;  
Best Local Similarity 49.3%; Pred. No. 4.5;  
RESULT 1019  
ID ABL34150 standard; DNA; 5376 BP.  
DE Human immune system associated gene SEQ ID NO: 2123.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 5376;  
Best Local Similarity 51.0%; Pred. No. 6.6;  
RESULT 1020  
ID ABK31491 standard; DNA; 6012 BP.  
DE Signal transduction associated gene modified complementary DNA #167.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 6012;  
Best Local Similarity 48.9%; Pred. No. 7;  
RESULT 1021  
ID ABL70464 standard; DNA; 6012 BP.  
DE Chemically treated cell signalling DNA sequence complementary to #177.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 6012;  
Best Local Similarity 48.9%; Pred. No. 7;  
RESULT 1022  
ID AAS46430 standard; DNA; 6106 BP.  
DE Tumour suppressor gene derived chemically modified sequence #152.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 4; Length 6106;  
Best Local Similarity 43.9%; Pred. No. 7;  
RESULT 1023  
ID ABK40032 standard; DNA; 6106 BP.  
DE Human chemically pretreated gene sequence #57 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 6106;  
Best Local Similarity 43.9%; Pred. No. 7;  
RESULT 1024  
ID ABL33473 standard; DNA; 6106 BP.  
DE Human immune system associated gene SEQ ID NO: 1446.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 6106;  
Best Local Similarity 43.9%; Pred. No. 7;  
RESULT 1025  
ID ABL32408 standard; DNA; 6317 BP.  
DE Human immune system associated gene SEQ ID NO: 381.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 6317;  
Best Local Similarity 45.9%; Pred. No. 7.1;  
RESULT 1026  
ID ABL49311 standard; DNA; 6317 BP.  
DE Human polynucleotide associated with DNA replication SEQ ID NO: 11.  
PN WO200177377-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 6317;  
Best Local Similarity 45.9%; Pred. No. 7.1;  
RESULT 1027  
ID ABL32832 standard; DNA; 6585 BP.  
DE Human immune system associated gene SEQ ID NO: 805.  
PN WO200200928-A2.  
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 6585;  
Best Local Similarity 51.9%; Pred. No. 7.2;  
RESULT 1028  
ID AAS61182 standard; DNA; 6585 BP.  
DE Human gene regulation-associated gene oligonucleotide #137.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 6585;  
Best Local Similarity 51.9%; Pred. No. 7.2;  
RESULT 1029  
ID ABL33476 standard; DNA; 6590 BP.  
DE Human immune system associated gene SEQ ID NO: 1449.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 6590;  
Best Local Similarity 45.8%; Pred. No. 7.2;  
RESULT 1030  
ID ABL33735 standard; DNA; 6942 BP.  
DE Human immune system associated gene SEQ ID NO: 1708.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 6942;  
Best Local Similarity 47.3%; Pred. No. 7.4;  
RESULT 1031  
ID AAS45403 standard; DNA; 7903 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #54.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 4; Length 7903;  
Best Local Similarity 47.0%; Pred. No. 7.8;  
RESULT 1032  
ID ABL33363 standard; DNA; 7903 BP.  
DE Human immune system associated gene SEQ ID NO: 1336.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 7903;  
Best Local Similarity 47.0%; Pred. No. 7.8;  
RESULT 1033  
ID ABK28248 standard; DNA; 7903 BP.  
DE DNA transcription associated complementary genomic DNA #61.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 7903;  
Best Local Similarity 47.0%; Pred. No. 7.8;  
RESULT 1034  
ID ACF62816 standard; DNA; 8222 BP.  
DE Colon cancer analysis related genomic DNA SEQ ID NO: 65.  
PN WO2003014388-A2.  
PD 20-FEB-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 8; Length 8222;  
Best Local Similarity 43.8%; Pred. No. 8;  
RESULT 1035  
ID ACF62794 standard; DNA; 8222 BP.  
DE Colon cancer analysis related genomic DNA SEQ ID NO: 43.  
PN WO2003014388-A2.  
PD 20-FEB-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 8; Length 8222;  
Best Local Similarity 43.8%; Pred. No. 8;  
RESULT 1036  
ID ABK40075 standard; DNA; 9021 BP.  
DE Human chemically pretreated gene sequence #79 strand 1.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.8%; Score 43.4; DB 6; Length 9021;  
Best Local Similarity 45.1%; Pred. No. 8.3;  
RESULT 1037  
ID ABL32190 standard; DNA; 9021 BP.  
DE Human immune system associated gene SEQ ID NO: 2205.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 9021;  
Best Local Similarity 45.1%; Pred. No. 8.3;  
RESULT 1038  
ID ABL33988 standard; DNA; 9021 BP.  
DE Human DNA for staging of Astrocytomas #37.  
PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 9021;  
Best Local Similarity 45.1%; Pred. No. 8.3;  
RESULT 1039  
ID ADA20388 standard; DNA; 9021 BP.  
DE Prostate tumour related genomic DNA sample #27.  
PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 8; Length 9021;  
Best Local Similarity 45.1%; Pred. No. 8.3;  
RESULT 1040  
ID ADA84195 standard; DNA; 9021 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:53.  
PN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 8; Length 9021;  
Best Local Similarity 45.1%; Pred. No. 8.3;  
RESULT 1041  
ID ADB54190 standard; DNA; 11222 BP.  
DE Pretreated genomic DNA region 114.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 10; Length 11222;  
Best Local Similarity 43.8%; Pred. No. 9.2;  
RESULT 1042  
ID ADB54318 standard; DNA; 11222 BP.  
DE Pretreated genomic DNA region 242.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 10; Length 11222;  
Best Local Similarity 43.8%; Pred. No. 9.2;  
RESULT 1043  
ID ABL39937 standard; DNA; 11422 BP.  
DE Human chemically pretreated gene sequence #9 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 11422;  
Best Local Similarity 49.3%; Pred. No. 9.2;  
RESULT 1044  
ID ABL32219 standard; DNA; 11422 BP.  
DE Human immune system associated gene SEQ ID NO: 192.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 11422;  
Best Local Similarity 49.3%; Pred. No. 9.2;  
RESULT 1045  
ID ABL33927 standard; DNA; 13427 BP.  
DE Human immune system associated gene SEQ ID NO: 1900.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 13427;

Best Local Similarity 47.8%; Pred. No. 9.9;  
RESULT 1046  
ID ABL32190 standard; DNA; 17137 BP.  
DE Human immune system associated gene SEQ ID NO: 163.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 17137;  
Best Local Similarity 46.1%; Pred. No. 11;  
RESULT 1047  
ID ABL70570 standard; DNA; 24939 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#230.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 24939;  
Best Local Similarity 48.2%; Pred. No. 13;  
RESULT 1048  
ID ABD33520 standard; DNA; 34722 BP.  
DE Human cancer-associated (CA) gene HD07-102.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 1.8%; Score 43.4; DB 13; Length 34722;  
Best Local Similarity 45.7%; Pred. No. 15;  
RESULT 1049  
ID ACN44638 standard; DNA; 35680 BP.  
DE Human genomic sequence hCG17117.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 1.8%; Score 43.4; DB 11; Length 35680;  
Best Local Similarity 51.9%; Pred. No. 15;  
RESULT 1050  
ID ABQ67150 standard; DNA; 40324 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 180.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.4; DB 6; Length 40324;  
Best Local Similarity 45.7%; Pred. No. 16;  
RESULT 1051  
ID ABS52847 standard; DNA; 90541 BP.  
DE Human SR protein-specific kinase 2, SRPK2, genomic DNA.  
PN US2002094560-A1.  
PD 18-JUL-2002.  
PA (ABUT/) ABU-THREIDEH J.  
PA (GONG/) GONG F.  
PA (KETC/) KETCHUM K A.  
PA (DFRA/) DI FRANCESCO V.  
PA (BEAS/) BEASLEY E M.  
Query Match 1.8%; Score 43.4; DB 6; Length 90541;  
Best Local Similarity 53.2%; Pred. No. 23;  
RESULT 1052  
ID ADJ37690 standard; DNA; 90541 BP.  
DE Human kinase genomic DNA.  
PN US2003175927-A1.  
PD 18-SEP-2003.  
PA (APPL-) APPLERA CORP.  
Query Match 1.8%; Score 43.4; DB 10; Length 90541;  
Best Local Similarity 53.2%; Pred. No. 23;  
RESULT 1053  
ID ADR31219 standard; DNA; 90541 BP.  
DE Human SRPK2 kinase protein alternative splice form genomic DNA.  
PN US2004157297-A1.  
PD 12-AUG-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 1.8%; Score 43.4; DB 13; Length 90541;  
Best Local Similarity 53.2%; Pred. No. 23;  
RESULT 1054  
ID AAL54213 standard; DNA; 113033 BP.  
DE SR protein-specific kinase-1 DNA, SEQ ID No 5.  
PN WO200299427-A1.

PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 1.8%; Score 43.4; DB 8; Length 113033;  
Best Local Similarity 53.2%; Pred. No. 25;  
RESULT 1055  
ID ADL17884 standard; cDNA; 158001 BP.  
DE Human phosphotyrosyl phosphatase activator, PTPA, gene.  
PN US2004023906-A1.  
PD 05-FEB-2004.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 1.8%; Score 43.4; DB 12; Length 158001;  
Best Local Similarity 48.7%; Pred. No. 29;  
RESULT 1056  
ID ABV56638 standard; cDNA; 469 BP.  
DE Human prostate expression marker cDNA 56629.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.8%; Score 43.2; DB 5; Length 469;  
Best Local Similarity 50.8%; Pred. No. 2.5;  
RESULT 1057  
ID ACN55408 standard; cDNA; 499 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-023-Q6-N6-C10, SEQ:10189.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.8%; Score 43.2; DB 13; Length 499;  
Best Local Similarity 47.4%; Pred. No. 2.6;  
RESULT 1058  
ID AAV40736 standard; cDNA; 1982 BP.  
DE C. felis esterase, nFE51982, coding sequence complementary strand.  
PN WO9821324-A1.  
PD 22-MAY-1998.  
PA (HESK-) HESKA CORP.  
Query Match 1.8%; Score 43.2; DB 2; Length 1982;  
Best Local Similarity 47.8%; Pred. No. 4.8;  
RESULT 1059  
ID AAV40735 standard; cDNA; 1982 BP.  
DE C. felis esterase, nFE51982, coding sequence.  
PN WO9821324-A1.  
PD 22-MAY-1998.  
PA (HESK-) HESKA CORP.  
Query Match 1.8%; Score 43.2; DB 2; Length 1982;  
Best Local Similarity 47.8%; Pred. No. 4.8;  
RESULT 1060  
ID AAD21167 standard; cDNA; 1982 BP.  
DE Ctenocephalides felis carboxylesterase cDNA, nFE51982.  
PN US6291222-B1.  
PD 18-SEP-2001.  
PA (HESK-) HESKA CORP.  
Query Match 1.8%; Score 43.2; DB 4; Length 1982;  
Best Local Similarity 47.8%; Pred. No. 4.8;  
RESULT 1061  
ID AAV40758 standard; cDNA; 2144 BP.  
DE C. felis esterase, nFE52144, coding sequence.  
PN WO9821324-A1.  
PD 22-MAY-1998.  
PA (HESK-) HESKA CORP.  
Query Match 1.8%; Score 43.2; DB 2; Length 2144;  
Best Local Similarity 47.8%; Pred. No. 5;  
RESULT 1062  
ID AAV40759 standard; cDNA; 2144 BP.  
DE C. felis esterase, nFE52144, coding sequence complementary strand.  
PN WO9821324-A1.  
PD 22-MAY-1998.  
PA (HESK-) HESKA CORP.  
Query Match 1.8%; Score 43.2; DB 2; Length 2144;  
Best Local Similarity 47.8%; Pred. No. 5;  
RESULT 1063  
ID AAD21182 standard; cDNA; 2144 BP.

DE Ctenocephalides felis carboxylesterase cDNA, nFE52144.  
PN US6291222-B1.  
PD 18-SEP-2001.  
PA (HESK-) HESKA CORP.  
Query Match 1.8%; Score 43.2; DB 4; Length 2144;  
Best Local Similarity 47.8%; Pred. No. 5;  
RESULT 1064  
ID ADB54116 standard; DNA; 2501 BP.  
DE Pretreated genomic DNA region 40.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.2; DB 10; Length 2501;  
Best Local Similarity 48.9%; Pred. No. 5.3;  
RESULT 1065  
ID ADS89272 standard; DNA; 2501 BP.  
DE Oligonucleotide of the invention SEQ ID NO:288.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.2; DB 13; Length 2501;  
Best Local Similarity 48.9%; Pred. No. 5.3;  
RESULT 1066  
ID AB281728 standard; cDNA; 2652 BP.  
DE Rat brain-enriched hyaluronan binding protein coding sequence.  
PN WO2003007880-A2.  
PD 30-JAN-2003.  
PA (UYVA) UNIV YALE.  
PA (HOCK/) HOCKFIELD S.  
PA (MATT/) MATTHEWS R T.  
Query Match 1.8%; Score 43.2; DB 8; Length 2652;  
Best Local Similarity 51.6%; Pred. No. 5.4;  
RESULT 1067  
ID AB281727 standard; cDNA; 2652 BP.  
DE Rat mutant brain-enriched hyaluronan binding protein coding sequence.  
PN WO2003007880-A2.  
PD 30-JAN-2003.  
PA (UYVA) UNIV YALE.  
PA (HOCK/) HOCKFIELD S.  
PA (MATT/) MATTHEWS R T.  
Query Match 1.8%; Score 43.2; DB 8; Length 2652;  
Best Local Similarity 51.6%; Pred. No. 5.4;  
RESULT 1068  
ID ADK67781 standard; DNA; 2652 BP.  
DE Rat glycosylation-variant BEHAB isoform coding sequence.  
PN WO2004013356-A1.  
PD 12-FEB-2004.  
PA (UYVA) UNIV YALE.  
Query Match 1.8%; Score 43.2; DB 12; Length 2652;  
Best Local Similarity 51.6%; Pred. No. 5.4;  
RESULT 1069  
ID ADK67780 standard; DNA; 2652 BP.  
DE Rat brain-enriched hyaluronan binding (BEHAB) mutant coding sequence.  
PN WO2004013356-A1.  
PD 12-FEB-2004.  
PA (UYVA) UNIV YALE.  
Query Match 1.8%; Score 43.2; DB 12; Length 2652;  
Best Local Similarity 51.6%; Pred. No. 5.4;  
RESULT 1070  
ID ADB59097 standard; DNA; 3077 BP.  
DE Toxicity-related gene, SEQ ID 4123.  
PN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match 1.8%; Score 43.2; DB 10; Length 3077;  
Best Local Similarity 51.6%; Pred. No. 5.8;  
RESULT 1071  
ID ADP72861 standard; DNA; 3077 BP.  
DE Renal toxin progression gene marker #1450.  
PN WO2004048598-A2.  
PD 10-JUN-2004.  
PA (GENE-) GENE LOGIC INC.  
Query Match 1.8%; Score 43.2; DB 12; Length 3077;

Best Local Similarity 51.6%; Pred. No. 5.8;  
RESULT 1072  
ID AD09331 standard; DNA; 3552 BP.  
DE Swinepox virus (SPV) DNA sequence #1.  
PN JP2003111591-A.  
PD 15-APR-2003.  
PA (JAPG ) NIPPON ZEON KK.  
Query Match  
Best Local Similarity 1.8%; Score 43.2; DB 10; Length 3552;  
52.2%; Pred. No. 6.2;  
RESULT 1073  
ID ADH51190 standard; DNA; 4597 BP.  
DE Soybean FAD2-2B gene intron 1.  
PN WO2004001000-A2.  
PD 31-DEC-2003.  
PA (MONS ) MONSANTO TECHNOLOGY LLC.  
Query Match  
Best Local Similarity 1.8%; Score 43.2; DB 12; Length 4597;  
44.2%; Pred. No. 6.9;  
RESULT 1074  
ID ADI03851 standard; DNA; 4597 BP.  
DE Soybean FAD2-2B intron 1 sequence.  
PN WO2004001001-A2.  
PD 31-DEC-2003.  
PA (CALJ ) CALGENE LLC.  
Query Match  
Best Local Similarity 1.8%; Score 43.2; DB 12; Length 4597;  
44.2%; Pred. No. 6.9;  
RESULT 1075  
ID ABL33070 standard; DNA; 5294 BP.  
DE Human immune system associated gene SEQ ID NO: 1043.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 43.2; DB 6; Length 5294;  
45.9%; Pred. No. 7.4;  
RESULT 1076  
ID ABK31282 standard; DNA; 5294 BP.  
DE Signal transduction associated gene modified DNA #63.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 43.2; DB 6; Length 5294;  
45.9%; Pred. No. 7.4;  
RESULT 1077  
ID AAA70199 standard; DNA; 6042 BP.  
DE Plasmidium falciparum chromosome 2 related DNA sequence SEQ ID NO:332.  
PN WO20025728-A2.  
PD 11-MAY-2000.  
PA (HOFF/) HOFFMAN S.  
PA (CARU/) CARUCCI D.  
PA (GARD/) GARDNER M.  
PA (VENT/) VENTER J C.  
Query Match  
Best Local Similarity 1.8%; Score 43.2; DB 3; Length 6042;  
44.8%; Pred. No. 7.8;  
RESULT 1078  
ID AAS46310 standard; DNA; 6095 BP.  
DE Tumour suppressor gene derived chemically modified sequence #32.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 43.2; DB 4; Length 6095;  
48.9%; Pred. No. 7.8;  
RESULT 1079  
ID ABL32361 standard; DNA; 6095 BP.  
DE Human immune system associated gene SEQ ID NO: 334.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 43.2; DB 6; Length 6095;  
48.9%; Pred. No. 7.8;  
RESULT 1080  
ID ABL34475 standard; DNA; 6095 BP.  
DE Human metastasis associated gene SEQ ID NO: 28.  
PN WO200177376-A2.  
PD 18-OCT-2001.

PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 43.2; DB 6; Length 6095;  
48.9%; Pred. No. 7.8;  
RESULT 1081  
ID ABL70150 standard; DNA; 6095 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#20.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 43.2; DB 6; Length 6095;  
48.9%; Pred. No. 7.8;  
RESULT 1082  
ID ADS99736 standard; DNA; 6095 BP.  
DE Complement of bisulphite treated metastasis-associated human gene #14.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match  
Best Local Similarity 1.8%; Score 43.2; DB 7; Length 6095;  
48.9%; Pred. No. 7.8;  
RESULT 1083  
ID ADH51189 standard; DNA; 6220 BP.  
DE Soybean FAD2-2 partial genomic clone.  
PN WO2004001000-A2.  
PD 31-DEC-2003.  
PA (MONS ) MONSANTO TECHNOLOGY LLC.  
Query Match  
Best Local Similarity 1.8%; Score 43.2; DB 12; Length 6220;  
44.2%; Pred. No. 7.9;  
RESULT 1084  
ID ADI03850 standard; DNA; 6220 BP.  
DE Soybean FAD2-2 partial genomic sequence.  
PN WO2004001001-A2.  
PD 31-DEC-2003.  
PA (CALJ ) CALGENE LLC.  
Query Match  
Best Local Similarity 1.8%; Score 43.2; DB 12; Length 6220;  
44.2%; Pred. No. 7.9;  
RESULT 1085  
ID ABL33496 standard; DNA; 6285 BP.  
DE Human immune system associated gene SEQ ID NO: 1469.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 43.2; DB 6; Length 6285;  
45.4%; Pred. No. 8;  
RESULT 1086  
ID AAS46591 standard; DNA; 6286 BP.  
DE Tumour suppressor gene derived chemically modified sequence #313.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 43.2; DB 4; Length 6286;  
43.8%; Pred. No. 8;  
RESULT 1087  
ID ABL32315 standard; DNA; 6641 BP.  
DE Human immune system associated gene SEQ ID NO: 288.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 43.2; DB 6; Length 6641;  
42.3%; Pred. No. 8.1;  
RESULT 1088  
ID ABL54336 standard; DNA; 6641 BP.  
DE Chemically treated apoptosis gene complementary to gene #18.  
PN WO200177164-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 43.2; DB 6; Length 6641;  
42.3%; Pred. No. 8.1;  
RESULT 1089  
ID ABK31323 standard; DNA; 6880 BP.  
DE Signal transduction associated gene modified complementary DNA #83.  
PN WO200200926-A2.

PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.2; DB 6; Length 6880;  
Best Local Similarity 46.9%; Pred. No. 8.3;  
RESULT 1090  
ID ABL70294 standard; DNA; 6880 BP.  
DE Human immune system associated gene sequence complementary to#92.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.2; DB 6; Length 6880;  
Best Local Similarity 46.9%; Pred. No. 8.3;  
RESULT 1091  
ID AAS61224 standard; DNA; 6880 BP.  
DE Human gene regulation-associated gene oligonucleotide #179.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.2; DB 6; Length 6880;  
Best Local Similarity 46.9%; Pred. No. 8.3;  
RESULT 1092  
ID ABL32893 standard; DNA; 10710 BP.  
DE Human immune system associated gene SEQ ID NO: 866.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.2; DB 6; Length 10710;  
Best Local Similarity 46.0%; Pred. No. 10;  
RESULT 1093  
ID ADS89562 standard; DNA; 11029 BP.  
DE Oligonucleotide of the invention SEQ ID NO:578.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.2; DB 13; Length 11029;  
Best Local Similarity 45.4%; Pred. No. 10;  
RESULT 1094  
ID ABL54326 standard; DNA; 11670 BP.  
DE Chemically treated apoptosis gene complementary to gene #13.  
PN WO200177164-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.2; DB 6; Length 11670;  
Best Local Similarity 46.0%; Pred. No. 10;  
RESULT 1095  
ID ABL33531 standard; DNA; 13712 BP.  
DE Human immune system associated gene SEQ ID NO: 1504.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.2; DB 6; Length 13712;  
Best Local Similarity 43.6%; Pred. No. 11;  
RESULT 1096  
ID ABL32729 standard; DNA; 14307 BP.  
DE Human immune system associated gene SEQ ID NO: 702.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.2; DB 6; Length 14307;  
Best Local Similarity 48.1%; Pred. No. 11;  
RESULT 1097  
ID ABL32467 standard; DNA; 15373 BP.  
DE Human immune system associated gene SEQ ID NO: 440.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.2; DB 6; Length 15373;  
Best Local Similarity 45.5%; Pred. No. 12;  
RESULT 1098  
ID ABL32625 standard; DNA; 16217 BP.  
DE Human immune system associated gene SEQ ID NO: 598.  
PN WO200200928-A2.  
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.2; DB 6; Length 16217;  
Best Local Similarity 46.2%; Pred. No. 12;  
RESULT 1099  
ID ABL34027 standard; DNA; 17594 BP.  
DE Human immune system associated gene SEQ ID NO: 2000.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.2; DB 6; Length 17594;  
Best Local Similarity 49.1%; Pred. No. 13;  
RESULT 1100  
ID AAC58017 standard; DNA; 20674 BP.  
DE Archidonic acid metabolism related genomic biallelic marker #651.  
PN WO200047771-A2.  
PD 17-AUG-2000.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.2; DB 3; Length 20674;  
Best Local Similarity 50.0%; Pred. No. 13;  
RESULT 1101  
ID ABL70570 standard; DNA; 24939 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#230.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43.2; DB 6; Length 24939;  
Best Local Similarity 46.2%; Pred. No. 15;  
RESULT 1102  
ID AAS16305 standard; DNA; 74586 BP.  
DE Genomic DNA encoding human transporter polypeptide.  
PN WO200181413-A2.  
Query Match 1.8%; Score 43.2; DB 6; Length 74586;  
Best Local Similarity 49.6%; Pred. No. 24;  
RESULT 1103  
ID ACN47472 standard; cDNA; 560 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-011-Q1-N6-C9, SEQ:2253.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.8%; Score 43; DB 13; Length 560;  
Best Local Similarity 45.4%; Pred. No. 3.1;  
RESULT 1104  
ID AB215647 standard; DNA; 1132 BP.  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 3452.  
PN WO200216655-A2.  
PD 28-FEB-2002.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 1.8%; Score 43; DB 6; Length 1132;  
Best Local Similarity 47.6%; Pred. No. 4.2;  
RESULT 1105  
ID ADS89486 standard; DNA; 4001 BP.  
DE Oligonucleotide of the invention SEQ ID NO:502.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 13; Length 4001;  
Best Local Similarity 48.2%; Pred. No. 7.3;  
RESULT 1106  
ID ABL33266 standard; DNA; 5218 BP.  
DE Human immune system associated gene SEQ ID NO: 1239.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 5218;  
Best Local Similarity 48.5%; Pred. No. 8.2;  
RESULT 1107  
ID ABK33945 standard; DNA; 5942 BP.  
DE Human DNA for staging of Astrocytomas, complement, #14.  
PN WO200202808-A2.

PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 5942;  
Best Local Similarity 47.2%; Pred. No. 8.7;  
RESULT 1108  
ID ABK31223 standard; DNA; 5942 BP.  
DE Signal transduction associated gene modified complementary DNA #33.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 5942;  
Best Local Similarity 47.2%; Pred. No. 8.7;  
RESULT 1109  
ID ABL70534 standard; DNA; 5942 BP.  
DE Chemically treated cell signalling DNA sequence complementary to #212.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 5942;  
Best Local Similarity 47.2%; Pred. No. 8.7;  
RESULT 1110  
ID AAS61135 standard; DNA; 5942 BP.  
DE Human gene regulation-associated gene oligonucleotide #90.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 5942;  
Best Local Similarity 47.2%; Pred. No. 8.7;  
RESULT 1111  
ID AB210002 standard; DNA; 5942 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #142.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 8; Length 5942;  
Best Local Similarity 47.2%; Pred. No. 8.7;  
RESULT 1112  
ID AB210234 standard; DNA; 5942 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #374.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 8; Length 5942;  
Best Local Similarity 47.2%; Pred. No. 8.7;  
RESULT 1113  
ID AB210088 standard; DNA; 5942 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #228.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 8; Length 5942;  
Best Local Similarity 47.2%; Pred. No. 8.7;  
RESULT 1114  
ID AB210148 standard; DNA; 5942 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #288.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 8; Length 5942;  
Best Local Similarity 47.2%; Pred. No. 8.7;  
RESULT 1115  
ID ADA20351 standard; DNA; 5942 BP.  
DE Prostate tumour related genomic DNA complement sample #8.  
PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 8; Length 5942;  
Best Local Similarity 47.2%; Pred. No. 8.7;  
RESULT 1116  
ID ADA84158 standard; DNA; 5942 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:16.  
PN WO2002103041-A2.  
PD 27-DEC-2002.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 8; Length 5942;  
Best Local Similarity 47.2%; Pred. No. 8.7;  
RESULT 1117  
ID ADE84068 standard; DNA; 5942 BP.  
DE Human lymphoid cell proliferative disorder gene derived DNA #4.  
PN WO2003044226-A2.  
PD 30-MAY-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 10; Length 5942;  
Best Local Similarity 47.2%; Pred. No. 8.7;  
RESULT 1118  
ID ADE84144 standard; DNA; 5942 BP.  
DE Human lymphoid cell proliferative disorder gene derived DNA #80.  
PN WO2003044226-A2.  
PD 30-MAY-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 10; Length 5942;  
Best Local Similarity 47.2%; Pred. No. 8.7;  
RESULT 1119  
ID ABL33246 standard; DNA; 6077 BP.  
DE Human immune system associated gene SEQ ID NO: 1219.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 6077;  
Best Local Similarity 44.2%; Pred. No. 8.8;  
RESULT 1120  
ID AAS46573 standard; DNA; 6126 BP.  
DE Tumour suppressor gene derived chemically modified sequence #295.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 4; Length 6126;  
Best Local Similarity 45.2%; Pred. No. 8.8;  
RESULT 1121  
ID ABL33830 standard; DNA; 6126 BP.  
DE Human immune system associated gene SEQ ID NO: 1803.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 6126;  
Best Local Similarity 45.2%; Pred. No. 8.8;  
RESULT 1122  
ID AAS46498 standard; DNA; 6233 BP.  
DE Tumour suppressor gene derived chemically modified sequence #220.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 4; Length 6233;  
Best Local Similarity 49.0%; Pred. No. 8.9;  
RESULT 1123  
ID ABL32409 standard; DNA; 6317 BP.  
DE Human immune system associated gene SEQ ID NO: 382.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 6317;  
Best Local Similarity 43.4%; Pred. No. 8.9;  
RESULT 1124  
ID ABL49312 standard; DNA; 6317 BP.  
DE Human polynucleotide associated with DNA replication SEQ ID NO 12.  
PN WO200177377-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 6317;  
Best Local Similarity 43.4%; Pred. No. 8.9;  
RESULT 1125  
ID ABK40057 standard; DNA; 7441 BP.  
DE Human chemically pretreated gene sequence #70 strand 1.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.



Query Match  
Best Local Similarity 1.8%; Score 43; DB 6; Length 7441;  
RESULT 1126  
ID AAS61424 standard; DNA; 7479 BP.  
DE Human gene regulation-associated gene oligonucleotide #379.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 7479;  
Best Local Similarity 49.5%; Pred. No. 9.6;  
RESULT 1127  
ID AAS46760 standard; DNA; 7900 BP.  
DE Tumour suppressor gene derived chemically modified sequence #484.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 4; Length 7900;  
Best Local Similarity 44.6%; Pred. No. 9.9;  
RESULT 1128  
ID ABL33993 standard; DNA; 8592 BP.  
DE Human immune system associated gene SEQ ID NO: 1956.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 8592;  
Best Local Similarity 46.2%; Pred. No. 10;  
RESULT 1129  
ID ADS89411 standard; DNA; 8900 BP.  
DE Oligonucleotide of the invention SEQ ID NO: 427.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 13; Length 8900;  
Best Local Similarity 48.2%; Pred. No. 10;  
RESULT 1130  
ID ABL32427 standard; DNA; 9810 BP.  
DE Human immune system associated gene SEQ ID NO: 400.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 9810;  
Best Local Similarity 46.1%; Pred. No. 11;  
RESULT 1131  
ID ABL92243 standard; DNA; 11787 BP.  
DE Chemically treated DNA repair gene fragment complementary to#26.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 11787;  
Best Local Similarity 45.0%; Pred. No. 12;  
RESULT 1132  
ID ADB54202 standard; DNA; 11787 BP.  
DE Pretreated genomic DNA region 126.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 10; Length 11787;  
Best Local Similarity 45.0%; Pred. No. 12;  
RESULT 1133  
ID ABL33316 standard; DNA; 13574 BP.  
DE Human immune system associated gene SEQ ID NO: 1289.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 13574;  
Best Local Similarity 46.3%; Pred. No. 13;  
RESULT 1134  
ID ABL70459 standard; DNA; 16228 BP.  
DE Chemically treated cell signalling DNA sequence#175.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 16228;

Best Local Similarity 45.9%; Pred. No. 14;  
RESULT 1135  
ID AAS61424 standard; DNA; 16228 BP.  
DE Human gene regulation-associated gene oligonucleotide #379.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 16228;  
Best Local Similarity 45.9%; Pred. No. 14;  
RESULT 1136  
ID ADB54118 standard; DNA; 16579 BP.  
DE Pretreated genomic DNA region 42.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 10; Length 16579;  
Best Local Similarity 43.1%; Pred. No. 14;  
RESULT 1137  
ID ADE37763 standard; DNA; 16579 BP.  
DE Human chemically treated TPEF nucleotide sequence SEQ ID NO: 9.  
PN WO2003072820-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 10; Length 16579;  
Best Local Similarity 43.1%; Pred. No. 14;  
RESULT 1138  
ID ADS89274 standard; DNA; 16579 BP.  
DE Oligonucleotide of the invention SEQ ID NO: 290.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 13; Length 16579;  
Best Local Similarity 43.1%; Pred. No. 14;  
RESULT 1139  
ID ABL32627 standard; DNA; 19082 BP.  
DE Human immune system associated gene SEQ ID NO: 600.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 19082;  
Best Local Similarity 44.3%; Pred. No. 15;  
RESULT 1140  
ID ABL32627 standard; DNA; 19082 BP.  
DE Human immune system associated gene SEQ ID NO: 600.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 19082;  
Best Local Similarity 53.6%; Pred. No. 15;  
RESULT 1141  
ID ABO67124 standard; DNA; 20933 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 154.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 20933;  
Best Local Similarity 44.3%; Pred. No. 15;  
RESULT 1142  
ID ADB37661 standard; DNA; 29993 BP.  
DE Human chemically pretreated EYA4 gene SEQ ID NO: 3.  
PN WO2003072812-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 10; Length 29993;  
Best Local Similarity 43.7%; Pred. No. 18;  
RESULT 1143  
ID ABO67078 standard; DNA; 37184 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 108.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 37184;  
Best Local Similarity 43.7%; Pred. No. 20;

RESULT 1144  
ID AAS46746 standard; DNA; 38342 BP.  
DE Tumour suppressor gene derived Chemically modified sequence #470.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 4; Length 38342;  
Best Local Similarity 43.7%; Pred. No. 20;  
RESULT 1145  
ID ABK31507 standard; DNA; 38342 BP.  
DE Signal transduction associated gene modified complementary DNA #175.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 43; DB 6; Length 38342;  
Best Local Similarity 43.7%; Pred. No. 20;  
RESULT 1146  
ID ABUS6202 standard; DNA; 50000 BP.  
DE AmEPV genome fragment#4.  
PN WO200212526-A2.  
PD 14-FEB-2002.  
PA (UYFL ) UNIV FLORIDA.  
Query Match 1.8%; Score 43; DB 6; Length 50000;  
Best Local Similarity 46.5%; Pred. No. 22;  
RESULT 1147  
ID ADQ97764 standard; DNA; 79544 BP.  
DE Human cancer associated sequence HD10-042, SEQ ID 741.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 1.8%; Score 43; DB 12; Length 79544;  
Best Local Similarity 55.8%; Pred. No. 27;  
RESULT 1148  
ID AB216071 standard; DNA; 2000 BP.  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 3876.  
PN WO200216655-A2.  
PD 28-FEB-2002.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 2000;  
Best Local Similarity 54.4%; Pred. No. 6;  
RESULT 1149  
ID AB132899 standard; DNA; 5204 BP.  
DE Human immune system associated gene SEQ ID NO: 872.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 5204;  
Best Local Similarity 47.6%; Pred. No. 9.2;  
RESULT 1150  
ID AAA70236 standard; DNA; 5454 BP.  
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:369.  
PN WO200025728-A2.  
PD 11-MAY-2000.  
PA (HOFF/) HOFFMAN S.  
PA (CARU/) CARUCCI D.  
PA (GARD/) GARDNER M.  
PA (VENT/) VENTER J C.  
Query Match 1.8%; Score 42.8; DB 3; Length 5454;  
Best Local Similarity 45.3%; Pred. No. 9.4;  
RESULT 1151  
ID AB067069 standard; DNA; 5611 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 99.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 5611;  
Best Local Similarity 44.6%; Pred. No. 9.5;  
RESULT 1152  
ID AB134086 standard; DNA; 5928 BP.  
DE Human immune system associated gene SEQ ID NO: 2059.  
PN WO200200928-A2.  
PD 03-JAN-2002.

PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 5928;  
Best Local Similarity 50.8%; Pred. No. 9.8;  
RESULT 1153  
ID ABL32194 standard; DNA; 6208 BP.  
DE Human immune system associated gene SEQ ID NO: 167.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 6208;  
Best Local Similarity 44.1%; Pred. No. 10;  
RESULT 1154  
ID ABL32359 standard; DNA; 6237 BP.  
DE Human immune system associated gene SEQ ID NO: 332.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 6237;  
Best Local Similarity 46.9%; Pred. No. 10;  
RESULT 1155  
ID AAS45344 standard; DNA; 6815 BP.  
DE Chemically pretreated genomic DNA associated with cell cycle #25.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 4; Length 6815;  
Best Local Similarity 51.6%; Pred. No. 10;  
RESULT 1156  
ID ABL32670 standard; DNA; 6815 BP.  
DE Human immune system associated gene SEQ ID NO: 643.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 6815;  
Best Local Similarity 51.6%; Pred. No. 10;  
RESULT 1157  
ID ABK28175 standard; DNA; 6815 BP.  
DE DNA transcription associated genomic DNA #25.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 6815;  
Best Local Similarity 51.6%; Pred. No. 10;  
RESULT 1158  
ID ADB54195 standard; DNA; 6815 BP.  
DE Pretreated genomic DNA region 119.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 10; Length 6815;  
Best Local Similarity 51.6%; Pred. No. 10;  
RESULT 1159  
ID ADB54323 standard; DNA; 6815 BP.  
DE Pretreated genomic DNA region 247.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 10; Length 6815;  
Best Local Similarity 51.6%; Pred. No. 10;  
RESULT 1160  
ID ADB84207 standard; DNA; 6815 BP.  
DE Human lymphoid cell proliferative disorder gene derived DNA #143.  
PN WO2003044226-A2.  
PD 30-MAY-2003.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 10; Length 6815;  
Best Local Similarity 51.6%; Pred. No. 10;  
RESULT 1161  
ID ADB84131 standard; DNA; 6815 BP.  
DE Human lymphoid cell proliferative disorder gene derived DNA #67.  
PN WO2003044226-A2.  
PD 30-MAY-2003.  
PA (EPiG-) EPIGENOMICS AG.

Query Match 1.8%; Score 42.8; DB 10; Length 6815;  
Best Local Similarity 51.6%; Pred. No. 10;  
RESULT 1162  
ID AAS46532 standard; DNA; 7008 BP.  
DE Tumour suppressor gene derived chemically modified sequence #254.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 4; Length 7008;  
Best Local Similarity 44.4%; Pred. No. 11;  
RESULT 1163  
ID ABL32345 standard; DNA; 7346 BP.  
DE Human immune system associated gene SEQ ID NO: 318.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 7346;  
Best Local Similarity 43.4%; Pred. No. 11;  
RESULT 1164  
ID ABK28131 standard; DNA; 7450 BP.  
DE DNA transcription associated genomic DNA #3.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 7450;  
Best Local Similarity 50.5%; Pred. No. 11;  
RESULT 1165  
ID ABL33761 standard; DNA; 7851 BP.  
DE Human immune system associated gene SEQ ID NO: 1734.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 7851;  
Best Local Similarity 45.2%; Pred. No. 11;  
RESULT 1166  
ID ABL32203 standard; DNA; 8246 BP.  
DE Human immune system associated gene SEQ ID NO: 176.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 8246;  
Best Local Similarity 46.7%; Pred. No. 11;  
RESULT 1167  
ID AAS45469 standard; DNA; 8588 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #87.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 4; Length 8588;  
Best Local Similarity 49.1%; Pred. No. 11;  
RESULT 1168  
ID ABK28325 standard; DNA; 8588 BP.  
DE DNA transcription associated genomic DNA #100.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 8588;  
Best Local Similarity 49.1%; Pred. No. 11;  
RESULT 1169  
ID ABL33241 standard; DNA; 9888 BP.  
DE Human immune system associated gene SEQ ID NO: 1214.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 9888;  
Best Local Similarity 47.7%; Pred. No. 12;  
RESULT 1170  
ID ABL34241 standard; DNA; 11691 BP.  
DE Human immune system associated gene SEQ ID NO: 2214.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 11691;

Best Local Similarity 45.5%; Pred. No. 13;  
RESULT 1171  
ID ABK28332 standard; DNA; 11745 BP.  
DE DNA transcription associated complementary genomic DNA #103.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 11745;  
Best Local Similarity 43.8%; Pred. No. 13;  
RESULT 1172  
ID ADB54256 standard; DNA; 12781 BP.  
DE Pretreated genomic DNA region 180.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 10; Length 12781;  
Best Local Similarity 43.8%; Pred. No. 14;  
RESULT 1173  
ID ABL32583 standard; DNA; 13376 BP.  
DE Human immune system associated gene SEQ ID NO: 556.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 13376;  
Best Local Similarity 46.8%; Pred. No. 14;  
RESULT 1174  
ID AAS45415 standard; DNA; 14649 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #60.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 4; Length 14649;  
Best Local Similarity 47.3%; Pred. No. 15;  
RESULT 1175  
ID ABK28268 standard; DNA; 14649 BP.  
DE DNA transcription associated complementary genomic DNA #71.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 14649;  
Best Local Similarity 47.3%; Pred. No. 15;  
RESULT 1176  
ID ABK31170 standard; DNA; 17293 BP.  
DE Signal transduction associated gene modified DNA #7.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 17293;  
Best Local Similarity 44.5%; Pred. No. 16;  
RESULT 1177  
ID ABL70125 standard; DNA; 17293 BP.  
DE Chemically treated cell signalling DNA sequence#8.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 17293;  
Best Local Similarity 44.5%; Pred. No. 16;  
RESULT 1178  
ID AAS61057 standard; DNA; 17293 BP.  
DE Human gene regulation-associated gene oligonucleotide #12.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.8; DB 6; Length 17293;  
Best Local Similarity 44.5%; Pred. No. 16;  
RESULT 1179  
ID ABA92787 standard; DNA; 640681 BP.  
DE Buchnera sp. genomic DNA SEQ ID NO:1.  
PN JP2001292771-A.  
PD 23-OCT-2001.  
PA (RIKA ) RIKAGAKU KENKYUSHO.  
Query Match 1.8%; Score 42.8; DB 6; Length 110000;  
Best Local Similarity 56.3%; Pred. No. 35;

RESULT 1180  
ID ABQ88198 standard; cDNA; 154902 BP.  
DE Human osteoblast differentiation related cDNA SEQ ID NO 105.  
PN WO200250301-A2.  
PD 27-JUN-2002.  
PA (GENE-) GENE LOGIC INC.  
PA (PROC) PROCTER & GAMBLE CO.  
Query Match  
Best Local Similarity 1.8%; Score 42.8; DB 6; Length 154902;  
RESULT 1181  
ID ABV46406 standard; cDNA; 535 BP.  
DE Human prostate expression marker cDNA 46397.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 1.8%; Score 42.6; DB 5; Length 535;  
RESULT 1182  
ID AAA59475 standard; DNA; 1117 BP.  
DE Nucleotide sequence of a soybean type III glutathione-S-transferase.  
PN WO200047728-A2.  
PD 17-AUG-2000.  
PA (DUFO) DU PONT DE NEMOURS & CO E I.  
Query Match  
Best Local Similarity 1.8%; Score 42.6; DB 3; Length 1117;  
RESULT 1183  
ID AAA97037 standard; DNA; 2486 BP.  
DE Nucleotide sequence encoding 48kd i-antigen.  
PN WO200046373-A1.  
PD 10-AUG-2000.  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
PA (CORR) CORNELL RES FOUND INC.  
PA (CIAR/) CLARK T G.  
PA (DICK/) DICKERSON H W.  
PA (LIN7/) LIN T.  
Query Match  
Best Local Similarity 1.8%; Score 42.6; DB 3; Length 2486;  
RESULT 1184  
ID ABK33946 standard; DNA; 2580 BP.  
DE Human DNA for staging of Astrocytomas #15.  
PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 42.6; DB 6; Length 2580;  
RESULT 1185  
ID ADA20402 standard; DNA; 2580 BP.  
DE Prostate tumour related genomic DNA sample #34.  
PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 42.6; DB 8; Length 2580;  
RESULT 1186  
ID ADA84209 standard; DNA; 2580 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:67.  
PN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 42.6; DB 8; Length 2580;  
RESULT 1187  
ID ABY10191 standard; DNA; 3287 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #331.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 42.6; DB 8; Length 3287;  
RESULT 1188  
ID ABJ33066 standard; DNA; 5107 BP.  
DE Human immune system associated Gene SEQ ID NO: 1039.  
PN WO200200928-A2.

PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 42.6; DB 6; Length 5107;  
RESULT 1189  
ID ABL32348 standard; DNA; 5145 BP.  
DE Human immune system associated gene SEQ ID NO: 321.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 42.6; DB 6; Length 5145;  
RESULT 1190  
ID ABL34464 standard; DNA; 5145 BP.  
DE Human metastasis associated gene SEQ ID NO: 17.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 42.6; DB 6; Length 5145;  
RESULT 1191  
ID AUS99725 standard; DNA; 5145 BP.  
DE Bisulphite treated human gene associated with metastasis #9.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match  
Best Local Similarity 1.8%; Score 42.6; DB 7; Length 5145;  
RESULT 1192  
ID ABL34021 standard; DNA; 5542 BP.  
DE Human immune system associated gene SEQ ID NO: 1994.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 42.6; DB 6; Length 5542;  
RESULT 1193  
ID ABL33577 standard; DNA; 5925 BP.  
DE Human immune system associated gene SEQ ID NO: 1550.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 42.6; DB 6; Length 5925;  
RESULT 1194  
ID ABL32708 standard; DNA; 5929 BP.  
DE Human immune system associated gene SEQ ID NO: 681.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 42.6; DB 6; Length 5929;  
RESULT 1195  
ID AAS46337 standard; DNA; 6063 BP.  
DE Tumour suppressor gene derived chemically modified sequence #59.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 42.6; DB 4; Length 6063;  
RESULT 1196  
ID ABL70595 standard; DNA; 6075 BP.  
DE Chemically treated cell signalling DNA sequence#243.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 1.8%; Score 42.6; DB 6; Length 6075;  
RESULT 1197  
ID AAS61316 standard; DNA; 6075 BP.  
DE Human gene regulation-associated gene oligonucleotide #271.

PD WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 6075;  
Best Local Similarity 53.6%; Pred. No. 11;  
RESULT 1198  
ID ABL70590 standard; DNA; 6129 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#240.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 6129;  
Best Local Similarity 49.8%; Pred. No. 11;  
RESULT 1199  
ID AA661301 standard; DNA; 6129 BP.  
DE Human gene regulation-associated gene oligonucleotide #256.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 6129;  
Best Local Similarity 49.8%; Pred. No. 11;  
RESULT 1200  
ID ABL33307 standard; DNA; 6175 BP.  
DE Human immune system associated gene SEQ ID NO: 1280.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 6175;  
Best Local Similarity 44.4%; Pred. No. 11;  
RESULT 1201  
ID ABL33393 standard; DNA; 6494 BP.  
DE Human immune system associated gene SEQ ID NO: 1366.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 6494;  
Best Local Similarity 45.8%; Pred. No. 11;  
RESULT 1202  
ID AAD28391 standard; DNA; 6494 BP.  
DE Human chemically treated genomic DNA #32.  
PN WO200202809-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 6494;  
Best Local Similarity 45.8%; Pred. No. 11;  
RESULT 1203  
ID ABL33709 standard; DNA; 6533 BP.  
DE Human immune system associated gene SEQ ID NO: 1682.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 6533;  
Best Local Similarity 46.2%; Pred. No. 11;  
RESULT 1204  
ID ABL33815 standard; DNA; 7312 BP.  
DE Human immune system associated gene SEQ ID NO: 1788.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 7312;  
Best Local Similarity 44.6%; Pred. No. 12;  
RESULT 1205  
ID ABL70402 standard; DNA; 7312 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#146.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 7312;  
Best Local Similarity 44.6%; Pred. No. 12;  
RESULT 1206  
ID AAS61350 standard; DNA; 7312 BP.  
DE Human gene regulation-associated gene oligonucleotide #305.  
PN WO200177375-A2.

PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 7312;  
Best Local Similarity 44.6%; Pred. No. 12;  
RESULT 1207  
ID AAS46436 standard; DNA; 8093 BP.  
DE Tumour suppressor gene derived chemically modified sequence #158.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 4; Length 8093;  
Best Local Similarity 47.2%; Pred. No. 13;  
RESULT 1208  
ID ABK33974 standard; DNA; 8093 BP.  
DE Human DNA for staging of Astrocytomas, complement, #29.  
PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 8093;  
Best Local Similarity 47.2%; Pred. No. 13;  
RESULT 1209  
ID ABL92237 standard; DNA; 8093 BP.  
DE Chemically treated DNA repair gene fragment complementary to#23.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 8093;  
Best Local Similarity 47.2%; Pred. No. 13;  
RESULT 1210  
ID ABL49332 standard; DNA; 8093 BP.  
DE Human polynucleotide associated with DNA replication SEQ ID NO 32.  
PN WO200177377-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 8093;  
Best Local Similarity 47.2%; Pred. No. 13;  
RESULT 1211  
ID AB210032 standard; DNA; 8093 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #172.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 8; Length 8093;  
Best Local Similarity 47.2%; Pred. No. 13;  
RESULT 1212  
ID ADA20361 standard; DNA; 8093 BP.  
DE Prostate tumour related genomic DNA complement sample #13.  
PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 8; Length 8093;  
Best Local Similarity 47.2%; Pred. No. 13;  
RESULT 1213  
ID ADA84168 standard; DNA; 8093 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:26.  
PN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 8; Length 8093;  
Best Local Similarity 47.2%; Pred. No. 13;  
RESULT 1214  
ID ADB54140 standard; DNA; 8093 BP.  
DE Pretreated genomic DNA region 64.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 10; Length 8093;  
Best Local Similarity 47.2%; Pred. No. 13;  
RESULT 1215  
ID ADE84114 standard; DNA; 8093 BP.  
DE Human lymphoid cell proliferative disorder gene derived DNA #50.  
PN WO2003044226-A2.  
PD 30-MAY-2003.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 10; Length 8093;  
Best Local Similarity 47.2%; Pred. No. 13;  
RESULT 1216  
ID ADS89292 standard; DNA; 8093 BP.  
DE Oligonucleotide of the invention SEQ ID NO:308.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 13; Length 8093;  
Best Local Similarity 47.2%; Pred. No. 13;  
RESULT 1217  
ID ABL33491 standard; DNA; 8392 BP.  
DE Human immune system associated gene SEQ ID NO: 1464.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 8392;  
Best Local Similarity 44.1%; Pred. No. 13;  
RESULT 1218  
ID ABL32990 standard; DNA; 9731 BP.  
DE Human immune system associated gene SEQ ID NO: 963.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 9731;  
Best Local Similarity 58.1%; Pred. No. 14;  
RESULT 1219  
ID ADF50895 standard; DNA; 11097 BP.  
DE Chemically modified promoter region of human melastatin gene (SeqID 3).  
PN EP1344832-A1.  
PD 17-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 10; Length 11097;  
Best Local Similarity 45.0%; Pred. No. 14;  
RESULT 1220  
ID ADF50897 standard; DNA; 11097 BP.  
DE Chemically modified promoter region of human melastatin gene (SeqID 5).  
PN EP1344832-A1.  
PD 17-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 10; Length 11097;  
Best Local Similarity 45.0%; Pred. No. 14;  
RESULT 1221  
ID AAS46698 standard; DNA; 11694 BP.  
DE Tumour suppressor gene derived chemically modified sequence #421.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 4; Length 11694;  
Best Local Similarity 45.7%; Pred. No. 15;  
RESULT 1222  
ID ABL34493 standard; DNA; 11996 BP.  
DE Human metastasis associated gene SEQ ID NO: 46.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 11996;  
Best Local Similarity 48.2%; Pred. No. 15;  
RESULT 1223  
ID ADS99754 standard; DNA; 11996 BP.  
DE Complement of bisulphite treated metastasis-associated human gene #23.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK)/ OLEK A.  
PA (PIEP)/ PIEPENBROCK C.  
PA (BERL)/ BERLIN K.  
Query Match 1.8%; Score 42.6; DB 7; Length 11996;  
Best Local Similarity 48.2%; Pred. No. 15;  
RESULT 1224  
ID AAS45331 standard; DNA; 12405 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #18.  
PN WO200168911-A2.

PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 4; Length 12405;  
Best Local Similarity 44.3%; Pred. No. 15;  
RESULT 1225  
ID ABK28170 standard; DNA; 12405 BP.  
DE DNA transcription associated complementary genomic DNA #22.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 12405;  
Best Local Similarity 44.3%; Pred. No. 15;  
RESULT 1226  
ID AAS61144 standard; DNA; 12405 BP.  
DE Human gene regulation-associated gene oligonucleotide #99.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 12405;  
Best Local Similarity 44.3%; Pred. No. 15;  
RESULT 1227  
ID ASN80146 standard; DNA; 14920 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 163.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 6; Length 14920;  
Best Local Similarity 47.9%; Pred. No. 16;  
RESULT 1228  
ID AAS46665 standard; DNA; 17144 BP.  
DE Tumour suppressor gene derived chemically modified sequence #387.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.6; DB 4; Length 17144;  
Best Local Similarity 52.5%; Pred. No. 17;  
RESULT 1229  
ID ADP84152 standard; DNA; 42347 BP.  
DE Human CA125 genomic DNA extracellular repeat sequence SeqID 2.  
Query Match 1.8%; Score 42.6; DB 12; Length 42347;  
Best Local Similarity 46.2%; Pred. No. 26;  
RESULT 1230  
ID AAL48890 standard; DNA; 53332 BP.  
DE Human Pftaire family kinase gene.  
PN WO200261060-A2.  
PD 08-AUG-2002.  
PA (PEKE ) PE CORP NY.  
Query Match 1.8%; Score 42.6; DB 6; Length 53332;  
Best Local Similarity 45.2%; Pred. No. 29;  
RESULT 1231  
ID AAL61370 standard; DNA; 127197 BP.  
DE Soybean 515002 region G2, SEQ ID NO: 1.  
PN WO200151627-A2.  
PD 19-JUL-2001.  
PA (MONS ) MONSANTO CO.  
Query Match 1.8%; Score 42.6; DB 5; Length 127197;  
Best Local Similarity 47.0%; Pred. No. 42;  
RESULT 1232  
ID ADL11800 standard; cDNA; 275 BP.  
DE Cat flea hindgut and malpighian tubule (HMT) protein cDNA #2205.  
PN US2004067516-A1.  
PD 08-APR-2004.  
PA (BRAN)/ BRANDT K S.  
PA (GAIN)/ GAINES P J.  
PA (STIN)/ STINCHCOMB D T.  
PA (WISN)/ WISNEWSKI N.  
Query Match 1.8%; Score 42.4; DB 12; Length 275;  
Best Local Similarity 49.1%; Pred. No. 3.2;  
RESULT 1233  
ID ADL11674 standard; cDNA; 549 BP.  
DE Cat flea hindgut and malpighian tubule (HMT) protein cDNA #2079.  
PN US2004067516-A1.  
PD 08-APR-2004.

PA (BRAN//) BRANDT K S.  
PA (GAIN//) GAINES P J.  
PA (STIN//) STINCHCOMB D T.  
PA (WISN//) WISNEWSKI N.  
Query Match 1.8%; Score 42.4; DB 12; Length 549;  
Best Local Similarity 46.0%; Pred. No. 4.3;  
RESULT 1234  
ID ACN45312 standard; cDNA; 552 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-K6-CS, SEQ:93.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK//) DEIKMAN J.  
PA (FENG//) FENG P C C.  
PA (FINC//) FINCHER K L.  
PA (ZIEG//) ZIEGLER T E.  
Query Match 1.8%; Score 42.4; DB 13; Length 552;  
Best Local Similarity 41.7%; Pred. No. 4.3;  
RESULT 1235  
ID ADR01846 standard; DNA; 828 BP.  
DE A. gossypii genomic DNA PAG1375RP.  
PN USG239264-B1.  
PD 29-MAY-2001.  
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.  
Query Match 1.8%; Score 42.4; DB 2; Length 828;  
Best Local Similarity 48.7%; Pred. No. 5.2;  
RESULT 1236  
ID ADP10611 standard; DNA; 1843 BP.  
DE Reference mRNA sequences for marker probe #288.  
PN WO2004042346-A2.  
PD 21-MAY-2004.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match 1.8%; Score 42.4; DB 12; Length 1843;  
Best Local Similarity 51.0%; Pred. No. 7.3;  
RESULT 1237  
ID ABL21456 standard; DNA; 4377 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 15841.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PRKE) PE CORP NY.  
Query Match 1.8%; Score 42.4; DB 4; Length 4377;  
Best Local Similarity 44.6%; Pred. No. 11;  
RESULT 1238  
ID ABK63337 standard; cDNA; 4537 BP.  
DE Human cDNA #337 differentially expressed in activated vascular tissue.  
PN US2002137081-A1.  
PD 26-SEP-2002.  
PA (BAND//) BANDMAN O.  
Query Match 1.8%; Score 42.4; DB 8; Length 4537;  
Best Local Similarity 60.3%; Pred. No. 11;  
RESULT 1239  
ID ABL32258 standard; DNA; 6079 BP.  
DE Human immune system associated gene SEQ ID NO: 231.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 6079;  
Best Local Similarity 45.7%; Pred. No. 12;  
RESULT 1240  
ID ABL33366 standard; DNA; 6104 BP.  
DE Human immune system associated gene SEQ ID NO: 1339.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 6104;  
Best Local Similarity 48.1%; Pred. No. 12;  
RESULT 1241  
ID AAS46344 standard; DNA; 6179 BP.  
DE Tumour suppressor gene derived chemically modified sequence #66.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 4; Length 6179;  
Best Local Similarity 45.3%; Pred. No. 13;

RESULT 1242  
ID ABK31251 standard; DNA; 6179 BP.  
DE Signal transduction associated gene modified complementary DNA #47.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 6179;  
Best Local Similarity 45.3%; Pred. No. 13;  
RESULT 1243  
ID AAS46498 standard; DNA; 6233 BP.  
DE Tumour suppressor gene derived chemically modified sequence #220.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 4; Length 6233;  
Best Local Similarity 49.5%; Pred. No. 13;  
RESULT 1244  
ID ABL32089 standard; DNA; 6283 BP.  
DE Human immune system associated gene SEQ ID NO: 62.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 6283;  
Best Local Similarity 44.6%; Pred. No. 13;  
RESULT 1245  
ID AAS46591 standard; DNA; 6286 BP.  
DE Tumour suppressor gene derived chemically modified sequence #313.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 4; Length 6286;  
Best Local Similarity 44.2%; Pred. No. 13;  
RESULT 1246  
ID AAS46735 standard; DNA; 6292 BP.  
DE Tumour suppressor gene derived chemically modified sequence #459.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 4; Length 6292;  
Best Local Similarity 46.8%; Pred. No. 13;  
RESULT 1247  
ID ABL49326 standard; DNA; 6583 BP.  
DE Human polynucleotide associated with DNA replication SEQ ID NO 26.  
PN WO200177377-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 6583;  
Best Local Similarity 51.0%; Pred. No. 13;  
RESULT 1248  
ID ABK39996 standard; DNA; 7108 BP.  
DE Human chemically pretreated gene sequence #39 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 7108;  
Best Local Similarity 47.1%; Pred. No. 13;  
RESULT 1249  
ID ABL33989 standard; DNA; 8238 BP.  
DE Human immune system associated gene SEQ ID NO: 1962.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 8238;  
Best Local Similarity 45.6%; Pred. No. 14;  
RESULT 1250  
ID AAS63349 standard; DNA; 8238 BP.  
DE Chemically pretreated metabolism associated gene #44.  
PN WO200176451-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 8238;  
Best Local Similarity 45.6%; Pred. No. 14;

ID AAK86270 standard; DNA; 9706 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41082.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.8%; Score 42.4; DB 4; Length 9706;  
Best Local Similarity 44.9%; Pred. No. 15;  
RESULT 1252  
ID ABK31243 standard; DNA; 9760 BP.  
DE Signal transduction associated gene modified complementary DNA #43.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 9760;  
Best Local Similarity 47.9%; Pred. No. 15;  
RESULT 1253  
ID ABL70198 standard; DNA; 9760 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#44.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 9760;  
Best Local Similarity 47.9%; Pred. No. 15;  
RESULT 1254  
ID AAS61136 standard; DNA; 9760 BP.  
DE Human gene regulation-associated gene oligonucleotide #111.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 9760;  
Best Local Similarity 47.9%; Pred. No. 15;  
RESULT 1255  
ID ABL33263 standard; DNA; 12393 BP.  
DE Human immune system associated gene SEQ ID NO: 1236.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 12393;  
Best Local Similarity 44.0%; Pred. No. 17;  
RESULT 1256  
ID ABK40038 standard; DNA; 16258 BP.  
DE Human chemically pretreated gene sequence #60 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 16258;  
Best Local Similarity 44.1%; Pred. No. 19;  
RESULT 1257  
ID ABL70376 standard; DNA; 16258 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#133.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 16258;  
Best Local Similarity 44.1%; Pred. No. 19;  
RESULT 1258  
ID ABL32619 standard; DNA; 16373 BP.  
DE Human immune system associated gene SEQ ID NO: 592.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 16373;  
Best Local Similarity 44.1%; Pred. No. 19;  
RESULT 1259  
ID AAD28383 standard; DNA; 16373 BP.  
DE Human chemically treated genomic DNA #24.  
PN WO200202809-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 16373;  
Best Local Similarity 44.1%; Pred. No. 19;  
RESULT 1260  
ID ABL32387 standard; DNA; 18598 BP.

DE Human immune system associated gene SEQ ID NO: 360.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 18598;  
Best Local Similarity 52.2%; Pred. No. 20;  
RESULT 1261  
ID ABL34495 standard; DNA; 18817 BP.  
DE Human metastasis associated gene SEQ ID NO: 48.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 18817;  
Best Local Similarity 46.1%; Pred. No. 20;  
RESULT 1262  
ID ABL70162 standard; DNA; 18817 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#26.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 18817;  
Best Local Similarity 46.1%; Pred. No. 20;  
RESULT 1263  
ID ADS99756 standard; DNA; 18817 BP.  
DE Complement of bisulphite treated metastasis-associated human gene #24.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 1.8%; Score 42.4; DB 7; Length 18817;  
Best Local Similarity 46.1%; Pred. No. 20;  
RESULT 1264  
ID ABO67059 standard; DNA; 34688 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 89.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 34688;  
Best Local Similarity 48.8%; Pred. No. 27;  
RESULT 1265  
ID ABO66998 standard; DNA; 37515 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 28.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 37515;  
Best Local Similarity 45.5%; Pred. No. 28;  
RESULT 1266  
ID ABD32684 standard; DNA; 41991 BP.  
DE Human cancer-associated genomic DNA HD13-117.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 1.8%; Score 42.4; DB 13; Length 41991;  
Best Local Similarity 44.9%; Pred. No. 29;  
RESULT 1267  
ID ABL34175 standard; DNA; 113515 BP.  
DE Human immune system associated gene SEQ ID NO: 2148.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.4; DB 6; Length 113515;  
Best Local Similarity 45.7%; Pred. No. 45;  
RESULT 1268  
ID ADO43653 standard; DNA; 127432 BP.  
DE Nucleotide sequence of BAC-64.  
PN WO2004039988-A1.  
PD 13-MAY-2004.  
PA (GENO-) GENOPLANTE-VALOR.  
Query Match 1.8%; Score 42.4; DB 12; Length 127432;  
Best Local Similarity 45.3%; Pred. No. 47;  
RESULT 1269



ID AA004525 standard; DNA; 134525 BP.  
DE Total base sequence of rice plant chloroplast DNA.  
PN JP02100682-A.  
PD 12-APR-1990.  
PA (MITK) MITSUI TOATSU CHEM INC.  
Query Match 1.8%; Score 42.4; DB 2; Length 134525;  
Best Local Similarity 49.5%; Pred. No. 49;  
RESULT 1270  
ID ADS36467 standard; DNA; 154799 BP.  
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1681.  
PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 1.8%; Score 42.4; DB 13; Length 154799;  
Best Local Similarity 46.4%; Pred. No. 52;  
RESULT 1271  
ID ADL37508 standard; DNA; 294 BP.  
DE Human ovarian cancer DNA marker #11398.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.8%; Score 42.2; DB 5; Length 294;  
Best Local Similarity 47.7%; Pred. No. 3.7;  
RESULT 1272  
ID AD172364 standard; DNA; 294 BP.  
DE Human ovarian cancer DNA marker #5106.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.8%; Score 42.2; DB 5; Length 294;  
Best Local Similarity 47.7%; Pred. No. 3.7;  
RESULT 1273  
ID ACN53339 standard; cDNA; 537 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-006-Q1-N6-D9, SEQ:8120.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.8%; Score 42.2; DB 13; Length 537;  
Best Local Similarity 43.2%; Pred. No. 4.8;  
RESULT 1274  
ID ACN47472 standard; cDNA; 560 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-011-Q1-N6-C9, SEQ:2253.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.8%; Score 42.2; DB 13; Length 560;  
Best Local Similarity 51.3%; Pred. No. 4.9;  
RESULT 1275  
ID AAL14642 standard; cDNA; 796 BP.  
DE Human breast cancer expressed polynucleotide 7099.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.8%; Score 42.2; DB 4; Length 796;  
Best Local Similarity 48.0%; Pred. No. 5.7;  
RESULT 1276  
ID ACN84679 standard; DNA; 839 BP.  
DE Breast cancer related marker, seq id 5829.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.8%; Score 42.2; DB 11; Length 839;  
Best Local Similarity 48.0%; Pred. No. 5.8;  
RESULT 1277  
ID ADA69044 standard; DNA; 2000 BP.  
DE Arabidopsis thaliana gene, SEQ ID 2367.  
PN WO2003000898-A1.

PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 1.8%; Score 42.2; DB 8; Length 2000;  
Best Local Similarity 51.0%; Pred. No. 8.5;  
RESULT 1278  
ID ADS54244 standard; DNA; 2501 BP.  
DE Pretreated genomic DNA region 168.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 10; Length 2501;  
Best Local Similarity 46.4%; Pred. No. 9.4;  
RESULT 1279  
ID ADS89546 standard; DNA; 2501 BP.  
DE Oligonucleotide of the invention SEQ ID NO:562.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 13; Length 2501;  
Best Local Similarity 46.4%; Pred. No. 9.4;  
RESULT 1280  
ID ABL32801 standard; DNA; 5070 BP.  
DE Human immune system associated gene SEQ ID NO: 774.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 5070;  
Best Local Similarity 47.9%; Pred. No. 13;  
RESULT 1281  
ID ABN80030 standard; DNA; 5942 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 47.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 5942;  
Best Local Similarity 56.2%; Pred. No. 14;  
RESULT 1282  
ID ABK31361 standard; DNA; 6013 BP.  
DE Signal transduction associated gene modified complementary DNA #102.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 6013;  
Best Local Similarity 46.2%; Pred. No. 14;  
RESULT 1283  
ID AAS61265 standard; DNA; 6013 BP.  
DE Human gene regulation-associated gene oligonucleotide #220.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 6013;  
Best Local Similarity 46.2%; Pred. No. 14;  
RESULT 1284  
ID AAS61405 standard; DNA; 6014 BP.  
DE Human gene regulation-associated gene oligonucleotide #360.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 6014;  
Best Local Similarity 44.1%; Pred. No. 14;  
RESULT 1285  
ID ABL32421 standard; DNA; 6079 BP.  
DE Human immune system associated gene SEQ ID NO: 394.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 6079;  
Best Local Similarity 48.5%; Pred. No. 14;  
RESULT 1286  
ID AAS46449 standard; DNA; 6337 BP.  
DE Tumour suppressor gene derived chemically modified sequence #171.  
PN WO200168912-A2.  
PD 20-SEP-2001.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 4; Length 6337;  
Best Local Similarity 47.3%; Pred. No. 14;  
RESULT 1287  
ID ABLJ3310 standard; DNA; 6337 BP.  
DE Human immune system associated gene SEQ ID NO: 1283.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 6337;  
Best Local Similarity 47.3%; Pred. No. 14;  
RESULT 1288  
ID AAS46336 standard; DNA; 7348 BP.  
DE Tumour suppressor gene derived chemically modified sequence #58.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 4; Length 7348;  
Best Local Similarity 45.0%; Pred. No. 15;  
RESULT 1289  
ID ABX77219 standard; DNA; 10094 BP.  
DE 5' sequence flanking human MDR1 contig.  
PN WO200283897-A1.  
PD 24-OCT-2002.  
PA (GENE-) GENE STREAM PTY LTD.  
Query Match 1.8%; Score 42.2; DB 10; Length 10094;  
Best Local Similarity 49.9%; Pred. No. 17;  
RESULT 1290  
ID AAS45315 standard; DNA; 11260 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #10.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 4; Length 11260;  
Best Local Similarity 44.1%; Pred. No. 18;  
RESULT 1291  
ID ABK28154 standard; DNA; 11260 BP.  
DE DNA transcription associated complementary genomic DNA #14.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 11260;  
Best Local Similarity 44.1%; Pred. No. 18;  
RESULT 1292  
ID ANR80039 standard; DNA; 11260 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 56.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 11260;  
Best Local Similarity 44.1%; Pred. No. 18;  
RESULT 1293  
ID ABLJ3943 standard; DNA; 12138 BP.  
DE Human immune system associated gene SEQ ID NO: 1916.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 12138;  
Best Local Similarity 49.1%; Pred. No. 19;  
RESULT 1294  
ID ABK28336 standard; DNA; 12138 BP.  
DE DNA transcription associated complementary genomic DNA #105.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 12138;  
Best Local Similarity 49.1%; Pred. No. 19;  
RESULT 1295  
ID AAS63312 standard; DNA; 12409 BP.  
DE Chemically pretreated metabolism associated gene #7.  
PN WO200176451-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.8%; Score 42.2; DB 6; Length 12409;  
Best Local Similarity 49.1%; Pred. No. 19;  
RESULT 1296  
ID ABL32298 standard; DNA; 12507 BP.  
DE Human immune system associated gene SEQ ID NO: 271.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 12507;  
Best Local Similarity 45.7%; Pred. No. 19;  
RESULT 1297  
ID ABL70458 standard; DNA; 15161 BP.  
DE Chemically treated cell signalling DNA sequence complementary to #174.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 15161;  
Best Local Similarity 48.8%; Pred. No. 21;  
RESULT 1298  
ID AAS61423 standard; DNA; 15161 BP.  
DE Human gene regulation-associated gene oligonucleotide #378.  
PN WO20017375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 15161;  
Best Local Similarity 48.8%; Pred. No. 21;  
RESULT 1299  
ID ABL32466 standard; DNA; 15373 BP.  
DE Human immune system associated gene SEQ ID NO: 439.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 15373;  
Best Local Similarity 48.2%; Pred. No. 21;  
RESULT 1300  
ID ABL33157 standard; DNA; 17538 BP.  
DE Human immune system associated gene SEQ ID NO: 1130.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 17538;  
Best Local Similarity 44.0%; Pred. No. 22;  
RESULT 1301  
ID ABL32571 standard; DNA; 18997 BP.  
DE Human immune system associated gene SEQ ID NO: 544.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 18997;  
Best Local Similarity 51.0%; Pred. No. 23;  
RESULT 1302  
ID ABK33949 standard; DNA; 18997 BP.  
DE Human DNA for staging of Astrocytomas, complement, #16.  
PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 18997;  
Best Local Similarity 51.0%; Pred. No. 23;  
RESULT 1303  
ID ADA20353 standard; DNA; 18997 BP.  
DE Prostate tumour related genomic DNA complement sample #9.  
PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 8; Length 18997;  
Best Local Similarity 51.0%; Pred. No. 23;  
RESULT 1304  
ID ADA84160 standard; DNA; 18997 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO: 18.  
PN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 8; Length 18997;  
Best Local Similarity 51.0%; Pred. No. 23;

Best Local Similarity 51.0%; Pred. No. 23;  
RESULT 1305  
ID AB33451 standard; DNA; 19787 BP.  
DE Human immune system associated gene SEQ ID NO: 1424.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 19787;  
Best Local Similarity 42.5%; Pred. No. 23;  
RESULT 1306  
ID AD337661 standard; DNA; 29993 BP.  
DE Human chemically pretreated EVA4 gene SEQ ID NO:3.  
PN WO2003072812-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 10; Length 29993;  
Best Local Similarity 46.7%; Pred. No. 28;  
RESULT 1307  
ID AA546746 standard; DNA; 38342 BP.  
DE Tumour suppressor gene derived chemically modified sequence #470.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 4; Length 38342;  
Best Local Similarity 46.7%; Pred. No. 31;  
RESULT 1308  
ID ABK31507 standard; DNA; 38342 BP.  
DE Signal transduction associated gene modified complementary DNA #175.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42.2; DB 6; Length 38342;  
Best Local Similarity 46.7%; Pred. No. 31;  
RESULT 1309  
ID ACN44642 standard; DNA; 69081 BP.  
DE Human genomic sequence hCG17195.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 1.8%; Score 42.2; DB 11; Length 69081;  
Best Local Similarity 46.6%; Pred. No. 41;  
RESULT 1310  
ID ABD33611 standard; DNA; 89567 BP.  
DE Human cancer-associated (CA) gene HD07-124.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 1.8%; Score 42.2; DB 13; Length 89567;  
Best Local Similarity 45.3%; Pred. No. 46;  
RESULT 1311  
Query Match 1.8%; Score 42.2; DB 2; Length 110000;  
Best Local Similarity 47.5%; Pred. No. 50;  
RESULT 1312  
ID ACF62751 standard; DNA; 177380 BP.  
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:683.  
PN WO2003013534-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 1.8%; Score 42.2; DB 8; Length 177380;  
Best Local Similarity 49.9%; Pred. No. 62;  
RESULT 1313  
ID ADB20870 standard; DNA; 177380 BP.  
DE MRP1 based cancer related nucleic acid SEQ ID NO:683.  
PN WO2003013533-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 1.8%; Score 42.2; DB 8; Length 177380;  
Best Local Similarity 49.9%; Pred. No. 62;  
RESULT 1314  
ID ADB87959 standard; DNA; 177380 BP.  
DE Human UGT1A1 gene sequence SEQ ID NO:683.  
PN WO2003013536-A2.  
PD 20-FEB-2003.

PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 1.8%; Score 42.2; DB 10; Length 177380;  
Best Local Similarity 49.9%; Pred. No. 62;  
RESULT 1315  
ID ADB96942 standard; DNA; 177380 BP.  
DE Human MDR1 related DNA sequence SEQ ID NO:683.  
PN WO2003013537-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 1.8%; Score 42.2; DB 10; Length 177380;  
Best Local Similarity 49.9%; Pred. No. 62;  
RESULT 1316  
ID ADB92133 standard; DNA; 177380 BP.  
DE Human MDR1 related DNA sequence SEQ ID NO:683.  
PN WO2003013535-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 1.8%; Score 42.2; DB 10; Length 177380;  
Best Local Similarity 49.9%; Pred. No. 62;  
RESULT 1317  
ID ADR02445 standard; DNA; 636 BP.  
DE A. Gossypii genomic DNA PAG1692RP.  
PN US6239264-B1.  
PD 29-MAY-2001.  
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.  
Query Match 1.8%; Score 42; DB 2; Length 636;  
Best Local Similarity 44.8%; Pred. No. 5.8;  
RESULT 1318  
ID AAX00617 standard; DNA; 683 BP.  
DE Human secreted protein gene 7 clone HBNBL77.  
PN WO9842738-A1.  
PD 01-OCT-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.8%; Score 42; DB 2; Length 683;  
Best Local Similarity 47.7%; Pred. No. 6;  
RESULT 1319  
ID AA197306 standard; cDNA; 804 BP.  
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 3381.  
PN WO200166719-A1.  
PD 13-SEP-2001.  
PA (CHIB-) CHIBA PREFECTURE.  
PA (HISM) HISAMITSU PHARM CO LTD.  
Query Match 1.8%; Score 42; DB 4; Length 804;  
Best Local Similarity 43.8%; Pred. No. 6.4;  
RESULT 1320  
ID AAC59297 standard; cDNA; 887 BP.  
DE Human secreted protein cDNA #21.  
PN WO200056753-A1.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.8%; Score 42; DB 3; Length 887;  
Best Local Similarity 47.4%; Pred. No. 6.7;  
RESULT 1321  
ID AA237079 standard; DNA; 1431 BP.  
DE DNA sequence encoding a modified yeast SceI endonuclease.  
PN EP972836-A2.  
PD 19-JAN-2000.  
PA (RIKA) INST PHYSICAL & CHEM RES.  
Query Match 1.8%; Score 42; DB 3; Length 1431;  
Best Local Similarity 45.9%; Pred. No. 8.3;  
RESULT 1322  
ID ABS67963 standard; DNA; 1431 BP.  
DE Platelet activating factor acetylhydrolase (PAF-AH) DNA.  
PN US2002102231-A1.  
PD 01-AUG-2002.  
PA (ICOS-) ICOS CORP.  
Query Match 1.8%; Score 42; DB 6; Length 1431;  
Best Local Similarity 45.9%; Pred. No. 8.3;  
RESULT 1323  
ID ADG34448 standard; DNA; 1431 BP.  
DE Platelet activating factor associated Yeast DNA sequence.  
PN US2003215439-A1.  
PD 20-NOV-2003.

PA (DIET/) DIETSCH G N.  
 PA (PETE/) PETERMAN G M.  
 PA (YUAS/) YU A S.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 10; Length 1431;  
 RESULT 1324  
 ID ACC60976 standard; DNA; 2000 BP.  
 DE Gene sequence #SEQ ID 734.  
 PN EPI258494-A1.  
 PD 20-NOV-2002.  
 PA (CELL-) CELLZOME AG.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 10; Length 2000;  
 RESULT 1325  
 ID ADK62537 standard; DNA; 2000 BP.  
 DE Disease treating protein complex-derived gene #394.  
 PN EPI338608-A2.  
 PD 27-AUG-2003.  
 PA (CELL-) CELLZOME AG.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 10; Length 2000;  
 RESULT 1326  
 ID ADG63205 standard; cDNA; 3708 BP.  
 DE Novel human cDNA sequence #366.  
 PN EPI440981-A2.  
 PD 28-JUL-2004.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 12; Length 3708;  
 RESULT 1327  
 ID ABLJ34109 standard; DNA; 5467 BP.  
 DE Human immune system associated gene SEQ ID NO: 2082.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 6; Length 5467;  
 RESULT 1328  
 ID ABLJ33773 standard; DNA; 5666 BP.  
 DE Human immune system associated gene SEQ ID NO: 1746.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 6; Length 5666;  
 RESULT 1329  
 ID AAS61186 standard; DNA; 5666 BP.  
 DE Human gene regulation-associated gene oligonucleotide #141.  
 PN WO200177375-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 6; Length 5666;  
 RESULT 1330  
 ID ABL49329 standard; DNA; 5666 BP.  
 DE Human polynucleotide associated with DNA replication SEQ ID NO 29.  
 PN WO200177377-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 6; Length 5666;  
 RESULT 1331  
 ID ADA20417 standard; DNA; 5881 BP.  
 DE Prostate tumour related genomic DNA complement sample #41.  
 PN WO2002103042-A2.  
 PD 27-DEC-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 8; Length 5881;  
 RESULT 1332  
 ID ADA84224 standard; DNA; 5881 BP.  
 DE Human renal/prostate carcinoma associated DNA SEQ ID NO:82.  
 PN WO2002103041-A2.

PD 27-DEC-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 8; Length 5881;  
 RESULT 1333  
 ID ABL33614 standard; DNA; 6127 BP.  
 DE Human immune system associated gene SEQ ID NO: 1587.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 6; Length 6127;  
 RESULT 1334  
 ID ABL32891 standard; DNA; 6131 BP.  
 DE Human immune system associated gene SEQ ID NO: 864.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 6; Length 6131;  
 RESULT 1335  
 ID AAS46644 standard; DNA; 6261 BP.  
 DE tumour suppressor gene derived chemically modified sequence #366.  
 PN WO200168912-A2.  
 PD 20-SEP-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 4; Length 6261;  
 RESULT 1336  
 ID ABK31161 standard; DNA; 6261 BP.  
 DE Signal transduction associated gene modified complementary DNA #2.  
 PN WO200200926-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 6; Length 6261;  
 RESULT 1337  
 ID ABL33872 standard; DNA; 6270 BP.  
 DE Human immune system associated gene SEQ ID NO: 1845.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 6; Length 6270;  
 RESULT 1338  
 ID ABN80070 standard; DNA; 6325 BP.  
 DE Human chemically modified disease associated gene SEQ ID NO 87.  
 PN WO200200927-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 6; Length 6325;  
 RESULT 1339  
 ID ABK31188 standard; DNA; 6509 BP.  
 DE Signal transduction associated gene modified DNA #16.  
 PN WO200200926-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 6; Length 6509;  
 RESULT 1340  
 ID AAS61085 standard; DNA; 6509 BP.  
 DE Human gene regulation-associated gene oligonucleotide #40.  
 PN WO200177375-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match  
 Best Local Similarity 1.8%; Score 42; DB 6; Length 6509;  
 RESULT 1341  
 ID ABL32639 standard; DNA; 6650 BP.  
 DE Human immune system associated gene SEQ ID NO: 612.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.

PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 6650;  
Best Local Similarity 47.0%; Pred. No. 16;  
RESULT 1342  
ID ABL32155 standard; DNA; 6681 BP.  
DE Human immune system associated gene SEQ ID NO: 128.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 6681;  
Best Local Similarity 46.9%; Pred. No. 16;  
RESULT 1343  
ID ABL32155 standard; DNA; 6681 BP.  
DE Human immune system associated gene SEQ ID NO: 128.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 6681;  
Best Local Similarity 45.3%; Pred. No. 16;  
RESULT 1344  
ID ABL54304 standard; DNA; 6681 BP.  
DE Chemically treated apoptosis gene complementary to gene #2.  
PN WO200177164-A2.  
PD 18-OCT-2001.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 6681;  
Best Local Similarity 46.9%; Pred. No. 16;  
RESULT 1345  
ID ABL54304 standard; DNA; 6681 BP.  
DE Chemically treated apoptosis gene complementary to gene #2.  
PN WO200177164-A2.  
PD 18-OCT-2001.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 6681;  
Best Local Similarity 45.3%; Pred. No. 16;  
RESULT 1346  
ID ABL32453 standard; DNA; 6980 BP.  
DE Human immune system associated gene SEQ ID NO: 426.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 6980;  
Best Local Similarity 48.4%; Pred. No. 17;  
RESULT 1347  
ID ABL31451 standard; DNA; 7131 BP.  
DE Signal transduction associated gene modified complementary DNA #147.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 7131;  
Best Local Similarity 65.3%; Pred. No. 17;  
RESULT 1348  
ID ABL70428 standard; DNA; 7131 BP.  
DE Chemically treated cell signalling DNA sequence complementary to #159.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 7131;  
Best Local Similarity 65.3%; Pred. No. 17;  
RESULT 1349  
ID ABL61361 standard; DNA; 7131 BP.  
DE Human gene regulation-associated gene oligonucleotide #316.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 7131;  
Best Local Similarity 65.3%; Pred. No. 17;  
RESULT 1350  
ID ABL32746 standard; DNA; 7384 BP.  
DE Human immune system associated gene SEQ ID NO: 719.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.

Query Match 1.8%; Score 42; DB 6; Length 7384;  
Best Local Similarity 44.2%; Pred. No. 17;  
RESULT 1351  
ID AAS45477 standard; DNA; 7657 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #91.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 4; Length 7657;  
Best Local Similarity 46.3%; Pred. No. 17;  
RESULT 1352  
ID ABL34022 standard; DNA; 7657 BP.  
DE Human immune system associated gene SEQ ID NO: 1995.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 7657;  
Best Local Similarity 46.3%; Pred. No. 17;  
RESULT 1353  
ID AAS45489 standard; DNA; 7823 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #97.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 4; Length 7823;  
Best Local Similarity 45.0%; Pred. No. 17;  
RESULT 1354  
ID ABL34060 standard; DNA; 7823 BP.  
DE Human immune system associated gene SEQ ID NO: 2033.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 7823;  
Best Local Similarity 45.0%; Pred. No. 17;  
RESULT 1355  
ID ABL31492 standard; DNA; 7823 BP.  
DE Signal transduction associated gene modified DNA #168.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 7823;  
Best Local Similarity 45.0%; Pred. No. 17;  
RESULT 1356  
ID ABL28417 standard; DNA; 7823 BP.  
DE DNA transcription associated genomic DNA #146.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 7823;  
Best Local Similarity 45.0%; Pred. No. 17;  
RESULT 1357  
ID ABL33793 standard; DNA; 8166 BP.  
DE Human immune system associated gene SEQ ID NO: 1766.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 8166;  
Best Local Similarity 46.5%; Pred. No. 18;  
RESULT 1358  
ID ABL33569 standard; DNA; 8305 BP.  
DE Human immune system associated gene SEQ ID NO: 1542.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPiG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 8305;  
Best Local Similarity 45.3%; Pred. No. 18;  
RESULT 1359  
ID AAZ29911 standard; DNA; 8310 BP.  
DE cDNA encoding a SC4 protein of soybean.  
PN WO9953067-A2.  
PD 21-OCT-1999.  
PA (MITAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA.  
Query Match 1.8%; Score 42; DB 2; Length 8310;

Best Local Similarity 46.9%; Pred. No. 18;  
RESULT 1360  
ID ABL34229 standard; DNA; 8576 BP.  
DE Human immune system associated gene SEQ ID NO: 2202.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 8576;  
Best Local Similarity 46.3%; Pred. No. 18;  
RESULT 1361  
ID ASK28366 standard; DNA; 9238 BP.  
DE DNA transcription associated complementary genomic DNA #120.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 9238;  
Best Local Similarity 44.5%; Pred. No. 19;  
RESULT 1362  
ID ABL34161 standard; DNA; 10189 BP.  
DE Human immune system associated gene SEQ ID NO: 2134.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 10189;  
Best Local Similarity 43.8%; Pred. No. 20;  
RESULT 1363  
ID AAS46360 standard; DNA; 10609 BP.  
DE Tumour suppressor gene derived chemically modified sequence #82.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 4; Length 10609;  
Best Local Similarity 46.9%; Pred. No. 20;  
RESULT 1364  
ID ASK31269 standard; DNA; 10609 BP.  
DE Signal transduction associated gene modified complementary DNA #56.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 10609;  
Best Local Similarity 46.9%; Pred. No. 20;  
RESULT 1365  
ID ABL32605 standard; DNA; 11155 BP.  
DE Human immune system associated gene SEQ ID NO: 578.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 11155;  
Best Local Similarity 47.5%; Pred. No. 20;  
RESULT 1366  
ID ASK31422 standard; DNA; 13123 BP.  
DE Signal transduction associated gene modified DNA #133.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 13123;  
Best Local Similarity 44.4%; Pred. No. 22;  
RESULT 1367  
ID ABL54363 standard; DNA; 13123 BP.  
DE Chemically treated apoptosis gene #32.  
PN WO200177164-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 13123;  
Best Local Similarity 44.4%; Pred. No. 22;  
RESULT 1368  
ID ABL34141 standard; DNA; 15698 BP.  
DE Human immune system associated gene SEQ ID NO: 2114.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 15698;  
Best Local Similarity 48.6%; Pred. No. 24;

RESULT 1369  
ID ADB54306 standard; DNA; 17897 BP.  
DE Pretreated genomic DNA region 230.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 10; Length 17897;  
Best Local Similarity 49.5%; Pred. No. 25;  
RESULT 1370  
ID ADB54178 standard; DNA; 17897 BP.  
DE Pretreated genomic DNA region 102.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 10; Length 17897;  
Best Local Similarity 49.5%; Pred. No. 25;  
RESULT 1371  
ID ADS89328 standard; DNA; 17897 BP.  
DE Oligonucleotide of the invention SEQ ID NO:344.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 13; Length 17897;  
Best Local Similarity 49.5%; Pred. No. 25;  
RESULT 1372  
ID ADS89602 standard; DNA; 17897 BP.  
DE Oligonucleotide of the invention SEQ ID NO:618.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 13; Length 17897;  
Best Local Similarity 49.5%; Pred. No. 25;  
RESULT 1373  
ID ABL32035 standard; DNA; 18011 BP.  
DE Human immune system associated gene SEQ ID NO: 8.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 18011;  
Best Local Similarity 45.7%; Pred. No. 25;  
RESULT 1374  
ID ASK67059 standard; DNA; 34688 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 89.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 42; DB 6; Length 34688;  
Best Local Similarity 50.0%; Pred. No. 34;  
RESULT 1375  
Query Match 1.8%; Score 42; DB 6; Length 40681;  
Best Local Similarity 51.0%; Pred. No. 36;  
RESULT 1376  
ID ADA03026 standard; DNA; 96588 BP.  
DE Human MBNL carcinoma associated gene, SEQ ID NO:1544.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 1.8%; Score 42; DB 9; Length 96588;  
Best Local Similarity 45.9%; Pred. No. 53;  
RESULT 1377  
ID ADB72764 standard; DNA; 96588 BP.  
DE Human MBNL gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 1.8%; Score 42; DB 10; Length 96588;  
Best Local Similarity 45.9%; Pred. No. 53;  
RESULT 1378  
ID ADC85506 standard; DNA; 96588 BP.  
DE Human Mbml genomic sequence.  
PN WO2003045230-A2.  
PD 05-JUN-2003.  
PA (SAGR-) SAGRES DISCOVERY.

PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.8%; Score 41.8; DB 5; Length 375;  
Best Local Similarity 41.7%; Pred. No. 5.1;  
RESULT 1386  
ID AAZ94422 standard; DNA; 1444 BP.  
DE Plasmodium falci parum ycf 24 gene.  
PN WO20016758-A2.  
PD 30-MAR-2000.  
PA (MEDI-) MEDICAL RES COUNCIL.  
Query Match 1.8%; Score 41.8; DB 3; Length 1444;  
Best Local Similarity 47.2%; Pred. No. 9.3;  
RESULT 1389  
ID AAX99552 standard; DNA; 2478 BP.  
DE Nucleic acid sequence from U. urealyticum.  
PN WO9939007-A1.  
PD 05-AUG-1999.  
PA (UABR-) UAB RES FOUND.  
Query Match 1.8%; Score 41.8; DB 2; Length 2478;  
Best Local Similarity 44.0%; Pred. No. 12;  
RESULT 1390  
ID AAR97037 standard; DNA; 2486 BP.  
DE Nucleotide sequence encoding 48kd i-antigen.  
PN WO200046373-A1.  
PD 10-AUG-2000.  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
PA (CORR ) CORNELL RES FOUND INC.  
PA (CLAR/) CLARK T G.  
PA (DICK/) DICKERSON H W.  
PA (LIN7/) LIN T.  
Query Match 1.8%; Score 41.8; DB 3; Length 2486;  
Best Local Similarity 45.2%; Pred. No. 12;  
RESULT 1391  
ID ADD93413 standard; cDNA; 2622 BP.  
DE Human lipid-associated molecule LIPAM-1 polynucleotide.  
PN WO2003083081-A2.  
PD 09-OCT-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 1.8%; Score 41.8; DB 10; Length 2622;  
Best Local Similarity 50.8%; Pred. No. 12;  
RESULT 1392  
ID AAB70149 standard; DNA; 3744 BP.  
DE Plasmodium falci parum chromosome 2 related DNA sequence SEQ ID NO:282.  
PN WO200025728-A2.  
PD 11-MAY-2000.  
PA (HOFF/) HOFFMAN S.  
PA (CARU/) CARUCCI D.  
PA (GARD/) GARDNER M.  
PA (VENT/) VENTER J C.  
Query Match 1.8%; Score 41.8; DB 3; Length 3744;  
Best Local Similarity 49.8%; Pred. No. 14;  
RESULT 1393  
ID ABZ10146 standard; DNA; 5033 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #286.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 8; Length 5033;  
Best Local Similarity 43.7%; Pred. No. 16;  
RESULT 1394  
ID ABZ10000 standard; DNA; 5033 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #140.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 8; Length 5033;  
Best Local Similarity 43.7%; Pred. No. 16;  
RESULT 1395  
ID ABL33066 standard; DNA; 5107 BP.  
DE Human immune system associated gene SEQ ID NO: 1039.  
PN WO200200928-A2.  
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 5107;  
Best Local Similarity 57.1%; Pred. No. 16;  
RESULT 1396  
ID ABN80305 standard; DNA; 6068 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 222.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 6068;  
Best Local Similarity 49.1%; Pred. No. 18;  
RESULT 1397  
ID ABL92289 standard; DNA; 6156 BP.  
DE Chemically treated DNA repair gene fragment complementary to#49.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 6156;  
Best Local Similarity 44.5%; Pred. No. 18;  
RESULT 1398  
ID ABL49360 standard; DNA; 6156 BP.  
DE Human polynucleotide associated with DNA replication SEQ ID NO 60.  
PN WO200177377-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 6156;  
Best Local Similarity 44.5%; Pred. No. 18;  
RESULT 1399  
ID ABL32391 standard; DNA; 6195 BP.  
DE Human immune system associated gene SEQ ID NO: 564.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 6195;  
Best Local Similarity 46.5%; Pred. No. 18;  
RESULT 1400  
ID ABL33145 standard; DNA; 6823 BP.  
DE Human immune system associated gene SEQ ID NO: 1118.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 6823;  
Best Local Similarity 59.8%; Pred. No. 18;  
RESULT 1401  
ID ABL33239 standard; DNA; 6894 BP.  
DE Human immune system associated gene SEQ ID NO: 1212.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 6894;  
Best Local Similarity 44.8%; Pred. No. 19;  
RESULT 1402  
ID ABK33970 standard; DNA; 6894 BP.  
DE Human DNA for staging of Astrocytomas, complement, #27.  
PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 6894;  
Best Local Similarity 44.8%; Pred. No. 19;  
RESULT 1403  
ID ADA20365 standard; DNA; 6894 BP.  
DE Prostate tumour related genomic DNA complement sample #15.  
PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 8; Length 6894;  
Best Local Similarity 44.8%; Pred. No. 19;  
RESULT 1404  
ID ADA84172 standard; DNA; 6894 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:30.  
PN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.8%; Score 41.8; DB 8; Length 6894;  
Best Local Similarity 44.8%; Pred. No. 19;  
RESULT 1405  
ID ABL32979 standard; DNA; 6963 BP.  
DE Human immune system associated gene SEQ ID NO: 952.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 6963;  
Best Local Similarity 43.4%; Pred. No. 19;  
RESULT 1406  
ID ABK40051 standard; DNA; 7058 BP.  
DE Human chemically pretreated gene sequence #67 strand 1.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 7058;  
Best Local Similarity 47.2%; Pred. No. 19;  
RESULT 1407  
ID AAS46423 standard; DNA; 7135 BP.  
DE Tumour suppressor gene derived chemically modified sequence #145.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 4; Length 7135;  
Best Local Similarity 53.3%; Pred. No. 19;  
RESULT 1408  
ID AAS46308 standard; DNA; 8033 BP.  
DE Tumour suppressor gene derived chemically modified sequence #30.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 4; Length 8033;  
Best Local Similarity 43.7%; Pred. No. 20;  
RESULT 1409  
ID ABK31203 standard; DNA; 8033 BP.  
DE Signal transduction associated gene modified complementary DNA #23.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 8033;  
Best Local Similarity 43.7%; Pred. No. 20;  
RESULT 1410  
ID ABL70170 standard; DNA; 8033 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#30.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 8033;  
Best Local Similarity 43.7%; Pred. No. 20;  
RESULT 1411  
ID AAS61117 standard; DNA; 8033 BP.  
DE Human gene regulation-associated gene oligonucleotide #72.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 8033;  
Best Local Similarity 43.7%; Pred. No. 20;  
RESULT 1412  
ID ABL34514 standard; DNA; 8197 BP.  
DE Human metastasis associated gene SEQ ID NO: 67.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 8197;  
Best Local Similarity 46.4%; Pred. No. 20;  
RESULT 1413  
ID ABL70541 standard; DNA; 8197 BP.  
DE Chemically treated cell signalling DNA sequence#216.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 8197;



Best Local Similarity 46.4%; Pred. No. 20;  
RESULT 1414  
ID ADS99775 standard; DNA; 8197 BP.  
DE Bisulphite treated human gene associated with metastasis #34.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 1.8%; Score 41.8; DB 7; Length 8197;  
Best Local Similarity 46.4%; Pred. No. 20;  
RESULT 1415  
ID ABK40068 standard; DNA; 8776 BP.  
DE Human chemically pretreated gene sequence #75 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 8776;  
Best Local Similarity 50.8%; Pred. No. 21;  
RESULT 1416  
ID AAS45437 standard; DNA; 8801 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #71.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 4; Length 8801;  
Best Local Similarity 50.2%; Pred. No. 21;  
RESULT 1417  
ID ABU33741 standard; DNA; 8801 BP.  
DE Human immune system associated gene SEQ ID NO: 1714.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 8801;  
Best Local Similarity 50.2%; Pred. No. 21;  
RESULT 1418  
ID ABK28286 standard; DNA; 8801 BP.  
DE DNA transcription associated complementary genomic DNA #80.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 8801;  
Best Local Similarity 50.2%; Pred. No. 21;  
RESULT 1419  
ID AAK86271 standard; DNA; 9599 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41083.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 1.8%; Score 41.8; DB 4; Length 9599;  
Best Local Similarity 48.2%; Pred. No. 21;  
RESULT 1420  
ID ABL33799 standard; DNA; 9848 BP.  
DE Human immune system associated gene SEQ ID NO: 1772.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 9848;  
Best Local Similarity 45.2%; Pred. No. 22;  
RESULT 1421  
ID ABL34043 standard; DNA; 10039 BP.  
DE Human immune system associated gene SEQ ID NO: 2016.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 10039;  
Best Local Similarity 46.7%; Pred. No. 22;  
RESULT 1422  
ID ABL34187 standard; DNA; 11944 BP.  
DE Human immune system associated gene SEQ ID NO: 2160.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 11944;  
Best Local Similarity 46.4%; Pred. No. 24;  
RESULT 1423  
ID ABL33052 standard; DNA; 17131 BP.  
DE Human immune system associated gene SEQ ID NO: 1025.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 17131;  
Best Local Similarity 46.7%; Pred. No. 28;  
RESULT 1424  
ID AAD52172 standard; DNA; 26000 BP.  
DE Human interferon gamma receptor 1 (IFNGR1) gene.  
PN WO200288162-A1.  
PD 07-NOV-2002.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 1.8%; Score 41.8; DB 10; Length 26000;  
Best Local Similarity 48.2%; Pred. No. 33;  
RESULT 1425  
ID ACN44852 standard; DNA; 34200 BP.  
DE Mouse genomic sequence mCG4860.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 1.8%; Score 41.8; DB 11; Length 34200;  
Best Local Similarity 47.2%; Pred. No. 38;  
RESULT 1426  
ID ABL55857 standard; DNA; 34337 BP.  
DE Human GABA transporter protein gene.  
PN US2002031800-A1.  
PD 14-MAR-2002.  
PA (LIZZ/) LI Z.  
PA (CHAT/) CHATURVEDI K.  
PA (ZHUS/) ZHU S.  
PA (WOOD/) WOODAGE T.  
PA (GUEG/) GUEGLER K.  
PA (WEBS/) WEBSTER M.  
PA (DFRA/) DI FRANCESCO V.  
PA (BEAS/) BEASLEY E M.  
Query Match 1.8%; Score 41.8; DB 6; Length 34337;  
Best Local Similarity 48.2%; Pred. No. 38;  
RESULT 1427  
ID ADG88376 standard; DNA; 34337 BP.  
DE Human transporter gene.  
PN US2003157649-A1.  
PD 21-AUG-2003.  
PA (APPL-) APPLERA CORP.  
Query Match 1.8%; Score 41.8; DB 10; Length 34337;  
Best Local Similarity 48.2%; Pred. No. 38;  
RESULT 1428  
ID ABO67094 standard; DNA; 83391 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 124.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.8; DB 6; Length 83391;  
Best Local Similarity 47.7%; Pred. No. 56;  
RESULT 1429  
ID ADI72102 standard; DNA; 299 BP.  
DE Human ovarian cancer DNA marker #4844.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.8%; Score 41.6; DB 5; Length 299;  
Best Local Similarity 45.3%; Pred. No. 5.2;  
RESULT 1430  
ID ADU37251 standard; DNA; 299 BP.  
DE Human ovarian cancer DNA marker #11141.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.8%; Score 41.6; DB 5; Length 299;  
Best Local Similarity 45.3%; Pred. No. 5.2;

RESULT 1431  
ID AAH93356 standard; DNA; 366 BP.  
DE Human chromosome 16 BAC clone CIT987SK-A-248F7 SEQ ID NO 77.  
PN WO200152616-A2.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.8%; Score 41.6; DB 4; Length 366;  
Best Local Similarity 48.7%; Pred. No. 5.7;  
RESULT 1432  
ID ACN32913 standard; cDNA; 411 BP.  
DE Cotton androecium tissue EST Clone ID: LTB3828-019-Q1-N6-D10, SEQ:7694.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FENG/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.8%; Score 41.6; DB 13; Length 411;  
Best Local Similarity 49.5%; Pred. No. 6;  
RESULT 1433  
ID ACN2049 standard; cDNA; 469 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-024-Q6-N6-E4, SEQ:16830.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FENG/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 1.8%; Score 41.6; DB 13; Length 469;  
Best Local Similarity 47.1%; Pred. No. 6.4;  
RESULT 1434  
ID ADL4372 standard; DNA; 539 BP.  
DE Human ovarian cancer DNA marker #17862.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 1.8%; Score 41.6; DB 5; Length 539;  
Best Local Similarity 48.0%; Pred. No. 6.8;  
RESULT 1435  
ID ABT18873 standard; DNA; 1569 BP.  
DE Aspergillus fumigatus essential gene #1231.  
PN WO200286090-A2.  
PD 31-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.8%; Score 41.6; DB 8; Length 1569;  
Best Local Similarity 52.3%; Pred. No. 11;  
RESULT 1436  
ID ABT20693 standard; DNA; 1569 BP.  
DE Aspergillus fumigatus essential gene #3051.  
PN WO200286090-A2.  
PD 31-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.8%; Score 41.6; DB 8; Length 1569;  
Best Local Similarity 52.3%; Pred. No. 11;  
RESULT 1437  
ID ABT20095 standard; DNA; 1689 BP.  
DE Aspergillus fumigatus essential gene #2453.  
PN WO200286090-A2.  
PD 31-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.8%; Score 41.6; DB 8; Length 1689;  
Best Local Similarity 52.3%; Pred. No. 11;  
RESULT 1438  
ID ABT18279 standard; DNA; 1714 BP.  
DE Aspergillus fumigatus essential gene #637.  
PN WO200286090-A2.  
PD 31-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.8%; Score 41.6; DB 8; Length 1714;  
Best Local Similarity 52.3%; Pred. No. 11;  
RESULT 1439  
ID AAV39373 standard; cDNA; 2115 BP.  
DE Beta(1 -> 4)-N-acetylglucosaminyl-transferase (Gnt-IV) a encoding cDNA.

PN WO9826053-A1.  
PD 18-JUN-1998.  
PA (KIRI) KIRIN BEER KK.  
Query Match 1.8%; Score 41.6; DB 2; Length 2115;  
Best Local Similarity 53.0%; Pred. No. 12;  
RESULT 1440  
ID AAD63209 standard; DNA; 2115 BP.  
DE Human DNA #34 used in the method for diagnosing cancer.  
PN US2003190656-A1.  
PD 09-OCT-2003.  
PA (WANG/) WANG Y.  
Query Match 1.8%; Score 41.6; DB 10; Length 2115;  
Best Local Similarity 53.0%; Pred. No. 12;  
RESULT 1441  
ID AAD62810 standard; DNA; 2115 BP.  
DE Human DNA #23 used in the method for diagnosing cancer.  
PN US2003194733-A1.  
PD 16-OCT-2003.  
PA (WANG/) WANG Y.  
Query Match 1.8%; Score 41.6; DB 10; Length 2115;  
Best Local Similarity 53.0%; Pred. No. 12;  
RESULT 1442  
ID ADP88305 standard; cDNA; 2115 BP.  
DE Metastatic breast cancer marker gene MGAT4A, SEQ ID NO:82.  
PN EP1349104-A2.  
PD 01-OCT-2003.  
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
Query Match 1.8%; Score 41.6; DB 11; Length 2115;  
Best Local Similarity 53.0%; Pred. No. 12;  
RESULT 1443  
ID ADR25531 standard; DNA; 2115 BP.  
DE Breast cancer prognosis marker #1392.  
PN WO2004065545-A2.  
PD 05-AUG-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
PA (NECA-) NETHERLANDS CANCER INST.  
Query Match 1.8%; Score 41.6; DB 13; Length 2115;  
Best Local Similarity 53.0%; Pred. No. 12;  
RESULT 1444  
ID ADS32721 standard; DNA; 2115 BP.  
DE Human MGAT4A coding sequence.  
PN WO2004074461-A2.  
PD 02-SEP-2004.  
PA (BOBR/) BOBROWICZ P.  
PA (HAM/) HAMILTON S R.  
PA (GERN/) GERNGROSS T U.  
PA (WILD/) WILDT S.  
PA (CHOI/) CHOI B.  
PA (NETT/) NETT J H.  
PA (DAVI/) DAVIDSON R C.  
Query Match 1.8%; Score 41.6; DB 13; Length 2115;  
Best Local Similarity 53.0%; Pred. No. 12;  
RESULT 1445  
ID ADR97303 standard; DNA; 2115 BP.  
DE Human MGAT4A DNA, an apoptosis related target Seq 11.  
PN WO2004078783-A2.  
PD 16-SEP-2004.  
PA (EIRX-) EIRX THERAPEUTICS LTD.  
Query Match 1.8%; Score 41.6; DB 13; Length 2115;  
Best Local Similarity 53.0%; Pred. No. 12;  
RESULT 1446  
ID AAD09955 standard; cDNA; 2339 BP.  
DE Human drug metabolising enzyme (DME-20) cDNA.  
PN WO200151638-A2.  
PD 19-JUL-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.8%; Score 41.6; DB 4; Length 2339;  
Best Local Similarity 53.0%; Pred. No. 13;  
RESULT 1447  
ID ABT19499 standard; DNA; 3689 BP.  
DE Aspergillus fumigatus essential gene #1857.  
PN WO200286090-A2.  
PD 31-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.8%; Score 41.6; DB 8; Length 3689;  
Best Local Similarity 52.3%; Pred. No. 16;  
RESULT 1448  
ID ABT17685 standard; DNA; 3714 BP.  
DE Aspergillus fumigatus essential gene #43.  
PN WO200286090-A2.  
PD 31-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.8%; Score 41.6; DB 8; Length 3714;  
Best Local Similarity 52.3%; Pred. No. 16;  
RESULT 1449  
ID ABLJ33676 standard; DNA; 5379 BP.  
DE Human immune system associated gene SEQ ID NO: 1649.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 5379;  
Best Local Similarity 45.2%; Pred. No. 19;  
RESULT 1450  
ID ABLJ34576 standard; DNA; 5379 BP.  
DE Human metastasis associated gene SEQ ID NO: 129.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 5379;  
Best Local Similarity 45.2%; Pred. No. 19;  
RESULT 1451  
ID ABL70369 standard; DNA; 5379 BP.  
DE Chemically treated cell signalling DNA sequence#130.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 5379;  
Best Local Similarity 45.2%; Pred. No. 19;  
RESULT 1452  
ID ADS99837 standard; DNA; 5379 BP.  
DE Bisulphite treated human gene associated with metastasis #65.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 1.8%; Score 41.6; DB 7; Length 5379;  
Best Local Similarity 45.2%; Pred. No. 19;  
RESULT 1453  
ID AB210204 standard; DNA; 5507 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #344.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 8; Length 5507;  
Best Local Similarity 43.8%; Pred. No. 19;  
RESULT 1454  
ID ABK31279 standard; DNA; 5526 BP.  
DE Signal transduction associated gene modified complementary DNA #61.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 5526;  
Best Local Similarity 53.0%; Pred. No. 19;  
RESULT 1455  
ID ABLJ33396 standard; DNA; 5641 BP.  
DE Human immune system associated gene SEQ ID NO: 1369.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 5641;  
Best Local Similarity 49.3%; Pred. No. 19;  
RESULT 1456  
ID AB210144 standard; DNA; 5660 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #284.  
PN WO200277272-A2.

PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 8; Length 5660;  
Best Local Similarity 49.1%; Pred. No. 19;  
RESULT 1457  
ID ABLJ32697 standard; DNA; 5663 BP.  
DE Human immune system associated gene SEQ ID NO: 670.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 5663;  
Best Local Similarity 49.5%; Pred. No. 19;  
RESULT 1458  
ID ABLJ22223 standard; DNA; 5663 BP.  
DE Chemically treated DNA repair gene fragment complementary to#16.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 5663;  
Best Local Similarity 49.5%; Pred. No. 19;  
RESULT 1459  
ID ACF62812 standard; DNA; 5666 BP.  
DE Colon cancer analysis related genomic DNA SEQ ID NO:61.  
PN WO2003014388-A2.  
PD 20-FEB-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 8; Length 5666;  
Best Local Similarity 49.1%; Pred. No. 19;  
RESULT 1460  
ID ABLJ33667 standard; DNA; 5798 BP.  
DE Human immune system associated gene SEQ ID NO: 1640.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 5798;  
Best Local Similarity 46.3%; Pred. No. 19;  
RESULT 1461  
ID AAS61416 standard; DNA; 5887 BP.  
DE Human gene regulation-associated gene oligonucleotide #371.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 5887;  
Best Local Similarity 45.4%; Pred. No. 19;  
RESULT 1462  
ID ABK31361 standard; DNA; 6013 BP.  
DE Signal transduction associated gene modified complementary DNA #102.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 6013;  
Best Local Similarity 47.0%; Pred. No. 20;  
RESULT 1463  
ID AAS61265 standard; DNA; 6013 BP.  
DE Human gene regulation-associated gene oligonucleotide #220.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 6013;  
Best Local Similarity 47.0%; Pred. No. 20;  
RESULT 1464  
ID ABLJ22288 standard; DNA; 6156 BP.  
DE Chemically treated DNA repair gene fragment#49.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 6156;  
Best Local Similarity 44.8%; Pred. No. 20;  
RESULT 1465  
ID ABL49359 standard; DNA; 6156 BP.  
DE Human polynucleotide associated with DNA replication SEQ ID NO 59.  
PN WO200177377-A2.  
PD 18-OCT-2001.

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PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 6; Length 6156;
  Best Local Similarity 44.8%; Pred. No. 20;
  RESULT 1466
  ID ABK28369 standard; DNA; 6167 BP.
  DE DNA transcription associated genomic DNA #122.
  PN WO200192565-A2.
  PD 06-DEC-2001.
  PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 6; Length 6167;
  Best Local Similarity 50.0%; Pred. No. 20;
  RESULT 1467
  ID AAS46497 standard; DNA; 6233 BP.
  DE Tumour suppressor gene derived chemically modified sequence #219.
  PN WO200168912-A2.
  PD 20-SEP-2001.
  PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 4; Length 6233;
  Best Local Similarity 48.4%; Pred. No. 20;
  RESULT 1468
  ID AAS45445 standard; DNA; 6327 BP.
  DE Chemically pretreated complementary DNA associated with cell cycle #75.
  PN WO200168911-A2.
  PD 20-SEP-2001.
  PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 4; Length 6327;
  Best Local Similarity 47.6%; Pred. No. 20;
  RESULT 1469
  ID ABK28294 standard; DNA; 6327 BP.
  DE DNA transcription associated complementary genomic DNA #84.
  PN WO200192565-A2.
  PD 06-DEC-2001.
  PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 6; Length 6327;
  Best Local Similarity 47.6%; Pred. No. 20;
  RESULT 1470
  ID ABN80023 standard; DNA; 6636 BP.
  DE Human chemically modified disease associated gene SEQ ID NO 40.
  PN WO200200927-A2.
  PD 03-JAN-2002.
  PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 6; Length 6636;
  Best Local Similarity 44.1%; Pred. No. 20;
  RESULT 1471
  ID ABU32315 standard; DNA; 6641 BP.
  DE Human immune system associated gene SEQ ID NO: 288.
  PN WO200200928-A2.
  PD 03-JAN-2002.
  PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 6; Length 6641;
  Best Local Similarity 45.3%; Pred. No. 20;
  RESULT 1472
  ID ABU54336 standard; DNA; 6641 BP.
  DE Chemically treated apoptosis gene complementary to gene #18.
  PN WO200177164-A2.
  PD 18-OCT-2001.
  PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 6; Length 6641;
  Best Local Similarity 45.3%; Pred. No. 20;
  RESULT 1473
  ID ABU33894 standard; DNA; 6899 BP.
  DE Human immune system associated gene SEQ ID NO: 1867.
  PN WO200200928-A2.
  PD 03-JAN-2002.
  PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 6; Length 6899;
  Best Local Similarity 54.6%; Pred. No. 21;
  RESULT 1474
  ID AAD28379 standard; DNA; 7340 BP.
  DE Human chemically treated genomic DNA #20.
  PN WO200202809-A2.
  PD 10-JAN-2002.
  PA (EPIG-) EPIGENOMICS AG.

  Query Match 1.8%; Score 41.6; DB 6; Length 7340;
  Best Local Similarity 48.0%; Pred. No. 21;
  RESULT 1475
  ID ABK28342 standard; DNA; 8260 BP.
  DE DNA transcription associated complementary genomic DNA #108.
  PN WO200192565-A2.
  PD 06-DEC-2001.
  PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 6; Length 8260;
  Best Local Similarity 46.5%; Pred. No. 23;
  RESULT 1476
  ID ADB54216 standard; DNA; 8404 BP.
  DE Pretreated genomic DNA region 140.
  PN WO2003072821-A2.
  PD 04-SEP-2003.
  PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 10; Length 8404;
  Best Local Similarity 43.8%; Pred. No. 23;
  RESULT 1477
  ID ADE84152 standard; DNA; 8404 BP.
  DE Human lymphoid cell proliferative disorder gene derived DNA #88.
  PN WO2003044226-A2.
  PD 30-MAY-2003.
  PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 10; Length 8404;
  Best Local Similarity 43.8%; Pred. No. 23;
  RESULT 1478
  ID ADS89516 standard; DNA; 8404 BP.
  DE Oligonucleotide of the invention SEQ ID NO:532.
  PN WO2004035803-A2.
  PD 29-APR-2004.
  PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 13; Length 8404;
  Best Local Similarity 43.8%; Pred. No. 23;
  RESULT 1479
  ID ADB54240 standard; DNA; 8666 BP.
  DE Pretreated genomic DNA region 164.
  PN WO2003072821-A2.
  PD 04-SEP-2003.
  PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 10; Length 8666;
  Best Local Similarity 49.1%; Pred. No. 23;
  RESULT 1480
  ID ADE84178 standard; DNA; 8666 BP.
  DE Human lymphoid cell proliferative disorder gene derived DNA #114.
  PN WO2003044226-A2.
  PD 30-MAY-2003.
  PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 10; Length 8666;
  Best Local Similarity 49.1%; Pred. No. 23;
  RESULT 1481
  ID ADS89542 standard; DNA; 8666 BP.
  DE Oligonucleotide of the invention SEQ ID NO:558.
  PN WO2004035803-A2.
  PD 29-APR-2004.
  PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 13; Length 8666;
  Best Local Similarity 49.1%; Pred. No. 23;
  RESULT 1482
  ID AQB6990 standard; DNA; 9118 BP.
  DE Human angiogenesis associated polynucleotide SEQ ID NO 20.
  PN WO200246454-A2.
  PD 13-JUN-2002.
  PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 6; Length 9118;
  Best Local Similarity 45.4%; Pred. No. 24;
  RESULT 1483
  ID ABN80049 standard; DNA; 9543 BP.
  DE Human chemically modified disease associated gene SEQ ID NO 66.
  PN WO200200927-A2.
  PD 03-JAN-2002.
  PA (EPIG-) EPIGENOMICS AG.
  Query Match 1.8%; Score 41.6; DB 6; Length 9543;
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Best Local Similarity 45.4%; Pred. No. 24;  
RESULT 1484  
ID ABL3323 standard; DNA; 9741 BP.  
DE Human immune system associated gene SEQ ID NO: 1296.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 9741;  
Best Local Similarity 45.9%; Pred. No. 24;  
RESULT 1485  
ID ABL32892 standard; DNA; 10710 BP.  
DE Human immune system associated gene SEQ ID NO: 865.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 10710;  
Best Local Similarity 45.6%; Pred. No. 25;  
RESULT 1486  
ID AAS46805 standard; DNA; 10996 BP.  
DE Tumour suppressor gene derived chemically modified sequence #531.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 4; Length 10996;  
Best Local Similarity 43.0%; Pred. No. 26;  
RESULT 1487  
ID ABK28465 standard; DNA; 10996 BP.  
DE DNA transcription associated genomic DNA #170.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 10996;  
Best Local Similarity 43.0%; Pred. No. 26;  
RESULT 1488  
ID AAS46414 standard; DNA; 11029 BP.  
DE Tumour suppressor gene derived chemically modified sequence #136.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 4; Length 11029;  
Best Local Similarity 45.2%; Pred. No. 26;  
RESULT 1489  
ID ADS89288 standard; DNA; 11029 BP.  
DE Oligonucleotide of the invention SEQ ID NO:304.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 13; Length 11029;  
Best Local Similarity 45.2%; Pred. No. 26;  
RESULT 1490  
ID AAS45479 standard; DNA; 11047 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #92.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 4; Length 11047;  
Best Local Similarity 45.9%; Pred. No. 26;  
RESULT 1491  
ID ABL33984 standard; DNA; 11047 BP.  
DE Human immune system associated gene SEQ ID NO: 1957.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 11047;  
Best Local Similarity 45.9%; Pred. No. 26;  
RESULT 1492  
ID ABK28401 standard; DNA; 11047 BP.  
DE DNA transcription associated genomic DNA #138.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 11047;  
Best Local Similarity 45.9%; Pred. No. 26;

RESULT 1493  
ID ABK39937 standard; DNA; 11422 BP.  
DE Human chemically pretreated gene sequence #9 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 11422;  
Best Local Similarity 46.3%; Pred. No. 26;  
RESULT 1494  
ID ABL32219 standard; DNA; 11422 BP.  
DE Human immune system associated gene SEQ ID NO: 192.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 11422;  
Best Local Similarity 46.3%; Pred. No. 26;  
RESULT 1495  
ID AAS46509 standard; DNA; 12356 BP.  
DE Tumour suppressor gene derived chemically modified sequence #231.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 4; Length 12356;  
Best Local Similarity 49.1%; Pred. No. 27;  
RESULT 1496  
ID ADS89729 standard; DNA; 13286 BP.  
DE Oligonucleotide of the invention SEQ ID NO:745.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 13; Length 13286;  
Best Local Similarity 44.7%; Pred. No. 28;  
RESULT 1497  
ID ADS89455 standard; DNA; 13286 BP.  
DE Oligonucleotide of the invention SEQ ID NO:471.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 13; Length 13286;  
Best Local Similarity 44.7%; Pred. No. 28;  
RESULT 1498  
ID ABK31518 standard; DNA; 14316 BP.  
DE Signal transduction associated gene modified DNA #181.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 14316;  
Best Local Similarity 51.8%; Pred. No. 29;  
RESULT 1499  
ID ABL70605 standard; DNA; 14316 BP.  
DE Chemically treated cell signalling DNA sequence#248.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 14316;  
Best Local Similarity 51.8%; Pred. No. 29;  
RESULT 1500  
ID AAS61444 standard; DNA; 14316 BP.  
DE Human gene regulation-associated gene oligonucleotide #399.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 1.8%; Score 41.6; DB 6; Length 14316;  
Best Local Similarity 51.8%; Pred. No. 29;

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GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2005, 08:30:38 ; Search time 10304 Seconds  
(without alignments)  
11154.481 Million cell updates/sec

Title: US-10-063-670-5  
Perfect score: 2372  
Sequence: 1 agcagggaatccggatgtc.....ttaaagcatttagaaaactt 2372

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sw.\*
- 13: gb.un.\*
- 14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2372	100.0	2372	6	BD172392
2	2372	100.0	2372	6	BD172711
3	2372	100.0	2372	6	BD173030
4	2372	100.0	2372	6	BD173349
5	2372	100.0	2372	6	BD175383
6	2372	100.0	2372	6	AR410761
7	2372	100.0	2372	6	AR439125
8	2372	100.0	2372	6	AR473145
9	2372	100.0	2372	6	AR527131
10	2372	100.0	2372	6	AR566164
11	2372	100.0	2372	6	AX092274
12	2372	100.0	2372	6	AX454446
13	2372	100.0	2372	6	AX490924
14	2372	100.0	2372	6	AX697609
15	2372	100.0	2372	6	BD075532
16	2372	100.0	2372	9	AY358925
17	2299.4	96.2	2312	9	CQ720788
18	2282.2	96.2	2313	9	AF118108
19	2245.4	94.7	2282	9	BC026231

93	106	4.5	106	6	CQ303364	Sequence	C 166	57.4	2.4	121958	2	CR759861	Danio rer
94	71.6	3.0	191887	2	CR407563	AL07563 Danio rer	c 167	57.4	2.4	161162	8	AB086179	Anthocero
95	65.4	2.8	83110	2	PFMAL13PB	AL109814 Plasmoidiu	c 168	57.4	2.4	169520	2	CR753882	Danio rer
96	65.4	2.8	110000	2	PFMAL13_13	Continuation (14 o	c 169	57.4	2.4	179603	6	CQ870485	Sequence
97	65.4	2.8	194327	2	CR385065	CR385065 Danio rer	c 170	57.4	2.4	201659	2	AC146419	Pan trogl
98	65	2.7	12240	3	AE001424	AE001424 Plasmoidiu	c 171	57.4	2.4	205671	2	CR385067	Danio rer
99	65	2.7	258658	3	AE014832	AE014832 Plasmoidiu	c 172	57.4	2.4	210511	5	BX470068	Zebrafish
100	64.2	2.7	172064	9	AL445195	AL445195 Human DNA	173	57.4	2.4	223904	2	CR759864	Danio rer
101	64.2	2.7	347050	3	PFA929351	AL929351 Plasmoidiu	174	57.4	2.4	250022	3	AE014824	Plasmoidiu
102	63.4	2.7	153459	2	CR847994	CR847994 Danio rer	c 175	57.4	2.4	313727	2	AX510958	Danio rer
103	62.8	2.6	170143	2	AC048384	AC048384 Homo sapi	c 176	57.4	2.4	349751	3	PFMAL4P3	Plasmoidiu
104	62.4	2.6	3322	5	BC074228	BC074228 Xenopus l	c 177	57.2	2.4	91723	6	AX083744	Sequence
105	62.4	2.6	297798	2	CR396591	CR396591 Danio rer	c 178	57.2	2.4	91723	9	AC010903	Homo sapi
106	62.2	2.6	86826	3	PFMAL3P5	AL034556 Plasmoidiu	179	57.2	2.4	110000	2	PFMAL13_07	Continuation (8 of
107	62.2	2.6	183417	5	AL845320	AL845320 Zebrafish	180	57	2.4	136372	9	AC103828	Homo sapi
108	62	2.6	192187	3	AC117072	AC117072 Dictyoste	c 181	57	2.4	169894	2	CR762466	Danio rer
109	61.8	2.6	152966	9	AL359713	AL359713 Human DNA	182	57	2.4	172578	2	CR812468	Danio rer
110	61.8	2.6	164399	3	PFMAL3P6	Z98551 Plasmoidiu	183	57	2.4	183584	9	AC012492	Homo sapi
111	61.8	2.6	258658	3	AE014832	AE014832 Plasmoidiu	184	56.8	2.4	5074	3	AY171197	Caenorhab
112	61.6	2.6	154492	2	AC149661	AC149661 Bos tauru	c 185	56.8	2.4	8056	6	AX598900	Sequence
113	61.6	2.6	217621	2	BX901924	BX901924 Danio rer	c 186	56.8	2.4	118301	9	AC121342	Homo sapi
114	61.6	2.6	226543	2	BX855598	BX855598 Danio rer	c 187	56.8	2.4	181557	2	CR847945	Danio rer
115	61.4	2.6	214709	2	CR749183	CR749183 Danio rer	c 188	56.8	2.4	223166	2	CR790362	Danio rer
116	61.2	2.6	132254	3	AC116330	AC116330 Dictyoste	189	56.8	2.4	340552	3	PFA929354	Plasmoidiu
117	61.2	2.6	153943	2	AC027417	AC027417 Homo sapi	190	56.6	2.4	2000	6	AX555393	Sequence
118	61.2	2.6	157544	9	AC098590	AC098590 Homo sapi	191	56.6	2.4	6216	6	AX348318	Sequence
119	61.2	2.6	196988	9	AP002761	AP002761 Homo sapi	192	56.6	2.4	6216	6	AX348571	Sequence
120	61	2.6	5075	3	AY171195	AY171195 Caenorhab	c 193	56.6	2.4	150323	2	CR848005	Danio rer
121	61	2.6	5075	3	AY171201	AY171201 Caenorhab	c 194	56.6	2.4	160892	2	BX248386	Danio rer
122	61	2.6	5075	3	AY171205	AY171205 Caenorhab	c 195	56.6	2.4	167245	2	CR628882	Danio rer
123	60.6	2.6	210548	2	CR751608	CR751608 Danio rer	196	56.6	2.4	177301	9	AC103949	Homo sapi
124	60.6	2.6	331039	3	AC116979	AC116979 Dictyoste	197	56.6	2.4	196762	2	CR759796	Danio rer
125	60.2	2.5	176837	2	CR392355	CR392355 Danio rer	c 198	56.4	2.4	158697	9	AL133281	Human DNA
126	60.2	2.5	250611	2	CR762484	CR762484 Danio rer	c 199	56.4	2.4	164443	2	CR751221	Danio rer
127	60	2.5	60	6	CQ541234	CQ541234 Sequence	c 200	56.4	2.4	230890	2	BX537109	Danio rer
128	60	2.5	162401	2	AC024024	AC024024 Homo sapi	c 201	56.4	2.4	348034	3	CR382400	Plasmoidiu
129	60	2.5	174311	2	CR678065	CR678065 Danio rer	c 202	56.2	2.4	104992	2	AC005504	Plasmoidiu
130	60	2.5	250053	3	AE014825	AE014825 Plasmoidiu	c 203	56.2	2.4	142275	2	CR788316	Danio rer
131	60	2.5	341050	3	PFA929357	AL929357 Plasmoidiu	c 204	56.2	2.4	169546	2	AC004157	Plasmoidiu
132	59.6	2.5	169800	2	CR847821	CR847821 Danio rer	c 205	56.2	2.4	190015	3	AE0140056	Rattus no
133	59.6	2.5	192320	2	CR762470	CR762470 Danio rer	c 206	56.2	2.4	250421	3	AE014849	Plasmoidiu
134	59.4	2.5	5074	3	AY171199	AY171199 Caenorhab	c 207	56.2	2.4	347050	3	PFA929351	Plasmoidiu
135	59.4	2.5	5074	3	AY171203	AY171203 Caenorhab	c 208	56	2.4	192581	2	PFMAL13P1	Plasmoidiu
136	59.4	2.5	5074	3	AY171204	AY171204 Caenorhab	c 209	56	2.4	214773	2	CR7597236	Danio rer
137	59.4	2.5	5074	3	AY171206	AY171206 Caenorhab	c 210	56	2.4	220158	2	CR678095	Danio rer
138	59.4	2.5	5074	3	AY171207	AY171207 Caenorhab	c 211	56	2.4	251551	3	AE014844	Plasmoidiu
139	59.4	2.5	5075	3	AY171194	AY171194 Caenorhab	c 212	56	2.4	1348	8	AY187636	Modiola c
140	59.4	2.5	5075	3	AY171196	AY171196 Caenorhab	c 213	55.8	2.4	8056	6	AX599046	Sequence
141	59.4	2.5	13794	3	MTCE	X54522 Caenorhabdi	c 214	55.8	2.4	38692	3	AC116919	Dictyoste
142	59.4	2.5	150199	9	AC087568	AC087568 Pan trogl	c 215	55.8	2.4	105686	9	AC012072	Homo sapi
143	59	2.5	76568	3	MBREV	AF538053 Monosiga	c 216	55.8	2.4	110000	2	PFMAL13_01	Continuation (2 of
144	59	2.5	156721	9	AC026839	AC026839 Homo sapi	c 217	55.8	2.4	120192	2	AC093220	Homo sapi
145	59	2.5	220495	9	AP000886	AP000886 Homo sapi	c 218	55.8	2.4	150209	2	CR759744	Danio rer
146	58.8	2.5	199551	2	AC006281	AC006281 Plasmoidiu	c 219	55.8	2.4	170796	2	AC069416	Homo sapi
147	58.8	2.5	251551	3	AE014844	AE014844 Plasmoidiu	c 220	55.8	2.4	15007	3	AB075955	Ixodes ho
148	58.6	2.5	5075	3	AY171198	AY171198 Caenorhab	c 221	55.6	2.3	152158	2	CR649301	Danio rer
149	58.6	2.5	131459	8	AL391538	AL391538 Human DNA	c 222	55.6	2.3	159835	2	CR87984	Danio rer
150	58.6	2.5	180915	9	GTAP10592	AL010592 Guillard	c 223	55.6	2.3	168153	2	CR628407	Danio rer
151	58.6	2.5	330050	3	PFA929355	AL529355 Plasmoidiu	c 224	55.6	2.3	172777	2	CR847809	Danio rer
152	58.2	2.5	164481	2	CR759908	CR759908 Danio rer	c 225	55.6	2.3	180765	2	CR407593	Danio rer
153	58	2.4	146570	3	AC117076	AC117076 Dictyoste	c 226	55.6	2.3	186431	2	AC022281	Homo sapi
154	58	2.4	250029	3	AE014838	AE014838 Plasmoidiu	c 227	55.6	2.3	190482	2	CR450828	Danio rer
155	58	2.4	349580	6	AX344572	AX344572 Sequence	c 228	55.6	2.3	223904	2	CR759864	Danio rer
156	57.8	2.4	5074	3	AY171202	AY171202 Caenorhab	c 229	55.6	2.3	251762	3	AE014851	Plasmoidiu
157	57.8	2.4	5075	3	AY171200	AY171200 Caenorhab	c 230	55.6	2.3	266371	2	AC020619	Mus muscu
158	57.8	2.4	33361	3	AF298624	AF298624 Dictyoste	c 231	55.6	2.3	310779	2	AC005140	Plasmoidiu
159	57.8	2.4	62268	9	HS1178121	AL109852 Human DNA	c 232	55.6	2.3	1368	5	CR386646	Gallus ga
160	57.8	2.4	154071	3	AC115598	AC115598 Dictyoste	c 233	55.4	2.3	2035	5	AF153205	Sequence
161	57.8	2.4	207516	9	AC097108	AC097108 Homo sapi	c 234	55.4	2.3	7218	6	I66494	Sequence
162	57.8	2.4	254050	3	PFA929358	AL929358 Plasmoidiu	c 235	55.4	2.3	110000	2	PFMAL7P1_09	Continuation (10 o
163	57.6	2.4	110000	2	PFMAL8P1_06	Continuation (7 of	c 236	55.4	2.3	169357	2	CR847871	Danio rer
164	57.6	2.4	170929	2	CR759865	CR759865 Danio rer	c 237	55.4	2.3	169357	2	CR847871	Danio rer
165	57.6	2.4	219461	2	BX842685	BX842685 Danio rer	c 238	55.4	2.3	169357	2	CR847871	Danio rer



C 239	55.4	2.3 181713	2	CR847903	CR847903	Danio rer
C 240	55.4	2.3 232548	2	AC125209	Mus muscu	
C 241	55.4	2.3 250078	3	AE014829	Plasmodiu	
C 242	55.4	2.3 349174	1	AB063322	Wiggleswo	
C 243	55.4	2.3 8056	6	AX599046	Sequence	
C 244	55.2	2.3 28862	9	AC012398	Homo sapi	
C 245	55.2	2.3 85779	8	SCF011856	AX011856	Saccharom
C 246	55.2	2.3 105940	9	AC010606	Homo sapi	
C 247	55.2	2.3 110000	8	CR382138_22	Continuation (23 o	
C 248	55.2	2.3 133877	2	AC120883	Homo sapi	
C 249	55.2	2.3 135121	9	AC069525	Homo sapi	
C 250	55.2	2.3 136098	9	AC006970	Homo sapi	
C 251	55.2	2.3 150199	9	AC087568	Pan trogl	
C 252	55.2	2.3 159066	9	AC103557	Homo sapi	
C 253	55.2	2.3 176906	2	CR354387	CR354387	Danio rer
C 254	55.2	2.3 182870	3	AC116960	Dictyoste	
C 255	55.2	2.3 223509	3	CR388007	CR388007	Danio rer
C 256	55.2	2.3 337203	3	CR382401	Plasmodiu	
C 257	55	2.3 1894	3	PF4428569	AX428569	Sequence
C 258	55	2.3 83391	6	AX458577	AX458577	Sequence
C 259	55	2.3 89086	9	AC104373	Homo sapi	
C 260	55	2.3 125744	5	AL954387	AL954387	Zebrafish
C 261	55	2.3 159603	2	CR762422	Danio rer	
C 262	55	2.3 163809	2	CR392044	CR392044	Danio rer
C 263	55	2.3 170668	9	AC104012	Homo sapi	
C 264	55	2.3 176142	2	CR388010	CR388010	Danio rer
C 265	55	2.3 197951	2	CR392343	Danio rer	
C 266	55	2.3 254050	3	PF49229358	AL929358	Plasmodiu
C 267	54.8	2.3 7079	3	AF3622375	Dictyoste	
C 268	54.8	2.3 14001	3	PF001018	X95276 P.falci	paru
C 269	54.8	2.3 41399	3	AC116984_5	Continuation (6 of	
C 270	54.8	2.3 110000	8	CR382131_03	Continuation (4 of	
C 271	54.8	2.3 120029	2	HSU282H10	AL332672	Homo sapi
C 272	54.8	2.3 154675	2	CR354440	CR354440	Danio rer
C 273	54.8	2.3 161641	9	AC109464	CR109464	Homo sapi
C 274	54.8	2.3 204430	2	CR792453	Danio rer	
C 275	54.8	2.3 225612	2	AC117641	AC117641	Mus muscu
C 276	54.8	2.3 246589	2	CR450749	CR450749	Danio rer
C 277	54.8	2.3 287510	2	CR753823	CR753823	Danio rer
C 278	54.8	2.3 348600	1	AB063521	AB063521	Wiggleswo
C 279	54.8	2.3 348600	1	AB063521	Wiggleswo	
C 280	54.6	2.3 33651	3	AC114261	Dictyoste	
C 281	54.6	2.3 34335	9	AC126776	AC126776	Homo sapi
C 282	54.6	2.3 84550	3	PFMAL1p2_3	Continuation (4 of	
C 283	54.6	2.3 110000	2	PFMAL1p3_23	Continuation (25 o	
C 284	54.6	2.3 110000	2	PFMAL1p3_24	Continuation (24 o	
C 285	54.6	2.3 110000	2	PFMAL1p1_05	Continuation (6 of	
C 286	54.6	2.3 155609	2	BX327284	CR387986	Danio rer
C 287	54.6	2.3 156395	2	CR387986	CR387986	Danio rer
C 288	54.6	2.3 163735	9	AC027277	AC027277	Homo sapi
C 289	54.6	2.3 163930	2	CR847885	CR847885	Danio rer
C 290	54.6	2.3 175559	2	AC145101	AC145101	Homo sapi
C 291	54.6	2.3 191191	2	CR847965	CR847965	Danio rer
C 292	54.6	2.3 211748	2	CR392346	CR392346	Danio rer
C 293	54.6	2.3 236823	2	CR394523	CR394523	Danio rer
C 294	54.6	2.3 245802	2	AC006279	AC006279	Plasmodiu
C 295	54.6	2.3 250029	3	AE014839	AE014839	Plasmodiu
C 296	54.6	2.3 250195	3	AE014831	Plasmodiu	
C 297	54.6	2.3 251762	3	AE014851	Plasmodiu	
C 298	54.6	2.3 251797	2	BX890543	BX890543	Danio rer
C 299	54.6	2.3 257570	2	CR354431	Danio rer	
C 300	54.6	2.3 260929	3	AE014852	Plasmodiu	
C 301	54.6	2.3 271546	3	AE014843	Plasmodiu	
C 302	54.6	2.3 287510	2	CR753823	CR753823	Danio rer
C 303	54.6	2.3 310779	2	AC005140	AC005140	Plasmodiu
C 304	54.4	2.3 110000	2	BX890596_1	Continuation (2 of	
C 305	54.4	2.3 110000	2	PFMAL1p3_04	Continuation (5 of	
C 306	54.4	2.3 125632	2	CR753868	CR753868	Danio rer
C 307	54.4	2.3 163167	9	AC099784	AC099784	Homo sapi
C 308	54.4	2.3 167592	2	CR847845	CR847845	Danio rer
C 309	54.4	2.3 170195	9	AC025452	AC025452	Homo sapi
C 310	54.4	2.3 175356	2	CR354555	Danio rer	
C 311	54.4	2.3 250029	3	AE014816	AE014816	Plasmodiu
C 312	54.4	2.3 261771	2	CR356223	CR356223	Danio rer
C 313	54.4	2.3 290874	2	CR847807	CR847807	Danio rer
C 314	54.4	2.3 293431	2	PFMAL1p34	PFMAL1p34	Plasmodiu
C 315	54.2	2.3 5075	3	AY171193	AY171193	Caenorhab
C 316	54.2	2.3 8622	8	YSMTCTYOC	YSMTCTYOC	Sequence
C 317	54.2	2.3 15373	6	AX345369	AX345369	Sequence
C 318	54.2	2.3 17470	3	AE001402	Plasmodiu	
C 319	54.2	2.3 85779	8	SCF011856	AX011856	Saccharom
C 320	54.2	2.3 110000	2	CR555291_2	Continuation (3 of	
C 321	54.2	2.3 154071	3	AC115598	AC115598	Dictyoste
C 322	54.2	2.3 154948	2	AC141985	AC141985	Rattus no
C 323	54.2	2.3 166014	2	CR762396	CR762396	Danio rer
C 324	54.2	2.3 169979	2	AX901942	AX901942	Danio rer
C 325	54.2	2.3 170534	2	CR391918	CR391918	Danio rer
C 326	54.2	2.3 173021	9	AC146376	AC146376	Pan trogl
C 327	54.2	2.3 174198	2	CR762438	CR762438	Danio rer
C 328	54.2	2.3 185409	9	AC018758	AC018758	Homo sapi
C 329	54.2	2.3 196613	2	CR735105	CR735105	Danio rer
C 330	54.2	2.3 349174	1	AB063522	AB063522	Wiggleswo
C 331	54	2.3 25769	3	AC117267	AC117267	Dictyoste
C 332	54	2.3 66448	9	AC091286	AC091286	Homo sapi
C 333	54	2.3 87845	9	AL583860	AL583860	Human DNA
C 334	54	2.3 113053	8	ATF12B17	ATF12B17	Arabidops
C 335	54	2.3 144765	2	CR759966	CR759966	Danio rer
C 336	54	2.3 158813	9	AC080091	AC080091	Homo sapi
C 337	54	2.3 163797	2	CR847851	CR847851	Danio rer
C 338	54	2.3 169850	2	CR847949	CR847949	Danio rer
C 339	54	2.3 250793	2	CR388030	CR388030	Danio rer
C 340	53.8	2.3 1905	3	AF336303	AF336303	Oestrinia
C 341	53.8	2.3 11790	6	AX345444	AX345444	Sequence
C 342	53.8	2.3 24036	3	CR55354A	CR55354A	Caenorhab
C 343	53.8	2.3 89665	9	AC063976	AC063976	Homo sapi
C 344	53.8	2.3 110000	2	AC116984_1	Continuation (2 of	
C 345	53.8	2.3 163660	2	AC046165	AC046165	Homo sapi
C 346	53.8	2.3 163930	2	CR847885	CR847885	Danio rer
C 347	53.8	2.3 170966	5	BX000091	BX000091	Zebrafish
C 348	53.8	2.3 174001	2	BX927081	BX927081	Danio rer
C 349	53.8	2.3 175959	2	AL450429	AL450429	Homo sapi
C 350	53.8	2.3 190058	2	CR628384	CR628384	Danio rer
C 351	53.8	2.3 198047	2	CR376763	CR376763	Danio rer
C 352	53.8	2.3 252632	3	AE014818	Plasmodiu	
C 353	53.8	2.3 254436	3	AE014827	Plasmodiu	
C 354	53.8	2.3 349418	3	CR382398	CR382398	Plasmodiu
C 355	53.8	2.3 349751	3	PFMAL1p3	PFMAL1p3	Plasmodiu
C 356	53.6	2.3 631	3	JALMTTGMDBL	LI6849 Jalmenus ev	
C 357	53.6	2.3 700	6	AX183285	AX183285	Sequence
C 358	53.6	2.3 46491	8	AP005666	AP005666	Lotus cor
C 359	53.6	2.3 48488	3	AF106589	AF106589	Caenorhab
C 360	53.6	2.3 88295	9	AC004612	AC004612	Homo sapi
C 361	53.6	2.3 110000	2	PFMAL1p1_08	Continuation (9 of	
C 362	53.6	2.3 110000	3	AC116305_3	Continuation (4 of	
C 363	53.6	2.3 112811	5	BX005301_3	BX005301	Zebrafish
C 364	53.6	2.3 147056	2	CR846095	CR846095	Danio rer
C 365	53.6	2.3 152224	2	AC141680	AC141680	Apis mell
C 366	53.6	2.3 155024	5	BX649446	BX649446	Zebrafish
C 367	53.6	2.3 156851	2	CR751546	CR751546	Danio rer
C 368	53.6	2.3 157865	2	CR450836	CR450836	Danio rer
C 369	53.6	2.3 167320	2	CR450810	CR450810	Danio rer
C 370	53.6	2.3 178427	2	CR392006	CR392006	Danio rer
C 371	53.6	2.3 203595	2	CR385054	CR385054	Danio rer
C 372	53.6	2.3 205190	2	CR391979	CR391979	Danio rer
C 373	53.6	2.3 205828	2	BX649409	BX649409	Danio rer
C 374	53.6	2.3 250029	3	AE014820	Plasmodiu	
C 375	53.6	2.3 271546	3	AE014843	AE014843	Plasmodiu
C 376	53.6	2.3 297798	2	CR396591	CR396591	Danio rer
C 377	53.4	2.3 403	3	AF102765	AF102765	Mirax sp.
C 378	53.4	2.3 1156	9	AF044862	AF044862	Phoebis a
C 379	53.4	2.3 1192	9	HS323759	HS323759	Homo sapi
C 380	53.4	2.3 110000	2	PFMAL1p1_07	Continuation (8 of	
C 381	53.4	2.3 110000	3	PFMAL1p2_1	Continuation (2 of	
C 382	53.4	2.3 121024	8	CHMPX	X04465	Marchantia
C 383	53.4	2.3 155490	2	CR749749	CR749749	Danio rer
C 384	53.4	2.3 160645	2	CR391949	CR391949	Danio rer



C 531	52	2.2	250029	3	AE014830	AE014830 Plasmodiu	C 604	51.4	2.2	145553	5	AL935272	AL935272 Zebrafish
C 532	52	2.2	250053	3	AE014825	AE014825 Plasmodiu	605	51.4	2.2	150882	5	CR392344	CR392344 Zebrafish
C 533	52	2.2	250823	3	AE014821	AE014821 Plasmodiu	606	51.4	2.2	151391	9	HSJ730H16	AL220006 Human DNA
C 534	51.8	2.2	721	3	AMU35790	UF5790 Anopheles m	C 607	51.4	2.2	155076	2	CR391987	Danio rer
C 535	51.8	2.2	809	3	AF293659	AF293659 Anopheles m	608	51.4	2.2	155176	2	AC084716	Homo sapi
C 536	51.8	2.2	9632	6	AX345558	AX345558 Sequence	C 609	51.4	2.2	157845	5	AX005079	Zebrafish
C 537	51.8	2.2	96630	9	AC120055	AC120055 Homo sapi	610	51.4	2.2	157845	2	CR376741	Danio rer
C 538	51.8	2.2	103344	9	HS1108E15	AL035551 Human DNA	C 611	51.4	2.2	174225	5	AX005071	Zebrafish
C 539	51.8	2.2	110000	2	PFMAL13_25	Continuation (26 o	C 612	51.4	2.2	174741	9	AC040977	Homo sapi
C 540	51.8	2.2	110000	2	PFMAL13_00	AL844507 Plasmodiu	C 613	51.4	2.2	176032	2	AX510656	Danio rer
C 541	51.8	2.2	110000	3	PFMAL13_09	Continuation (10 o	C 614	51.4	2.2	179266	2	CR847966	Danio rer
C 542	51.8	2.2	110000	3	AC116957_1	Continuation (2 of	C 615	51.4	2.2	183498	5	AX072578	Zebrafish
C 543	51.8	2.2	114000	5	AX572104_1	BS072104 Zebrafish	C 616	51.4	2.2	198301	8	ATCHRIV31	Arabidops
C 544	51.8	2.2	138342	2	CR376794	CR376794 Danio rer	C 617	51.4	2.2	198296	2	CR753895	Danio rer
C 545	51.8	2.2	142012	9	AL591428	AL591428 Human DNA	C 618	51.4	2.2	205807	2	CR388418	Danio rer
C 546	51.8	2.2	148394	2	CR753884	CR753884 Danio rer	C 619	51.4	2.2	206216	2	AC148586	Pan trogl
C 547	51.8	2.2	156975	2	CR394534	CR394534 Danio rer	C 620	51.4	2.2	216721	2	AX901924	Homo sapi
C 548	51.8	2.2	162954	2	AX548252	AX548252 Danio rer	C 621	51.4	2.2	245072	2	CR381551	Danio rer
C 549	51.8	2.2	163377	9	BS000042	BS000042 Pan trogl	C 622	51.4	2.2	243050	3	PF8929353	Plasmodiu
C 550	51.8	2.2	166719	9	AC136957	AC136957 Homo sapi	C 623	51.4	2.2	349980	6	AX344569	Sequence 68
C 551	51.8	2.2	170597	9	CNS01DRR	AL118556 Human chr	C 624	51.2	2.2	724	6	AR155517	Sequence
C 552	51.8	2.2	180629	2	CR388025	CR388025 Danio rer	C 625	51.2	2.2	724	6	AR155517	Sequence
C 553	51.8	2.2	185926	5	AX548066	AX548066 Zebrafish	C 626	51.2	2.2	724	6	E66042	Genome DNA
C 554	51.8	2.2	198434	9	AC109994	AC109994 Homo sapi	C 627	51.2	2.2	738	8	AF264668	Cryptomit
C 555	51.8	2.2	209491	2	CR392365	CR392365 Danio rer	C 628	51.2	2.2	963	8	YSCMTRP2	YSCMTRP2
C 556	51.8	2.2	212528	2	AX914719	AX914719 Danio rer	C 629	51.2	2.2	1536	3	AF503869	AF503869 Plasmodiu
C 557	51.8	2.2	212881	2	CR450705	CR450705 Danio rer	C 630	51.2	2.2	2305	3	DTMTRNA	AX54011 D.teissi
C 558	51.8	2.2	245072	2	CR381551	CR381551 Danio rer	C 631	51.2	2.2	4601	3	DMU37541	DMU37541 Drosophila
C 559	51.8	2.2	248140	2	AX901898	AX901898 Danio rer	C 632	51.2	2.2	19517	3	PMU37541	PMU37541 Drosophila
C 560	51.8	2.2	346940	2	AC107420	AC107420 Homo sapi	C 633	51.2	2.2	67970	3	PFMAL1P3	PFMAL1P3 Plasmodiu
C 561	51.6	2.2	715	3	AMU35794	U35794 Anopheles m	C 634	51.2	2.2	71217	9	AL590306	AL590306 Human DNA
C 562	51.6	2.2	1809	1	AF267221	AF267221 Candidatu	C 635	51.2	2.2	73639	2	AC055834	AC055834 Homo sapi
C 563	51.6	2.2	9424	8	SDO404228	AX404228 Saccharom	C 636	51.2	2.2	104791	9	AC084364	AC084364 Homo sapi
C 564	51.6	2.2	16750	6	AX251068	AX251068 Sequence	C 637	51.2	2.2	108902	2	AC011430	AC011430 Homo sapi
C 565	51.6	2.2	16750	6	AX345423	AX345423 Sequence	C 638	51.2	2.2	110000	3	AC116305_1	AC091145 Homo sapi
C 566	51.6	2.2	47812	9	HS12714	Z83839 Human DNA	C 639	51.2	2.2	122986	3	AC004915	AC004915 Homo sapi
C 567	51.6	2.2	73666	9	HS3333B15	AL109954 Human DNA	C 640	51.2	2.2	125623	3	AC115599	AC115599 Dictyoste
C 568	51.6	2.2	89357	9	AC109472	AC109472 Homo sapi	C 641	51.2	2.2	147640	5	AX323035	AX323035 Zebrafish
C 569	51.6	2.2	91012	2	AC147363	AC147363 Medicago	C 642	51.2	2.2	151802	3	AC114263	AC114263 Dictyoste
C 570	51.6	2.2	101628	9	AF130350	AF130350 Homo sapi	C 643	51.2	2.2	152878	3	CEY18D10A	AL034393 Caenorhab
C 571	51.6	2.2	110000	2	PFMAL7P1_08	Continuation (9 of	C 644	51.2	2.2	160645	2	CR391949	Danio rer
C 572	51.6	2.2	110621	2	CR762468	CR762468 Danio rer	C 645	51.2	2.2	164262	2	AC147723	AC147723 Pongo pyg
C 573	51.6	2.2	113880	3	PFMAL3P4	AL008970 Plasmodiu	C 646	51.2	2.2	167336	2	AC021350	AC021350 Homo sapi
C 574	51.6	2.2	118018	9	AF227510	AF227510 Homo sapi	C 647	51.2	2.2	168054	2	AX936460	AX936460 Danio rer
C 575	51.6	2.2	151151	5	AX005294	AX005294 Zebrafish	C 648	51.2	2.2	168103	2	CR751601	CR751601 Danio rer
C 576	51.6	2.2	151370	9	AC147148	AC147148 Pan trogl	C 649	51.2	2.2	168538	5	AX537314	AX537314 Zebrafish
C 577	51.6	2.2	153477	2	AC006278	AC006278 Plasmodiu	C 650	51.2	2.2	168686	9	AC097066	AC097066 Homo sapi
C 578	51.6	2.2	156849	2	CR405684	CR405684 Danio rer	C 651	51.2	2.2	169842	2	AX914195	AX914195 Homo sapi
C 579	51.6	2.2	170664	5	AX276096	AX276096 Zebrafish	C 652	51.2	2.2	172288	2	AC138859	AC138859 Homo sapi
C 580	51.6	2.2	180346	9	AC092615	AC092615 Homo sapi	C 653	51.2	2.2	174765	2	AC073103	AC073103 Homo sapi
C 581	51.6	2.2	181381	2	CR450818	CR450818 Danio rer	C 654	51.2	2.2	175959	2	AL450429	AL450429 Homo sapi
C 582	51.6	2.2	181792	9	AC098822	AC098822 Homo sapi	C 655	51.2	2.2	180450	3	AE014835	AE014835 Plasmodiu
C 583	51.6	2.2	197054	2	CR450840	CR450840 Danio rer	C 656	51.2	2.2	182738	2	CR407564	CR407564 Danio rer
C 584	51.6	2.2	209195	5	AL954309	AL954309 Zebrafish	C 657	51.2	2.2	185085	2	CR762404	CR762404 Danio rer
C 585	51.6	2.2	217307	2	AX324165	AX324165 Danio rer	C 658	51.2	2.2	185926	5	AX548066	AX548066 Zebrafish
C 586	51.6	2.2	256172	2	AC005139	AC005139 Plasmodiu	C 659	51.2	2.2	209515	2	AX571687	AX571687 Danio rer
C 587	51.6	2.2	311860	2	AX537353	AX537353 Danio rer	C 660	51.2	2.2	213891	2	CR387983	CR387983 Homo sapi
C 588	51.6	2.2	340000	9	HS21C048	AL163248 Homo sapi	C 661	51.2	2.2	237869	5	AX537326	AX537326 Zebrafish
C 589	51.6	2.2	349980	6	AX951695	AX951695 Sequence	C 662	51.2	2.2	253924	3	AE014822	AE014822 Plasmodiu
C 590	51.4	2.2	1449	3	AF151384	AF151384 Cochliomy	C 663	51	2.2	1141	6	AX083744	AX083744 Sequence
C 591	51.4	2.2	6591	8	YSCMTCG06	L38890 Saccharomyc	C 664	51	2.2	19209	1	AF274444	AF274444 Carsonell
C 592	51.4	2.2	17429	3	PF13PB1	AE001416 Plasmodiu	C 665	51	2.2	20579	6	AX458558	AX458558 Sequence
C 593	51.4	2.2	18168	3	PF13PB1	AL929365 Plasmodiu	C 666	51	2.2	64394	9	AL928596	AL928596 Human DNA
C 594	51.4	2.2	18556	9	AY527817	AY527817 Homo sapi	C 667	51	2.2	79170	9	AC026705	AC026705 Homo sapi
C 595	51.4	2.2	47601	9	AC078802	AC078802 Homo sapi	C 668	51	2.2	92348	5	AL935295	AL935295 Zebrafish
C 596	51.4	2.2	47916	8	YL1307410	AJ307410 Yarrowia	C 669	51	2.2	94384	9	AC011718	AC011718 Homo sapi
C 597	51.4	2.2	53932	2	AC023371	AC023371 Homo sapi	C 670	51	2.2	110000	2	AX649285_0	AX649285 Danio rer
C 598	51.4	2.2	74406	8	F2P3	AF080120 Arabidops	C 671	51	2.2	110000	2	PFMAL7P1_02	Continuation (3 of
C 599	51.4	2.2	87731	9	AT105148	AL05148 Arabidops	C 672	51	2.2	110000	3	PFMAL7P1_05	Continuation (6 of
C 600	51.4	2.2	108598	8	ATT2284	AL049876 Arabidops	C 673	51	2.2	110000	3	AC116957_1	Continuation (2 of
C 601	51.4	2.2	115990	5	AX890614	AX890614 Zebrafish	C 674	51	2.2	110001	9	AX005439	AX005439 Human DNA
C 602	51.4	2.2	116810	9	AC112657	AC112657 Homo sapi	C 675	51	2.2	127560	5	AX005077	AX005077 Zebrafish
C 603	51.4	2.2	145306	2	AX8999179	AX8999179 Danio rer	C 676	51	2.2	134597	2	CR391983	CR391983 Danio rer

c 677	51	2.2	150671	2	CR847829	Danio rer	CR847829	Danio rer	c 750	50.6	2.1	159593	9	AC004832	Homo sapi	AC004832	Homo sapi
c 678	51	2.2	151391	9	HSJ730H16	Human DNA	AL122006	Human DNA	c 751	50.6	2.1	159693	10	AL646042	Mouse DNA	AL646042	Mouse DNA
c 679	51	2.2	151932	2	CR450747	Danio rer	CR450747	Danio rer	752	50.6	2.1	162929	5	BX323842	Zebrafish	BX323842	Zebrafish
c 680	51	2.2	160891	9	AL512410	Human DNA	AL512410	Human DNA	753	50.6	2.1	164219	5	EX005205	Zebrafish	EX005205	Zebrafish
c 681	51	2.2	161444	2	BX897740	Danio rer	BX897740	Danio rer	754	50.6	2.1	167054	9	AP006303	Homo sapi	AP006303	Homo sapi
c 682	51	2.2	166076	2	AC114292	Homo sapi	AC114292	Homo sapi	755	50.6	2.1	168637	5	AL844187	Zebrafish	AL844187	Zebrafish
c 683	51	2.2	169418	9	AC104163	Homo sapi	AC104163	Homo sapi	756	50.6	2.1	169895	2	CR396587	Danio rer	CR396587	Danio rer
c 684	51	2.2	172036	9	AC046181	Homo sapi	AC046181	Homo sapi	757	50.6	2.1	171382	2	CR392331	Danio rer	CR392331	Danio rer
c 685	51	2.2	175216	5	BX276115	Zebrafish	BX276115	Zebrafish	758	50.6	2.1	172816	9	AC093899	Homo sapi	AC093899	Homo sapi
c 686	51	2.2	177152	9	BX544879	Human DNA	BX544879	Human DNA	759	50.6	2.1	172880	9	AC027419	Homo sapi	AC027419	Homo sapi
c 687	51	2.2	179223	2	AC141463	Homo sapi	AC141463	Homo sapi	c 760	50.6	2.1	173532	2	AC040890	Homo sapi	AC040890	Homo sapi
c 688	51	2.2	180450	3	AE014835	Plasmid	AE014835	Plasmid	761	50.6	2.1	173611	2	CR846100	Danio rer	CR846100	Danio rer
c 689	51	2.2	183648	3	AC117081	Dictyoste	AC117081	Dictyoste	762	50.6	2.1	179641	2	AC119139	Rattus no	AC119139	Rattus no
c 690	51	2.2	226020	2	AC087689	Homo sapi	AC087689	Homo sapi	c 763	50.6	2.1	181792	2	CR388184	Danio rer	CR388184	Danio rer
c 691	51	2.2	230844	5	AL954831	Zebrafish	AL954831	Zebrafish	764	50.6	2.1	182666	2	AL929172	Zebrafish	AL929172	Zebrafish
c 692	51	2.2	243066	2	AC120999	Rattus no	AC120999	Rattus no	c 765	50.6	2.1	184431	2	CR628331	Danio rer	CR628331	Danio rer
c 693	51	2.2	257570	2	CR354431	Danio rer	CR354431	Danio rer	c 766	50.6	2.1	187174	9	AC109484	Homo sapi	AC109484	Homo sapi
c 694	51	2.2	257570	3	AE014837	Plasmid	AE014837	Plasmid	767	50.6	2.1	187523	5	BX005369	Zebrafish	BX005369	Zebrafish
c 695	51	2.2	302156	3	AC116977	Dictyoste	AC116977	Dictyoste	768	50.6	2.1	192265	9	CNS018P3	Human chr	AL110118	Human chr
c 696	51	2.2	341050	3	PFA929357	Plasmid	AL929357	Plasmid	c 769	50.6	2.1	193793	9	AC099780	Homo sapi	AC099780	Homo sapi
c 697	51	2.2	348174	3	CR832399	Plasmid	CR832399	Plasmid	770	50.6	2.1	197913	2	BX572087	Danio rer	BX572087	Danio rer
c 698	50.8	2.1	1192	9	HA3323759	Homo sapi	AL323759	Homo sapi	c 771	50.6	2.1	224076	2	AC084019	Mus muscu	AC084019	Mus muscu
c 699	50.8	2.1	4601	3	DMU11584	Drosophila	U11584	Drosophila	772	50.6	2.1	233296	2	CR318636	Danio rer	CR318636	Danio rer
c 700	50.8	2.1	5407	6	AX346992	Sequence	AX346992	Sequence	c 773	50.6	2.1	249943	3	AE014823	Plasmid	AE014823	Plasmid
c 701	50.8	2.1	15470	3	AC117073	Dictyoste	AC117073	Dictyoste	774	50.6	2.1	249943	3	AE014840	Plasmid	AE014840	Plasmid
c 702	50.8	2.1	18724	3	AC115605	Dictyoste	AC115605	Dictyoste	775	50.6	2.1	251448	3	AE014819	Plasmid	AE014819	Plasmid
c 703	50.8	2.1	19517	3	DMU37541	Drosophila	U37541	Drosophila	c 776	50.6	2.1	253151	3	AE014842	Plasmid	AE014842	Plasmid
c 704	50.8	2.1	72808	8	AC007660	Arabidops	AC007660	Arabidops	c 777	50.6	2.1	333321	3	AC116986	Dictyoste	AC116986	Dictyoste
c 705	50.8	2.1	89807	2	CR536602	Danio rer	CR536602	Danio rer	c 778	50.6	2.1	347582	3	PFMAL4P1	Plasmid	AL034557	Plasmid
c 706	50.8	2.1	100697	5	AL672072	Zebrafish	AL672072	Zebrafish	c 779	50.4	2.1	560	8	MISC26	Yeast mitoc	X00887	Yeast mitoc
c 707	50.8	2.1	105682	3	AC116992	Continuation (4 of	Continuation (4 of	Continuation (4 of	c 780	50.4	2.1	2353	9	HSM801942	Homo sapi	U60086	Dictyosteli
c 708	50.8	2.1	105673	9	AP002091	Homo sapi	AP002091	Homo sapi	c 781	50.4	2.1	5890	3	DDU60086	Homo sapi	U60086	Dictyosteli
c 709	50.8	2.1	110000	3	PFMAL13_19	Continuation (20 of	Continuation (20 of	Continuation (20 of	c 782	50.4	2.1	8056	6	AX598900	Sequence	AX598900	Sequence
c 710	50.8	2.1	110000	3	AC116984_4	Continuation (5 of	Continuation (5 of	Continuation (5 of	c 783	50.4	2.1	12237	6	AX347260	Sequence	AX347260	Sequence
c 711	50.8	2.1	129020	8	AP004871	Oryza sat	AP004871	Oryza sat	c 784	50.4	2.1	20063	8	CGLS11533	Candida g	AU51533	Candida g
c 712	50.8	2.1	136098	9	AC006970	Homo sapi	AC006970	Homo sapi	785	50.4	2.1	110000	2	PFMAL8P1_03	Continuation (4 of	Continuation (4 of	Continuation (4 of
c 713	50.8	2.1	146841	9	AC020549	Homo sapi	AC020549	Homo sapi	786	50.4	2.1	110000	3	AC116305_1	Continuation (2 of	Continuation (2 of	Continuation (2 of
c 714	50.8	2.1	149720	2	AC135210	Danio rer	AC135210	Danio rer	787	50.4	2.1	121958	2	CR759861	Danio rer	CR759861	Danio rer
c 715	50.8	2.1	154591	5	BX510907	Zebrafish	BX510907	Zebrafish	c 788	50.4	2.1	14124	5	AL845435	Zebrafish	AL845435	Zebrafish
c 716	50.8	2.1	157865	2	CR450836	Danio rer	CR450836	Danio rer	c 789	50.4	2.1	141861	2	CR318612	Danio rer	CR318612	Danio rer
c 717	50.8	2.1	167953	2	AC010948	Homo sapi	AC010948	Homo sapi	c 790	50.4	2.1	146570	3	AC117076	Dictyoste	AC117076	Dictyoste
c 718	50.8	2.1	169250	5	BX511251	Zebrafish	BX511251	Zebrafish	c 791	50.4	2.1	148978	2	AL391536	Homo sapi	AL391536	Homo sapi
c 719	50.8	2.1	172399	2	CR762388	Danio rer	CR762388	Danio rer	c 792	50.4	2.1	157011	2	AC140115	Rattus no	AC140115	Rattus no
c 720	50.8	2.1	173012	9	AC040170	Homo sapi	AC040170	Homo sapi	c 793	50.4	2.1	157293	2	AL441926	Homo sapi	AL441926	Homo sapi
c 721	50.8	2.1	173532	2	AC040890	Homo sapi	AC040890	Homo sapi	794	50.4	2.1	159603	2	CR762422	Danio rer	CR762422	Danio rer
c 722	50.8	2.1	177578	2	CR846089	Danio rer	CR846089	Danio rer	795	50.4	2.1	160432	5	AL925072	Zebrafish	AL925072	Zebrafish
c 723	50.8	2.1	180395	5	AL844152	Zebrafish	AL844152	Zebrafish	796	50.4	2.1	173320	9	AC068787	Homo sapi	AC068787	Homo sapi
c 724	50.8	2.1	181794	2	AC145186	Bos tauru	AC145186	Bos tauru	797	50.4	2.1	192389	2	CR751229	Danio rer	CR751229	Danio rer
c 725	50.8	2.1	184524	2	CR376827	Danio rer	CR376827	Danio rer	c 798	50.4	2.1	196168	2	CR376839	Danio rer	CR376839	Danio rer
c 726	50.8	2.1	188777	2	CR774179	Danio rer	CR774179	Danio rer	c 799	50.4	2.1	210548	2	CR815608	Danio rer	CR815608	Danio rer
c 727	50.8	2.1	189756	9	AC092327	Homo sapi	AC092327	Homo sapi	c 800	50.4	2.1	210806	2	CR812928	Danio rer	CR812928	Danio rer
c 728	50.8	2.1	193324	2	AC147653	Pan trogl	AC147653	Pan trogl	c 801	50.4	2.1	219753	2	AC108723	Homo sapi	AC108723	Homo sapi
c 729	50.8	2.1	199027	2	AC137061	Plasmid	AC137061	Plasmid	c 802	50.4	2.1	232004	2	AC023584	Homo sapi	AC023584	Homo sapi
c 730	50.8	2.1	254449	3	AE014817	Plasmid	AE014817	Plasmid	c 803	50.4	2.1	238215	2	CR848028	Danio rer	CR848028	Danio rer
c 731	50.6	2.1	4193	3	AV263399	Dictyoste	AV263399	Dictyoste	c 804	50.4	2.1	250531	3	AE014845	Plasmid	AE014845	Plasmid
c 732	50.6	2.1	4550	3	AE362376	Dictyoste	AE362376	Dictyoste	c 805	50.4	2.1	250743	3	AE014836	Plasmid	AE014836	Plasmid
c 733	50.6	2.1	5504	6	AX258009	Sequence	AX258009	Sequence	c 806	50.4	2.1	253001	3	AE014834	Plasmid	AE014834	Plasmid
c 734	50.6	2.1	5504	6	AX348782	Sequence	AX348782	Sequence	c 807	50.4	2.1	299511	1	AE015941	Clostridi	AE015941	Clostridi
c 735	50.6	2.1	13383	3	AE001374	Plasmid	AE001374	Plasmid	c 808	50.4	2.1	302718	2	AC027292	Homo sapi	AC027292	Homo sapi
c 736	50.6	2.1	13383	3	AE001374	Plasmid	AE001374	Plasmid	c 809	50.4	2.1	348034	3	CR382400	Plasmid	CR382400	Plasmid
c 737	50.6	2.1	13437	3	AE001407	Plasmid	AE001407	Plasmid	c 810	50.2	2.1	5701	3	AY047363	Dictyoste	AY047363	Dictyoste
c 738	50.6	2.1	17839	3	AE001384	Plasmid	AE001384	Plasmid	c 811	50.2	2.1	14287	3	AC115588	Dictyoste	AC115588	Dictyoste
c 739	50.6	2.1	19161	14	AE632322	Cotesia C	AE632322	Cotesia C	c 812	50.2	2.1	14973	3	AE001391	Plasmid	AE001391	Plasmid
c 740	50.6	2.1	50304	5	AL929168	Zebrafish	AL929168	Zebrafish	c 813	50.2	2.1	15363	3	MSQMTG	Anopheles g	L20934	Anopheles g
c 741	50.6	2.1	87841	8	AB005247	Arabidops	AB005247	Arabidops	c 814	50.2	2.1	58437	9	BX276094	Human DNA	BX276094	Human DNA
c 742	50.6	2.1	121131	2	AC138564	Felis cat	AC138564	Felis cat	c 815	50.2	2.1	83296	2	AC022588	Homo sapi	AC022588	Homo sapi
c 743	50.6	2.1	126999	9	AL513328	Human DNA	AL513328	Human DNA	c 816	50.2	2.1	94784	9	AL355309	Human DNA	AL355309	Human DNA
c 744	50.6	2.1	140661	2	AC012425	Homo sapi	AC012425	Homo sapi	c 817	50.2	2.1	113906	2	AC136589	Homo sapi	AC136589	Homo sapi
c 745	50.6	2.1	140677	9	AC005922	Homo sapi	AC005922	Homo sapi	c 818	50.2	2.1	146850	2	CR394559	Danio rer	CR394559	Danio rer
c 746	50.6	2.1	144333	9	AC105036	Homo sapi	AC105036	Homo sapi	c 819	50.2	2.1	148075	2	AC110014	Homo sapi	AC110014	Homo sapi
c 747	50.6	2.1	145650	2	CR762412	Danio rer	CR762412	Danio rer	c 820	50.2	2.1	148715	5	AL935049	Zebrafish	AL935049	Zebrafish
c 748	50.6	2.1	148289	5	AL845421	Zebrafish	AL845421	Zebrafish	c 821	50.2	2.1	150833	2	BX294162	Danio rer	BX294162	Danio rer
c 749	50.6	2.1	150162	9	AC026722	Homo sapi	AC026722	Homo sapi	c 822	50.2	2.1</						

C 823	50.2	2.1	159548	3	PFMAL3P2	AL034558	Plasmodiu	896	50	2.1	217006	2	BX248241	BX248241	Danio rer
C 824	50.2	2.1	159448	2	CR627500	CR627500	Danio rer	897	50	2.1	218074	9	AC023283	AC023283	Homo sapi
C 825	50.2	2.1	162884	9	AC016558	AC016558	Homo sapi	c 898	50	2.1	249995	3	AE014840	AE014840	Plasmodiu
C 826	50.2	2.1	162884	9	AC020936	AC020936	Homo sapi	899	50	2.1	250029	3	AE014838	AE014838	Plasmodiu
C 827	50.2	2.1	165277	5	AL954184	AL954184	Zebrafish	900	50	2.1	257109	3	AC116963	AC116963	Diclyoste
C 828	50.2	2.1	166189	2	CR847575	CR847575	Danio rer	901	50	2.1	293431	2	PFMAL13P4	PFMAL13P4	Plasmodiu
C 829	50.2	2.1	166281	2	CR790386	CR790386	Danio rer	902	49.8	2.1	1162	3	AE044851	AE044851	Colias cr
C 830	50.2	2.1	167373	2	CR354397	CR354397	Danio rer	903	49.8	2.1	1260	1	AF086618	AF086618	Lootah wi
C 831	50.2	2.1	170425	5	BX465867	BX465867	Zebrafish	c 904	49.8	2.1	1809	1	AF267216	AF267216	Candidatu
C 832	50.2	2.1	171255	9	AL691447	AL691447	Human DNA	c 905	49.8	2.1	14851	2	PFMAL1P5	PFMAL1P5	Plasmodiu
C 833	50.2	2.1	173288	2	AC138859	AC138859	Homo sapi	c 906	49.8	2.1	61952	2	AC123513	AC123513	Diclyoste
C 834	50.2	2.1	174187	10	AC121781	AC121781	Mus muscu	c 907	49.8	2.1	67970	3	PFMAL1P3	PFMAL1P3	Diclyoste
C 835	50.2	2.1	175916	9	AC018842	AC018842	Homo sapi	c 908	49.8	2.1	68887	2	AC067755	AC067755	Homo sapi
C 836	50.2	2.1	176704	2	CR628364	CR628364	Homo sapi	c 909	49.8	2.1	87731	9	AC105148	AC105148	Homo sapi
C 837	50.2	2.1	197310	10	BX005240	BX005240	Mouse DNA	c 910	49.8	2.1	88549	3	AC116924	AC116924	Diclyoste
C 838	50.2	2.1	206358	2	CR450701	CR450701	Danio rer	c 911	49.8	2.1	110000	2	PFMAL13_06	PFMAL13_06	Continuation (7 of
C 839	50.2	2.1	209360	5	BX470128	BX470128	Zebrafish	c 912	49.8	2.1	110000	2	PFMAL13_21	PFMAL13_21	Continuation (22 of
C 840	50.2	2.1	245046	2	CR846103	CR846103	Danio rer	913	49.8	2.1	110000	2	PFMAL13P1_04	PFMAL13P1_04	Continuation (5 of
C 841	50.2	2.1	273275	3	AE014828	AE014828	Plasmodiu	914	49.8	2.1	116121	2	CR352337	CR352337	Danio rer
C 842	50.2	2.1	330050	3	PF9A29355	PF9A29355	Plasmodiu	915	49.8	2.1	119483	5	BX470158	BX470158	Zebrafish
C 843	50.2	2.1	333321	3	AC116986	AC116986	Diclyoste	c 916	49.8	2.1	124497	9	AC120053	AC120053	Homo sapi
C 844	50.2	2.1	335050	3	PF9A29356	PF9A29356	Plasmodiu	c 917	49.8	2.1	136240	3	AC117070	AC117070	Diclyoste
C 845	50.2	2.1	50	6	BD172396	BD172396	Secreted	c 918	49.8	2.1	136503	2	AC068939	AC068939	Homo sapi
C 846	50.2	2.1	50	6	BD172715	BD172715	Secreted	c 919	49.8	2.1	137457	9	AC067947	AC067947	Homo sapi
C 847	50.2	2.1	50	6	BD173034	BD173034	Secreted	c 920	49.8	2.1	144041	2	CR392045	CR392045	Danio rer
C 848	50.2	2.1	50	6	BD173353	BD173353	Secreted	c 921	49.8	2.1	149223	2	CR382382	CR382382	Danio rer
C 849	50.2	2.1	50	6	BD175387	BD175387	Secretory	c 922	49.8	2.1	150830	5	BX470190	BX470190	Zebrafish
C 850	50.2	2.1	50	6	AR410765	AR410765	Sequence	c 923	49.8	2.1	150788	5	AL935300	AL935300	Zebrafish
C 851	50.2	2.1	50	6	AR439129	AR439129	Sequence	c 924	49.8	2.1	157544	9	AC098590	AC098590	Homo sapi
C 852	50.2	2.1	50	6	AR473149	AR473149	Sequence	c 925	49.8	2.1	157613	9	AC018769	AC018769	Homo sapi
C 853	50.2	2.1	50	6	AR527135	AR527135	Sequence	c 926	49.8	2.1	159621	9	AC083801	AC083801	Homo sapi
C 854	50.2	2.1	50	6	AR566168	AR566168	Sequence	c 927	49.8	2.1	161233	2	BX927409	BX927409	Danio rer
C 855	50.2	2.1	50	6	BD075536	BD075536	Secretory	c 928	49.8	2.1	163443	2	AC006280	AC006280	Plasmodiu
C 856	50.2	2.1	50	6	BD075536	BD075536	Secretory	c 929	49.8	2.1	165326	9	AL159974	AL159974	Human DNA
C 857	50.2	2.1	542	4	AF165781	AF165781	Apyceros	c 930	49.8	2.1	166904	9	AL627309	AL627309	Human DNA
C 858	50.2	2.1	1647	3	AF275219	AF275219	Gryllopro	c 931	49.8	2.1	169448	2	CR385039	CR385039	Danio rer
C 859	50.2	2.1	15635	3	AB083339	AB083339	Bombyx mo	c 932	49.8	2.1	170102	9	AC008079	AC008079	Homo sapi
C 860	50.2	2.1	15643	3	AF149768	AF149768	Bombyx mo	c 933	49.8	2.1	172476	9	AC007736	AC007736	Homo sapi
C 861	50.2	2.1	15656	3	AB070264	AB070264	Bombyx mo	c 934	49.8	2.1	179066	2	CR450782	CR450782	Danio rer
C 862	50.2	2.1	15664	3	AY048187	AY048187	Bombyx mo	c 935	49.8	2.1	180861	2	CR391970	CR391970	Danio rer
C 863	50.2	2.1	26565	2	AC119399	AC119399	Homo sapi	c 936	49.8	2.1	181880	9	BS000198	BS000198	Pan trogl
C 864	50.2	2.1	34750	3	AY217738	AY217738	Bimaria t	c 937	49.8	2.1	182871	3	AC117176	AC117176	Diclyoste
C 865	50.2	2.1	36977	2	AC092304	AC092304	Homo sapi	c 938	49.8	2.1	187466	2	CR388371	CR388371	Danio rer
C 866	50.2	2.1	37515	6	AX458482	AX458482	Sequence	c 939	49.8	2.1	188248	2	AC119128	AC119128	Rattus no
C 867	50.2	2.1	57203	3	AC115581	AC115581	Diclyoste	c 940	49.8	2.1	200260	2	CR753814	CR753814	Danio rer
C 868	50.2	2.1	96106	9	AC074119	AC074119	Homo sapi	c 941	49.8	2.1	209215	2	CR751543	CR751543	Danio rer
C 869	50.2	2.1	103775	2	AP002739	AP002739	Homo sapi	c 942	49.8	2.1	218311	2	CR749741	CR749741	Danio rer
C 870	50.2	2.1	108451	2	AP002739	AP002739	Homo sapi	c 943	49.8	2.1	218311	2	CR522882	CR522882	Danio rer
C 871	50.2	2.1	110000	2	PFMAL13_11	PFMAL13_11	Continuation (12 of	c 944	49.8	2.1	226929	2	AE014852	AE014852	Plasmodiu
C 872	50.2	2.1	110000	2	PFMAL13_12	PFMAL13_12	Continuation (13 of	c 945	49.8	2.1	226929	2	AE014852	AE014852	Plasmodiu
C 873	50.2	2.1	110000	2	PFMAL13_25	PFMAL13_25	Continuation (26 of	c 946	49.8	2.1	226929	2	AE014852	AE014852	Plasmodiu
C 874	50.2	2.1	110000	2	PFMAL13_06	PFMAL13_06	Continuation (7 of	c 947	49.8	2.1	226929	2	AE014852	AE014852	Plasmodiu
C 875	50.2	2.1	116696	3	PFMAL3P3	PFMAL3P3	Plasmodiu	c 948	49.8	2.1	253151	3	AE014842	AE014842	Plasmodiu
C 876	50.2	2.1	118758	9	HS450C20	HS450C20	Human DNA	c 949	49.8	2.1	253151	3	AE014842	AE014842	Plasmodiu
C 877	50.2	2.1	124330	3	PFMAL1P1	PFMAL1P1	Plasmodiu	c 950	49.8	2.1	263169	2	BX927111	BX927111	Danio rer
C 878	50.2	2.1	132427	5	BX323806	BX323806	Zebrafish	c 951	49.8	2.1	263169	2	BX927111	BX927111	Danio rer
C 879	50.2	2.1	137028	2	BS000643	BS000643	Pan trogl	c 952	49.8	2.1	266371	2	AC020619	AC020619	Mus muscu
C 880	50.2	2.1	139111	9	AL158048	AL158048	Human DNA	c 953	49.8	2.1	286208	2	AC117140	AC117140	Rattus no
C 881	50.2	2.1	143802	9	AL161431	AL161431	Human DNA	c 954	49.8	2.1	288385	2	AC092430	AC092430	Homo sapi
C 882	50.2	2.1	146285	9	AC005083	AC005083	Homo sapi	c 955	49.6	2.1	318221	2	PFMAL13P3	PFMAL13P3	Plasmodiu
C 883	50.2	2.1	155106	9	AC104069	AC104069	Homo sapi	c 956	49.6	2.1	7137	9	HUMAGPRO	HUMAGPRO	Human large
C 884	50.2	2.1	155758	2	CR792441	CR792441	Danio rer	c 957	49.6	2.1	9043	1	AE263924	AE263924	Peanut wi
C 885	50.2	2.1	163816	9	AC012308	AC012308	Homo sapi	c 958	49.6	2.1	14867	3	AE001398	AE001398	Plasmodiu
C 886	50.2	2.1	172862	2	AL645796	AL645796	Homo sapi	c 959	49.6	2.1	16022	3	AF260826	AF260826	Cochlioni
C 887	50.2	2.1	175919	2	CR786574	CR786574	Danio rer	c 960	49.6	2.1	23564	8	AE016821	AE016821	Eremothec
C 888	50.2	2.1	181435	2	BX927092	BX927092	Danio rer	c 961	49.6	2.1	34119	8	AF222718	AF222718	Chrysodid
C 889	50.2	2.1	183584	9	AC012492	AC012492	Homo sapi	c 962	49.6	2.1	47108	6	AX344507	AX344507	Sequence
C 890	50.2	2.1	186335	2	CR7888251	CR7888251	Danio rer	c 963	49.6	2.1	68444	9	AL731768	AL731768	Human DNA
C 891	50.2	2.1	189646	9	AC140909	AC140909	Homo sapi	c 964	49.6	2.1	70788	2	AL353144	AL353144	Homo sapi
C 892	50.2	2.1	193047	9	CNS000000	CNS000000	Human chr	c 965	49.6	2.1	73345	8	AL0294725	AL0294725	Dictyosia 1
C 893	50.2	2.1	194513	2	CR524482	CR524482	Danio rer	c 966	49.6	2.1	82139	3	AC115684	AC115684	Diclyoste
C 894	50.2	2.1	199551	2	AC006281	AC006281	Plasmodiu	c 967	49.6	2.1	103728	9	AL445219	AL445219	Human DNA
C 895	50.2	2.1	216648	2	BX901972	BX901972	Danio rer	c 968	49.6	2.1	104992	2	AC005504	AC005504	Plasmodiu
										2.1	110000	2	PFMAL13_05	PFMAL13_05	Continuation (6 of

969	49.6	2.1	113201	9	AC117509	1042	49.4	2.1	202533	2	CR392031	Danio rer
970	49.6	2.1	138504	9	AC092665	1043	49.4	2.1	202634	2	CR339052	Danio rer
971	49.6	2.1	144361	2	CR318608	1044	49.4	2.1	203958	5	AL954339	Zebrafish
972	49.6	2.1	144644	8	AP006155	1045	49.4	2.1	216185	5	EX842696	Zebrafish
973	49.6	2.1	144734	2	AC148922	1046	49.4	2.1	220888	2	CR450804	Danio rer
974	49.6	2.1	144788	2	AC032036	c1047	49.4	2.1	227073	2	CR846086	Danio rer
975	49.6	2.1	148782	9	AP006213	1048	49.4	2.1	229435	2	CR457452	Danio rer
976	49.6	2.1	150317	8	AP005739	1049	49.4	2.1	261771	2	CR356223	Danio rer
977	49.6	2.1	161078	9	AP003500	c1050	49.2	2.1	663	6	A85532	Sequence 19
978	49.6	2.1	161286	2	AC025120	c1051	49.2	2.1	663	6	AR155025	Sequence
979	49.6	2.1	167103	9	AC147065	c1052	49.2	2.1	663	6	E65550	Genome DNA
980	49.6	2.1	169524	2	AC023111	1053	49.2	2.1	669	3	AF504324	Andrena b
981	49.6	2.1	169546	2	AC004157	1054	49.2	2.1	732	6	A86377	Sequence 10
982	49.6	2.1	169894	2	CR762466	1055	49.2	2.1	732	6	AR155870	Sequence
983	49.6	2.1	170627	2	AC125567	1056	49.2	2.1	732	6	E66395	Genome DNA
984	49.6	2.1	172285	2	CR381538	c1057	49.2	2.1	854	6	A85875	Sequence 53
985	49.6	2.1	176063	9	AC022911	c1058	49.2	2.1	854	6	AR155368	Sequence
986	49.6	2.1	178273	2	AC005308	c1059	49.2	2.1	854	6	E65893	Genome DNA
987	49.6	2.1	183648	3	AC117081	c1060	49.2	2.1	1098	3	OFU560796	Ostrinia
988	49.6	2.1	187466	9	AC016322	c1061	49.2	2.1	1098	3	OFU560797	Ostrinia
989	49.6	2.1	189406	2	CR381547	c1062	49.2	2.1	1099	3	OFU560800	Ostrinia
990	49.6	2.1	191528	9	AC104260	1063	49.2	2.1	2418	3	DDRASGG	Z11533 D. discoidu
991	49.6	2.1	205242	9	AC146375	1064	49.2	2.1	7038	3	PFGLP195A	X15063 Plasmodium
992	49.6	2.1	205479	2	CR847506	1065	49.2	2.1	7347	1	AF211124	Carsonell
993	49.6	2.1	206784	9	HS93L7	1066	49.2	2.1	7461	6	AX346686	Sequence
994	49.6	2.1	215231	2	CR385085	1067	49.2	2.1	14374	3	AC024748	Caenorhab
995	49.6	2.1	234796	2	CR318626	1068	49.2	2.1	21354	6	AX251544	Sequence
996	49.6	2.1	250029	3	AE014816	c1069	49.2	2.1	37957	8	U17009	Phytophthor
997	49.6	2.1	250421	3	AE014849	c1070	49.2	2.1	62028	8	AB025631	Arabidops
998	49.6	2.1	251237	2	CR812792	c1071	49.2	2.1	81035	8	AB025631	Arabidops
999	49.4	2.1	1055	6	AX083745	c1072	49.2	2.1	90373	3	AC115680	Dictyoste
1000	49.4	2.1	1072	5	AF332869	1073	49.2	2.1	93122	8	AC006283	Arabidops
1001	49.4	2.1	1183	4	RABAGGRECA	1074	49.2	2.1	101800	9	AC021659	Homo sapi
1002	49.4	2.1	1314	3	AF489476	c1075	49.2	2.1	101970	2	CR383670	Danio rer
1003	49.4	2.1	1618	5	AX029553	1076	49.2	2.1	103244	3	AC090524	Caenorhab
1004	49.4	2.1	2872	3	DIUBIRPB	1077	49.2	2.1	110000	2	PFMAL13_10	Continuation (2 of
1005	49.4	2.1	4362	3	U60170	c1078	49.2	2.1	110000	2	PFMAL13_10	Continuation (11 of
1006	49.4	2.1	7347	1	AF211124	1079	49.2	2.1	110000	2	PFMAL13_19	Continuation (20 o
1007	49.4	2.1	8305	6	AX346471	c1080	49.2	2.1	110000	2	PFMAL8P1_09	Continuation (10 o
1008	49.4	2.1	11929	3	AE001431	c1081	49.2	2.1	111037	2	AC090067	Homo sapi
1009	49.4	2.1	12600	2	AC013952	1082	49.2	2.1	111728	5	EX470096	Zebrafish
1010	49.4	2.1	13599	3	AE001390	c1083	49.2	2.1	127392	9	AC008570	Homo sapi
1011	49.4	2.1	30630	3	AC116032	c1084	49.2	2.1	138964	2	EX950176	Danio rer
1012	49.4	2.1	47841	6	AX504842	1085	49.2	2.1	145160	2	CR847935	Danio rer
1013	49.4	2.1	73334	6	AX347027	c1086	49.2	2.1	145299	5	EX005348	Zebrafish
1014	49.4	2.1	73334	6	AX356494	1087	49.2	2.1	148061	9	AC010727	Homo sapi
1015	49.4	2.1	82139	3	AC115684	1088	49.2	2.1	148929	2	CR847848	Danio rer
1016	49.4	2.1	91875	9	AL512286	c1089	49.2	2.1	149238	2	CR847833	Danio rer
1017	49.4	2.1	110000	2	PFMAL13_14	1090	49.2	2.1	149450	2	AC067880	Homo sapi
1018	49.4	2.1	110000	2	PFMAL13P2_1	c1091	49.2	2.1	153300	9	AC073387	Homo sapi
1019	49.4	2.1	110000	2	PFMAL8P1_01	c1092	49.2	2.1	154792	2	EX511299	Homo sapi
1020	49.4	2.1	110000	3	PFMAL1P2_0	c1093	49.2	2.1	155443	9	AC106740	Homo sapi
1021	49.4	2.1	140677	9	AC005922	1094	49.2	2.1	159618	9	AC096750	Homo sapi
1022	49.4	2.1	144610	2	CR387981	c1095	49.2	2.1	160621	5	EX005014	Zebrafish
1023	49.4	2.1	144765	2	CR759966	1096	49.2	2.1	163288	2	CR812925	Danio rer
1024	49.4	2.1	144784	9	AC009324	c1097	49.2	2.1	163957	9	AC104786	Homo sapi
1025	49.4	2.1	149603	9	AC022100	1098	49.2	2.1	164819	9	AC092335	Homo sapi
1026	49.4	2.1	150656	5	EX649530	1099	49.2	2.1	169122	2	AC106803	Homo sapi
1027	49.4	2.1	155106	9	AC104069	c1100	49.2	2.1	170736	2	AC013658	Homo sapi
1028	49.4	2.1	157111	3	VTIVD10	1101	49.2	2.1	175946	9	AC141000	Homo sapi
1029	49.4	2.1	158548	9	AC034558	1102	49.2	2.1	179380	9	AL354803	Human DNA
1030	49.4	2.1	160896	9	AC025540	1103	49.2	2.1	179400	9	AC087481	Homo sapi
1031	49.4	2.1	163448	2	CR846088	1104	49.2	2.1	186979	2	CR631129	Danio rer
1032	49.4	2.1	163809	9	CR392044	c1105	49.2	2.1	187647	2	AC073220	Homo sapi
1033	49.4	2.1	172738	9	AC091953	1106	49.2	2.1	193806	2	AC148824	Pan trogl
1034	49.4	2.1	174162	2	CR759781	1107	49.2	2.1	204609	2	EX322531	Danio rer
1035	49.4	2.1	174412	2	CR381542	c1108	49.2	2.1	204652	2	PFMAL13P6	Plasmodium
1036	49.4	2.1	174482	2	AC139870	1109	49.2	2.1	206513	5	AL928728	Zebrafish
1037	49.4	2.1	180096	2	CR391999	1110	49.2	2.1	206832	2	CR759927	Danio rer
1038	49.4	2.1	180124	2	CR450699	c1111	49.2	2.1	229081	2	CR753897	Danio rer
1039	49.4	2.1	180540	2	CR847859	c1112	49.2	2.1	229237	5	EX323548	Zebrafish
1040	49.4	2.1	182871	3	AC117176	1113	49.2	2.1	236266	2	CR392026	Danio rer
1041	49.4	2.1	191191	2	CR847965	1114	49.2	2.1	246007	2	EX914205	Danio rer





c1261	48.8	2.1	211429	2	BX324152	Danio rer	BX324152	c1334	48.6	2.0	221637	2	AC097553	Rattus no
1262	48.8	2.1	226160	5	BX004838	Zebrafish	BX004838	c1335	48.6	2.0	239335	2	AC146635	Otolemur
c1263	48.8	2.1	232392	14	AF250284	Amasacta m	AF250284	c1336	48.6	2.0	250707	3	AE014848	Plasmodiu
1264	48.8	2.1	239484	2	CR759895	Danio rer	CR759895	c1337	48.6	2.0	282355	2	AC104401	Rattus no
1265	48.8	2.1	241111	2	CR385051	Danio rer	CR385051	1338	48.6	2.0	300050	1	AP004171	Mycoplas
c1266	48.8	2.1	246651	2	CR847857	Danio rer	CR847857	c1339	48.6	2.0	340000	9	AP001667	Homo sapi
c1267	48.8	2.1	250022	2	AE014824	Plasmodiu	AE014824	1340	48.6	2.0	349980	6	AX344555	Sequence
c1268	48.8	2.1	251237	2	CR812792	Danio rer	CR812792	c1341	48.4	2.0	716	3	AMU35786	U15786 Anopheles m
1269	48.8	2.1	253305	3	PFMAL3P7	Plasmodiu	AL034559	c1342	48.4	2.0	1154	3	AF044864	Pieris ra
c1270	48.8	2.1	253755	2	CR812465	Danio rer	CR812465	c1343	48.4	2.0	1442	8	MISDA1P9A	Z25399 S. douglasii
c1271	48.8	2.1	254449	3	AE014817	Plasmodiu	AE014817	c1344	48.4	2.0	1815	1	AF267201	AF267201 Candidatu
c1272	48.8	2.1	256879	3	AC116982	Dictyoste	AC116982	1345	48.4	2.0	5500	3	PFAMDF	M29154 P. falciparu
c1273	48.8	2.1	263615	5	BX927240	Zebrafish	BX927240	c1346	48.4	2.0	6775	6	AX458644	AX458644 Sequence
c1274	48.8	2.1	272698	3	PFMAL4P4	Plasmodiu	AL035477	c1347	48.4	2.0	8574	3	AF057019	AF057019 Dictyoste
1275	48.8	2.1	273275	3	AE014828	Danio rer	AE014828	c1348	48.4	2.0	8633	3	PPFMDR1	PPFMDR1 P. falciparu
c1276	48.8	2.1	340000	9	AP001715	Homo sapi	AP001715	c1349	48.4	2.0	14535	3	AF442957	AF442957 Ostrinia
c1277	48.6	2.0	718	3	AQ035792	U35792 Anopheles q	U35792	c1350	48.4	2.0	14536	3	AF467260	AF467260 Ostrinia
1278	48.6	2.0	1717	3	DISP70B	M98546 Dictyosteli	M98546	c1351	48.4	2.0	20816	3	AY325300	AY325300 Parameciu
c1279	48.6	2.0	1865	8	MISCAAP1	X00960 Yeast mitoc	X00960	c1352	48.4	2.0	26561	9	AL929515	AL929515 Human DNA
1280	48.6	2.0	1958	8	RCH296505	AJ296505 Revemia c	AJ296505	c1353	48.4	2.0	29143	3	AC115594	AC115594 Dictyoste
1281	48.6	2.0	4197	3	AF163835	AF163835 Dictyoste	AF163835	c1354	48.4	2.0	30849	2	AC117082	AC117082 Dictyoste
1282	48.6	2.0	6154	6	AX251808	AX251808 Sequence	AX251808	c1355	48.4	2.0	55372	2	CR759965	CR759965 Danio rer
1283	48.6	2.0	6154	6	AX344196	AX344196 Sequence	AX344196	1356	48.4	2.0	73666	9	HSJ333B15	HSJ333B15 Human DNA
c1284	48.6	2.0	6154	6	AX346955	AX346955 Sequence	AX346955	c1357	48.4	2.0	102306	5	BX571980	BX571980 Zebrafish
c1285	48.6	2.0	11172	6	AX346955	AX346955 Sequence	AX346955	c1358	48.4	2.0	104153	2	AX890590	AX890590 3
1286	48.6	2.0	14591	3	AE001406	AE001406 Plasmodiu	AE001406	c1359	48.4	2.0	105940	9	AC010606	AC010606 Homo sapi
1287	48.6	2.0	15575	3	AV242996	AV242996 Antherea	AV242996	c1360	48.4	2.0	107635	8	AC136955	AC136955 Medicago
c1288	48.6	2.0	15723	3	AY521251	AY521251 Aleurodic	AY521251	c1361	48.4	2.0	108908	3	PFMAL3P8	PFMAL3P8 Plasmodiu
1289	48.6	2.0	17137	6	AX345093	AX345093 Sequence	AX345093	c1362	48.4	2.0	110000	2	PFMAL13_14	PFMAL13_14 Continuation (15 o
c1290	48.6	2.0	24565	9	AL162498	AL162498 Human DNA	AL162498	c1363	48.4	2.0	110000	2	PFMAL7P1_06	PFMAL7P1_06 Continuation (7 o
c1291	48.6	2.0	34750	3	AY217738	AY217738 Eimeria t	AY217738	c1364	48.4	2.0	110000	6	AC116984	AC116984 4 Continuation (5 o
1292	48.6	2.0	36849	1	AE000788	AE000788 Borrelia	AE000788	1365	48.4	2.0	110000	6	AR409405	AR409405 3 Continuation (4 o
c1293	48.6	2.0	67607	2	AC116911	AC116911 Homo sapi	AC116911	1366	48.4	2.0	110000	6	BD061520	BD061520 3 Continuation (4 o
1294	48.6	2.0	70204	9	AC010737	AC010737 Homo sapi	AC010737	c1367	48.4	2.0	110664	8	AC074360	AC074360 Arabidops
1295	48.6	2.0	97817	9	AC063922	AC063922 Homo sapi	AC063922	1368	48.4	2.0	114676	9	BX323048	BX323048 Human DNA
c1296	48.6	2.0	110000	2	PFMAL8P1_05	PFMAL8P1_05 Continuation (6 of	PFMAL8P1_05	c1369	48.4	2.0	121248	8	AC137554	AC137554 Medicago
c1297	48.6	2.0	110000	2	AC116305	AC116305 Dictyoste	AC116305	1370	48.4	2.0	125958	3	AC115592	AC115592 Dictyoste
1298	48.6	2.0	110000	8	CR382138	CR382138 16 Continuation (17 o	CR382138	1371	48.4	2.0	131992	9	AF170801	AF170801 Homo sapi
1299	48.6	2.0	110621	2	CR762468	CR762468 Danio rer	CR762468	c1372	48.4	2.0	142257	5	BX005151	BX005151 Zebrafish
c1300	48.6	2.0	111882	3	AC115612	AC115612 Dictyoste	AC115612	1373	48.4	2.0	146098	9	AC105459	AC105459 Homo sapi
1301	48.6	2.0	142476	9	AC011355	AC011355 Homo sapi	AC011355	c1374	48.4	2.0	148061	9	AC010727	AC010727 Homo sapi
1302	48.6	2.0	142476	9	AC011355	AC011355 Homo sapi	AC011355	1375	48.4	2.0	150197	2	CR394568	CR394568 Danio rer
c1303	48.6	2.0	142475	2	CR788316	CR788316 Danio rer	CR788316	1376	48.4	2.0	152356	2	CR762406	CR762406 Danio rer
c1304	48.6	2.0	143903	2	CR391976	CR391976 Danio rer	CR391976	1377	48.4	2.0	152359	9	AC093790	AC093790 Homo sapi
1305	48.6	2.0	145598	9	AC008132	AC008132 Homo sapi	AC008132	1378	48.4	2.0	153026	9	AL391280	AL391280 Human DNA
c1306	48.6	2.0	145886	9	AP003438	AP003438 Homo sapi	AP003438	c1379	48.4	2.0	154564	5	BX640522	BX640522 Zebrafish
c1307	48.6	2.0	145114	9	AP001172	AP001172 Homo sapi	AP001172	1380	48.4	2.0	155711	3	VYIVD10	AL360354 Plasmodiu
1308	48.6	2.0	149230	2	AC018790	AC018790 Homo sapi	AC018790	c1381	48.4	2.0	158091	9	AC140171	AC140171 Homo sapi
c1309	48.6	2.0	153061	9	AC023943	AC023943 Homo sapi	AC023943	1382	48.4	2.0	162806	9	AC099675	AC099675 Homo sapi
1310	48.6	2.0	154486	2	CR847972	CR847972 Danio rer	CR847972	1383	48.4	2.0	163461	2	AC115050	AC115050 Mus muscu
c1311	48.6	2.0	154838	5	BX855622	BX855622 Zebrafish	BX855622	c1384	48.4	2.0	165933	1	AP004174	AP004174 Mycoplasm
1312	48.6	2.0	155429	5	BX255922	BX255922 Zebrafish	BX255922	c1385	48.4	2.0	165995	9	AC103776	AC103776 Homo sapi
c1313	48.6	2.0	150606	2	AC004153	AC004153 Plasmodiu	AC004153	c1386	48.4	2.0	167068	2	BX323866	BX323866 Danio rer
1314	48.6	2.0	156662	5	BX323995	BX323995 Zebrafish	BX323995	1387	48.4	2.0	172464	2	CR792425	CR792425 Danio rer
1315	48.6	2.0	159240	9	AC090629	AC090629 Homo sapi	AC090629	c1388	48.4	2.0	173256	2	AC073301	AC073301 Homo sapi
1316	48.6	2.0	159274	9	AC112651	AC112651 Homo sapi	AC112651	1389	48.4	2.0	174007	9	AC023831	AC023831 Homo sapi
c1317	48.6	2.0	159942	9	AC025018	AC025018 Homo sapi	AC025018	c1390	48.4	2.0	176837	2	CR392355	CR392355 Danio rer
c1318	48.6	2.0	164399	3	PFMAL3P6	PFMAL3P6 Danio rer	PFMAL3P6	c1391	48.4	2.0	176845	2	CR450808	CR450808 Homo sapi
1319	48.6	2.0	164668	2	CR847986	CR847986 Danio rer	CR847986	c1392	48.4	2.0	178066	2	AC013557	AC013557 Homo sapi
c1320	48.6	2.0	164929	2	CR548626	CR548626 Danio rer	CR548626	1393	48.4	2.0	180124	2	CR450699	CR450699 Danio rer
1321	48.6	2.0	169357	2	CR847871	CR847871 Danio rer	CR847871	1394	48.4	2.0	180664	2	AC006706	AC006706 Caenorhab
1322	48.6	2.0	169794	2	AC004688	AC004688 Plasmodiu	AC004688	c1395	48.4	2.0	182305	9	AC138940	AC138940 Homo sapi
1323	48.6	2.0	173520	9	AL732423	AL732423 Human DNA	AL732423	1396	48.4	2.0	182748	2	CR388066	CR388066 Danio rer
1324	48.6	2.0	180634	9	AL16015	AL16015 Homo sapi	AL16015	c1397	48.4	2.0	185618	2	CR847796	CR847796 Danio rer
1325	48.6	2.0	189082	9	AL733537	AL733537 Human DNA	AL733537	c1398	48.4	2.0	201413	2	AC129583	AC129583 Plasmodiu
1326	48.6	2.0	194152	5	BX465198	BX465198 Zebrafish	BX465198	1399	48.4	2.0	205429	2	AC005506	AC005506 Plasmodiu
1327	48.6	2.0	195080	2	AC019111	AC019111 Homo sapi	AC019111	1400	48.4	2.0	211099	5	AL954717	AL954717 Zebrafish
1328	48.6	2.0	195228	10	AL845281	AL845281 Mouse DNA	AL845281	c1401	48.4	2.0	211723	2	CR749164	CR749164 Danio rer
1329	48.6	2.0	201397	9	AC091628	AC091628 Homo sapi	AC091628	1402	48.4	2.0	223754	5	BX323557	BX323557 Zebrafish
1330	48.6	2.0	208710	2	CR788244	CR788244 Danio rer	CR788244	c1403	48.4	2.0	236763	5	BX649352	BX649352 Zebrafish
c1331	48.6	2.0	210777	2	BX323020	BX323020 Danio rer	BX323020	1404	48.4	2.0	227211	2	CR847561	CR847561 Danio rer
1332	48.6	2.0	211750	9	AP006306	AP006306 Homo sapi	AP006306	1405	48.4	2.0	243235	2	CR318614	CR318614 Danio rer
c1333	48.6	2.0	214709	2	CR749183	CR749183 Danio rer	CR749183	c1406	48.4	2.0	243899	5	BX510919	BX510919 Zebrafish





24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI JIAN ZHENG, PI JEAN YUAN PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC C12N5/10, PC C12P21/02/C12P21/08,(C12P21/02,C12R1:19),(C12P21/02,C12R1:91), PC (C12P21/02,C12R1:645),C12N15/00,C12N5/00 CC Secreted and transmembrane polypeptides and nucleic CC acids encoding the same FH Key Location/Qualifiers FT source 1..2372 FT /organism='Homo sapiens (human)'. FEATURES source 1..2372 /organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606'									
ORIGIN									
Query Match 100.0%; Score 2372; DB 6; Length 2372; Best Local Similarity 100.0%; Pred. No. 0; Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	AGCAGGGAATCCGGATGCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCGCTCAACATA	60						
Db	1	AGCAGGGAATCCGGATGCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCGCTCAACATA	60						
Qy	61	GTTCCAGAACTCTCCATCCGACTAGTATTATGAGCATCTGCTCTCATATCACCAGTGGC	120						
Db	61	GTTCCAGAACTCTCCATCCGACTAGTATTATGAGCATCTGCTCTCATATCACCAGTGGC	120						
Qy	121	CATCTGAGGTGTTCCCTGGCTCTGAAGGTAGGCAGATGGCCAGGTGCTTCAGCGTG	180						
Db	121	CATCTGAGGTGTTCCCTGGCTCTGAAGGTAGGCAGATGGCCAGGTGCTTCAGCGTG	180						
Qy	181	GTGTGCTTCTCACTTCCATCTGACACACGAGGCTCCTGGTCCAAGGCTCTTTGGGTGCA	240						
Db	181	GTGTGCTTCTCACTTCCATCTGACACACGAGGCTCCTGGTCCAAGGCTCTTTGGGTGCA	240						
Qy	241	GAAGAGCTTTCCATCCAGGTGCTATGAGCAATATGAGGATCACCCCTTGTGAGCAAAAAG	300						
Db	241	GAAGAGCTTTCCATCCAGGTGCTATGAGCAATATGAGGATCACCCCTTGTGAGCAAAAAG	300						
Qy	301	CGACACGAGCTGAATTTACAGAGCTTAAGAGGCTTAGGCTGCTGGACTAAGT	360						
Db	301	CGACACGAGCTGAATTTACAGAGCTTAAGAGGCTTAGGCTGCTGGACTAAGT	360						
Qy	361	TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTAT	420						
Db	361	TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTAT	420						
Qy	421	GGCTGGGTGGAGATGGATTCGTGTCATCTTAGGATTAAGCCCAACCCCAAGTGGG	480						
Db	421	GGCTGGGTGGAGATGGATTCGTGTCATCTTAGGATTAAGCCCAACCCCAAGTGGG	480						
Qy	481	AAAAATGGGTGGGTGCTCTGATTTGGAAAGTTCCAGTGAGCCGACATTTGCAGCCTAT	540						
Db	481	AAAAATGGGTGGGTGCTCTGATTTGGAAAGTTCCAGTGAGCCGACATTTGCAGCCTAT	540						
Qy	541	TGTTACAACTCATCTGATCTTGAAGTAACTCGTGATTCAGAAATATCACCACCAAA	600						
Db	541	TGTTACAACTCATCTGATCTTGAAGTAACTCGTGATTCAGAAATATCACCACCAAA	600						
Qy	601	GATCCCATATTTCAACACTCAAACTGCAACACAAACACAGAAATTTATTTGTCAGTGACAGT	660						
Db	601	GATCCCATATTTCAACACTCAAACTGCAACACAAACACAGAAATTTATTTGTCAGTGACAGT	660						
Qy	661	ACCTACTCGGTGGCATCCCTTACTCTACATATACCTGCCCTACTACTCTCTCTCGCT	720						
Db	661	ACCTACTCGGTGGCATCCCTTACTCTACATATACCTGCCCTACTACTCTCTCTCGCT	720						

Qy	721	CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGATTTGTGTACAGAAAGTTTTTATG	780						
Db	721	CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGATTTGTGTACAGAAAGTTTTTATG	780						
Qy	781	GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAAG	840						
Db	781	GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAAG	840						
Qy	841	AATCAAGCTGCTGGTTTGGAGGTGTCCCAACGGCTCTGCTAGTGTCTCTCTCTCTTC	900						
Db	841	AATGAAGCTGCTGGTTTGGAGGTGTCCCAACGGCTCTGCTAGTGTCTCTCTCTCTTC	900						
Qy	901	TTTGGTGTGCAGCTGGTCTTGGATTTTGGTATGTCAAAAGGTATGTCAAGGCCCTCCCT	960						
Db	901	TTTGGTGTGCAGCTGGTCTTGGATTTTGGTATGTCAAAAGGTATGTGAAGGCCCTCCCT	960						
Qy	961	TTTACAAACAAAGATCAGCAGAGAAATGATCGAAACCAAAAGTAGTAAAGGAGAGAG	1020						
Db	961	TTTACAAACAAAGATCAGCAGAGAAATGATCGAAACCAAAAGTAGTAAAGGAGAGAG	1020						
Qy	1021	GCCAAATGATAGCAACCTTAATGAGGAATCAAGAAAACTGATAAAAAACCCAGAAAGATCC	1080						
Db	1021	GCCAAATGATAGCAACCTTAATGAGGAATCAAGAAAACTGATAAAAAACCCAGAAAGATCC	1080						
Qy	1081	AAGAGTCCAAGCAAACTACCGTCCGATGCGTGAAGCTGAAGTTTAGATGAGACAGAAA	1140						
Db	1081	AAGAGTCCAAGCAAACTACCGTCCGATGCGTGAAGCTGAAGTTTAGATGAGACAGAAA	1140						
Qy	1141	TGAGGAGACACACTGAGGCTGGTTCTTTCATGCTCTTACCTGCCCGCAGCTGGGGAA	1200						
Db	1141	TGAGGAGACACACTGAGGCTGGTTCTTTCATGCTCTTACCTGCCCGCAGCTGGGGAA	1200						
Qy	1201	ATCAAAAGGGCCAAAGAACCAAGAAAGTCCACCTTGGTTCCTAACTGGAATCAGC	1260						
Db	1201	ATCAAAAGGGCCAAAGAACCAAGAAAGTCCACCTTGGTTCCTAACTGGAATCAGC	1260						
Qy	1261	TCAGGACTGCCATTGGACTATGAGTGCACCAAGAGAAATGCCCTTCTCTTATTGTAAAC	1320						
Db	1261	TCAGGACTGCCATTGGACTATGAGTGCACCAAGAGAAATGCCCTTCTCTTATTGTAAAC	1320						
Qy	1321	CCTGCTGGATCTCTATCCTCTTACCTCAAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT	1380						
Db	1321	CCTGCTGGATCTCTATCCTCTTACCTCAAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT	1380						
Qy	1381	GTCTCTAATATATCCACTGGGAGAAAGGAGTTTGCAGAGTGAAGACCTAAAAACATC	1440						
Db	1381	GTCTCTAATATATCCACTGGGAGAAAGGAGTTTGCAGAGTGAAGACCTAAAAACATC	1440						
Qy	1441	TCATCAGTATCCAGTGGTAAAAAGCCCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGC	1500						
Db	1441	TCATCAGTATCCAGTGGTAAAAAGCCCTCCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGC	1500						
Qy	1501	CAAGGAGTCACTGAGACCAAGGCTTTCTACTGATTCGGCAGCTCAGACCCCTTCTTCA	1560						
Db	1501	CAAGGAGTCACTGAGACCAAGGCTTTCTACTGATTCGGCAGCTCAGACCCCTTCTTCA	1560						
Qy	1561	GCTCTGAAGAGAAACACGATCCACCTGACATGCTCTCTGAGCCGGTAAAGAGCAA	1620						
Db	1561	GCTCTGAAGAGAAACACGATCCACCTGACATGCTCTCTGAGCCGGTAAAGAGCAA	1620						
Qy	1621	AGAAATGCGAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1680						
Db	1621	AGAAATGCGAGAAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1680						
Qy	1681	TCTCTGTAAGCTAAAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA	1740						
Db	1681	TCTCTGTAAGCTAAAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCA	1740						
Qy	1741	GCAGGACTGTAAACACAGACAGGCTCAAGTGTCTCTGTAACACATTGAGTTGGAAT	1800						
Db	1741	GCAGGACTGTAAACACAGACAGGCTCAAGTGTCTCTGTAACACATTGAGTTGGAAT	1800						
Qy	1801	CACCTGTTTAGAACACACACACTTACTTTTCTGCTCTCTACCACTGCTGATATTTTCTCT	1860						



Qy	481	AAAAATGGGGTGGGTGCTCTGATTTGGAAAGTTCCAGTGCAGCCGACAGATTTCAGAGCCTAT	540
Db	481	AAAAATGGGGTGGGTGCTCTGATTTGGAAGGTTCACGTGAGCCGACAGATTTCAGAGCCTAT	540
Qy	541	TGTTACAACTCATCTGATACTTGGACTAACTCGTGCATTCCAGAAATTTATCACACCACAAA	600
Db	541	TGTTACAACTCATCTGATACTTGGACTTAACCTGTGCATTCAGNAATTTATCACACCACAAA	600
Qy	601	GATCCCATATTTCAAACACTCAAACACTGCAACACAAAACACAGAAATTTATGTCAGTGACAGT	660
Db	601	GATCCCATATTTCAAACACTCAAACACTGCAACACAAAACACAGAAATTTATGTCAGTGACAGT	660
Qy	661	ACCTACTCGGTGGGATCCCTTACTCTACAAATACCTGCCCCCTACTACTCTCTCTGCT	720
Db	661	ACCTACTCGGTGGGATCCCTTACTCTACAAATACCTGCCCCCTACTACTCTCTCTCTGCT	720
Qy	721	CCAGCTTCCACTCTATTTCCACGAGAGAAAATAATGATTTGTCACAGAAATTTTATG	780
Db	721	CCAGCTTCCACTCTATTTCCACGAGAGAAAATAATGATTTGTCACAGAAATTTTATG	780
Qy	781	GAAACTAGCACCATGTCTACAGAAACTGAAACCATTTGTCGAAAATAAGCAGCATTTCAAG	840
Db	781	GAAACTAGCACCATGTCTACAGAAACTGAAACCATTTGTCGAAAATAAGCAGCATTTCAAG	840
Qy	841	AATGAAAGCTGCTGGTTTGGAGGTGCCCCACGGCTCTGCTAGTGTGCTCTCTCTCTTC	900
Db	841	AATGAAAGCTGCTGGTTTGGAGGTGCCCCACGGCTCTGCTAGTGTGCTCTCTCTCTTC	900
Qy	901	TTTTGGTCTGCAGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCTTTCCCT	960
Db	901	TTTTGGTCTGCAGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCTTTCCCT	960
Qy	961	TTTACAAAACAGAAATCAGCAGAGGAAATGATCGAAACCAAAGTAGTAAAAGGAGGAGAAG	1020
Db	961	TTTACAAAACAGAAATCAGCAGAGGAAATGATCGAAACCAAAGTAGTAAAAGGAGGAGAAG	1020
Qy	1021	GCCAAATGATAGCAACCTTAATGAGGAATCAAGAAAACTGATAAAAACCCAGAGAAGTCC	1080
Db	1021	GCCAAATGATAGCAACCTTAATGAGGAATCAAGAAAACTGATAAAAACCCAGAGAAGTCC	1080
Qy	1081	AAGAGTCCAGCAAAACTACCGTCGATGCTTGAAGCTGAAGTTTAGATGACACAGAAA	1140
Db	1081	AAGAGTCCAGCAAAACTACCGTCGATGCTTGAAGCTGAAGTTTAGATGACACAGAAA	1140
Qy	1141	TGAGGAGACACACTGAGGCTGGTTCTTTTCATGCTCTTACCTGCTGCCCGCAGCTGGGAA	1200
Db	1141	TGAGGAGACACACTGAGGCTGGTTCTTTTCATGCTCTTACCTGCTGCCCGCAGCTGGGAA	1200
Qy	1201	ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTTGGTTCTTAACCTGGAATCAGC	1260
Db	1201	ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTTGGTTCTTAACCTGGAATCAGC	1260
Qy	1261	TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCTTATTTGTAAC	1320
Db	1261	TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGCCCTTCTCTTATTTGTAAC	1320
Qy	1321	CCTGCTGGATCTTATCCTCTCACTCCAAGCTTCCACGGCTTTCTAGCCCTGGCTAT	1380
Db	1321	CCTGCTGGATCTTATCCTCTCACTCCAAGCTTCCACGGCTTTCTAGCCCTGGCTAT	1380
Qy	1381	GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAAGTCAAGGACCTAAAAACATC	1440
Db	1381	GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAAGTCAAGGACCTAAAAACATC	1440
Qy	1441	TCATCAGTATCCAGTGTGTAAGAGGCTCTCTGGCTGTCTGAGGCTAGGTGGGTGAAAGC	1500
Db	1441	TCATCAGTATCCAGTGTGTAAGAGGCTCTCTGGCTGTCTGAGGCTAGGTGGGTGAAAGC	1500
Qy	1501	CAAGGACTCACTGAGACCAAGGCTTCTCTACTGATTTCCGAGCTCAGACCCCTTCTTCA	1560
Db	1501	CAAGGACTCACTGAGACCAAGGCTTCTCTACTGATTTCCGAGCTCAGACCCCTTCTTCA	1560
Qy	1561	GCTCTGAAAGAGAAACAGTATCCACCTGACATGTCTCTTCTGAGCCCGGTGAAGAGCATA	1620

[illegible]

JOURNAL	Patent: JP 2002238587-A 165 27-AUG-2002;
COMMENT	GENENTECH INC OS Homo sapiens (human) PN JP 2002238587-A/165 PD 27-AUG-2002 PF 18-DEC-2001 JP 2001385248 PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR 17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR 17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR 17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR 18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR 18-SEP-1997 US 60/062287,17-OCT-1997 US 60/062285 PR 21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR 24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR 24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR 24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR 27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR 28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR 28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR 28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR 29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR 29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR 29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063735 PR 29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR 31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR 07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR 17-NOV-1997 US 60/065846,18-NOV-1997 US 60/065693 PR 21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR 24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR 24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR 24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI JIAN ZHENG, PI JEAN YUAN PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC C12N15/02, PC C12P21/02, C12P21/08// (C12P21/02, C12R1:91), (C12P21/02, C12R1:19), PC (C12P21/02, C12R1:645), C12N15/00, C12N5/00, C12N15/00 CC Secreted and transmembrane polypeptides and nucleic acids encoding the same FH Key Location/Qualifiers FT source 1..2372 /organism='Homo sapiens (human)'. FT Location/Qualifiers source 1..2372 /organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606'
FEATURES	Query Match 100.0%; Score 2372; DB 6; Length 2372; Best Local Similarity 100.0%; Pred. No. 0; Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ORIGIN	QY 1 AGCAGGAAATCCGGATGTCGTTATGAAGTGGACGTGAGTGTCAGGCTCAACATA 60 DB       1 AGCAGGAAATCCGGATGTCGTTATGAAGTGGACGTGAGTGTCAGGCTCAACATA 60 QY 61 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACAGTGGC 120 DB       61 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACAGTGGC 120 QY 121 CATCTGAGTGTTCCCTCGCTCTGNAGGGTAGGCAGTGGCCAGTGTCCTCAGCGCTG 180 DB       121 CATCTGAGTGTTCCCTCGCTCTGAAAGGGTAGGCAGTGGCCAGTGTCCTCAGCGCTG 180 QY 181 GTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCTGTGTCGAAGGCTCTTTCGGTGCA 240 DB       181 GTGTGCTTCTCACTTCCATCTGGACCACGAGGCTCTGTGTCGAAGGCTCTTTCGGTGCA 240 QY 241 GAAGAGCTTTCCATCCAGGTGTCTGCAGAATATTGGGGATCACCCCTTGTGAGCAAAAAG 300

Qy	1381	GTCTTAATAATATCCACTGGGAGAAAGGAGTTTTGCAAGTGCAAGGACCTAAAAACATC	1440
Ds	1381		
Qy	1441	GTCTTAATAATATCCACTGGGAGAAAGGAGTTTTGCAAGTGCAAGGACCTAAAAACATC	1440
Ds	1441		
Qy	1441	TCATCAGTATCCAGTGGTAAAGGCCCTCTGGCTGTCTGAGGCTAGTGCGTTGAAAGC	1500
Ds	1441	TCATCAGTATCCAGTGGTAAAGGCCCTCTGGCTGTCTGAGGCTAGTGCGTTGAAAGC	1500
Qy	1501	CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGGAGCTCAGACCTTCTTCA	1560
Ds	1501		
Qy	1561	GCTCTGAAAGAGAAACAGCTATCCACCTGACATGCTCTCTGAGCCGGTAAAGCAAA	1620
Ds	1561		
Qy	1621	AGAATGGCAGAAAAGTTTGTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1680
Ds	1621		
Qy	1681	TCTCTGTAAGCTAAATATAGAAATAGAAAGGCTGAGGATACGAGTACACTGTCA	1740
Ds	1681		
Qy	1741	TCCTCTGTAAGCTAAATATAGAAATAGAAAGGCTGAGGATACGAGTACACTGTCA	1740
Ds	1741		
Qy	1741	CGAGGAGTGTAAACACACAGAGGCTCAAGGTGTTTTCTCTGAAACACATTCAGTTGGAAT	1800
Ds	1741		
Qy	1801	CACCTGTTAGAACACACACACTTACTTTTTCTGGTCTCTACACCTGCTGATATTTCTCT	1860
Ds	1801		
Qy	1861	AGGAAATATCTTTTACAGTAAACAAATATAAACTCTTTATAATTTCTATTTTATCT	1920
Ds	1861		
Qy	1921	GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAAATAAA	1980
Ds	1921		
Qy	1981	TTCAACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTGTGCAAGGTATTACACTC	2040
Ds	1981		
Qy	2041	TGTAATTCAATATTATTCCTCAAAAATTTGCACATAGTAGACGCTATCTGGGAAGCTAT	2100
Ds	2041		
Qy	2101	TTTTTTCAGTTTTCATATTTCTAGCTTATCTACTTCCAAACTTAATTTTATTTTGTCTGA	2160
Ds	2101		
Qy	2161	GACTAACTTATTCATTTTCTTAATATGGCAACATTAACCTTAATTTATTTATTAAC	2220
Ds	2161		
Qy	2221	ATACCTAAGAGTACATTTGTTACCTCTATATACCAAGCACATTTTAAAGTGCCATTAA	2280
Ds	2221		
Qy	2281	CAAAATGTATCTACTAGCCCTCTCTTTTCCAAACAAAGAGGAGCTGAGAGATGAGAAATAT	2340
Ds	2281		
Qy	2341	TGTGACAAAAAATTAAAGCATTTAGAAACTT	2372
Ds	2341		

RESULT 4  
BD173349  
LOCUS

DEFINITION	Secreted and transmembrane polypeptides and nucleic acids encoding the same.		
ACCESSION	BD173349		
VERSION	BD173349.1 GI:28414660		
KEYWORDS	JP 2002238588-A/165.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (Bases 1 to 2372)		
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: JP 2002238588-A 165 27-AUG-2002;		
COMMENT	GENENTECH INC		
	OS	Homo sapiens (human)	
	PN	JP 2002238588-A/165	
	PD	27-AUG-2002	
	PF	18-DEC-2001	JP 2001385315
	PR	17-SEP-1997 US	60/059115, 17-SEP-1997 US 60/059184 PR
	17-SEP-1997 US	60/059122, 17-SEP-1997 US	60/059117 PR
	17-SEP-1997 US	60/059113, 17-SEP-1997 US	60/059121 PR
	17-SEP-1997 US	60/059119, 18-SEP-1997 US	60/059263 PR
	18-SEP-1997 US	60/059266, 15-OCT-1997 US	60/062125 PR
	17-OCT-1997 US	60/062287, 17-OCT-1997 US	60/062285 PR
	21-OCT-1997 US	60/063486, 24-OCT-1997 US	60/062816 PR
	24-OCT-1997 US	60/062814, 24-OCT-1997 US	60/063127 PR
	24-OCT-1997 US	60/063120, 24-OCT-1997 US	60/063121 PR
	24-OCT-1997 US	60/063045, 24-OCT-1997 US	60/063128 PR
	27-OCT-1997 US	60/063329, 27-OCT-1997 US	60/063327 PR
	28-OCT-1997 US	60/063549, 28-OCT-1997 US	60/063541 PR
	28-OCT-1997 US	60/063550, 28-OCT-1997 US	60/063542 PR
	28-OCT-1997 US	60/063544, 28-OCT-1997 US	60/063564 PR
	29-OCT-1997 US	60/063734, 29-OCT-1997 US	60/063738 PR
	29-OCT-1997 US	60/063704, 29-OCT-1997 US	60/063435 PR
	29-OCT-1997 US	60/064215, 29-OCT-1997 US	60/063735 PR
	29-OCT-1997 US	60/063732, 31-OCT-1997 US	60/064103 PR
	31-OCT-1997 US	60/063870, 03-NOV-1997 US	60/064248 PR
	07-NOV-1997 US	60/064809, 12-NOV-1997 US	60/065186 PR
	17-NOV-1997 US	60/065846, 18-NOV-1997 US	60/065693 PR
	21-NOV-1997 US	60/066120, 21-NOV-1997 US	60/066364 PR
	24-NOV-1997 US	60/066772, 24-NOV-1997 US	60/066466 PR
	24-NOV-1997 US	60/066770, 24-NOV-1997 US	60/066511 PR
	24-NOV-1997 US	60/066453, 25-NOV-1997 US	60/066840 PI
	WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI		
	JIAN ZHENG,		
	PI JEAN YUAN		
	PC	C12N15/09, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC	
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RESULT 5  
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DEFINITION Secretory and transmembrane polypeptide and nucleic acid encoding  
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ACCESSION BD175383  
VERSION BD175383.1 GI:29121079  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE 1 (bases 1 to 2372)  
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and  
Yuan,J.  
TITLE Secretory and transmembrane polypeptide and nucleic acid encoding  
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JOURNAL Patent: JP 2002253280-A 165 10-SEP-2002;  
GENENTECH INC.

COMMENT OS Homo sapiens (human)  
PN JP 2002253280-A/165  
PD 10-SEP-2002  
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WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI  
JIAN ZHENG,  
PI JEAN YUAN  
PC C12N15/09,A61K45/00,A61P1/00,A61P13/12,A61P17/00,A61P17/06, PC  
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VERSION AR410761.1 GI:40162261  
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SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2372)  
AUTHORS Ashkenazi, A., Botstein, D., Desnovers, L., Eaton, D.L., Ferrara, N.,  
Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E.,  
Goddard, A., Godowski, P., Grimaldi, J.C., Gurney, A.L., Hillan, K.J.,  
Kljasin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A.,  
Stewart, T.A., Tamas, D., Williams, P.M. and Wood, W.I.  
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AR439125 AR439125 2372 bp DNA linear PAT 20-FEB-2004  
LOCUS Sequence 200 from patent US 6664376.  
DEFINITION AR439125  
ACCESSION AR439125  
VERSION AR439125.1 GI:42664974  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2372)  
AUTHORS Ashkenazi, A., Botstein, D., Desnovers, L., Eaton, D.L., Ferrara, N.,  
Pilveroff, E., Fong, S., Gao, W.-O., Gerber, H., Gerritsen, M.E.,  
Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J.,  
Kljavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A.,  
Stewart, J.A., Tumas, D., Williams, P.M. and Wood, W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: US 6664376-A 200 16-DEC-2003;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 2372; DB 6; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DEFINITION	Sequence 200 from patent US 6686451.		
ACCESSION	AR473145		
VERSION	AR473145.1 GI:42708520		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 2372)		
AUTHORS	Desnoyers, L., Goddard, A., Godowski, P. J., Gurney, A. L., Mather, J. P., Williams, P. M. and Wood, W. I.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: US 6686451-A 200 03-FEB-2004;		
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RESULT 9  
ARS27131  
LOCUS ARS27131 2372 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 200 from patent US 6723535.  
ACCESSION ARS27131  
VERSION ARS27131.1 GI:53914048  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2372)  
AUTHORS Ashkenazi, A., Botstein, D., Desnovers, L., Eaton, D.L., Ferrara, N., Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J., Kljavin, I.J., Macher, J.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tamas, D., Williams, P.M. and Wood, W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: US 6723535-A 200 20-APR-2004;  
FEATURES Location/Qualifiers  
source 1..2372  
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/mol\_type="genomic DNA"  
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Query Match 100.0%; Score 2372; DB 6; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Qy	421	GCCTGGTGGAGAGTGGATTCGTGGTCACTCTAGGATTTAGCCCAACCCCAAGTGGG	480
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RESULT 11  
AX092274 2372 bp DNA linear PAT 21-MAR-2001  
LOCUS Sequence 5 from Patent WO0116318.  
DEFINITION AX092274  
ACCESSION AX092274  
VERSION AX092274.1 GI:13444451  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,  
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and  
Wood,W.I.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0116318-A 5 08-MAR-2001;  
Genentech, Inc. (US)  
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Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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AX454446  
LOCUS AX454446 2372 bp DNA linear PAT 06-JUL-2002  
DEFINITION Sequence 31 from Patent WO0208284.  
ACCESSION AX454446  
VERSION AX454446.1 GI:21713847

KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.
AUTHORS	
TITLE	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis
JOURNAL	Patent: WO 0208284-A 31 31-JAN-2002; Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)
FEATURES	Location/Qualifiers 1..2372 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
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VERSION AX490924.1 GI:22323799  
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REFERENCE 1  
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
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TITILE Compositions and methods for the diagnosis and treatment of  
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Genentech, Inc. (US)  
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DEFINITION Sequence 200 from Patent WO0104311.

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VERSION AX697609.1 GI:29498705

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

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Ashkenazi, A.J., Botstein, D., Desnovers, L., Eaton, D.L., Ferrara, N., Filvaroff, E., Fong, S., Gao, W.Q., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Hillan, K.J., Kljavin, I.J., Mathers, J.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.

Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0104311-A 200 18-JAN-2001;

Genentech Inc. (US)

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PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDLEY GODDARD,DIANE PENICA, PI
JEAN CHEN,
PI JEAN YUAN
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1 (bases 1 to 2372)
Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.
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PI JEAN YUAN
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Db 601 GATCCCATATTCAACACTCAAACTGCAACACAAACAGAAATTTATTTGTGTCAGTGACAGT 660  
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Db 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTCTCTCTCTGCT 720  
Qy 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGATTTGTGTCACAGAAATTTTATG 780  
Db 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGATTTGTGTCACAGAAATTTTATG 780  
Qy 781 GAACTAGCACCATGCTCTACAGAACTGAACCAATTTGTTGAAATTAAGAGCAGCATTTCAAG 840  
Db 781 GAACTAGCACCATGCTCTACAGAACTGAACCAATTTGTTGAAATTAAGAGCAGCATTTCAAG 840  
Qy 841 AATGAAGCTGTGGGTTTGGAGGTGTCGCCACGGCTCTGCTAGTGTGCTCTCTCTCTTC 900  
Db 841 AATGAAGCTGTGGGTTTGGAGGTGTCGCCACGGCTCTGCTAGTGTGCTCTCTCTCTTC 900  
Qy 901 TTTGGTGTGAGCTGGTCTTGATTTTGTATGTCAAAAGGTATGTGAAGGCTTCCCT 960  
Db 901 TTTGGTGTGAGCTGGTCTTGATTTTGTATGTCAAAAGGTATGTGAAGGCTTCCCT 960  
Qy 961 TTTCAACAAGAAATCAGCAGAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAG 1020  
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Db 1081 AAGAGTCCAAGCAAACTACCGTGCATGCTGGAAGCTGAAGTTAGATGAGACAGAAA 1140  
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Db 1141 TGAGGAGACACACTGAGGCTGTTCTTTATGTCTCTTACCTGCCCGCCAGCTGGGAA 1200  
Qy 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCTTAACCTGGAATCAGC 1260  
Db |||||

Db 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCCTTGGTTCTTAACCTGGAATCAGC 1260  
Qy 1261 TCAGGACTGCCATTTGGACTATGGAGTGCACAAAGAGAAATGCCCTTCTCCTTATTTGTAAC 1320  
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